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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 43.7968 Seconds
(without alignments)
256.908 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 611

Sequence: 1 MPSPTVCSLLLLGLMLDL.....LGKFLQDILWEEAKEAPADK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|-------|-------|--------|----------|--------------------|
| 1 | 611 | 100.0 | 117 | 1 A59316 | ghrelin precursor |
| 2 | 518 | 84.8 | 117 | 1 B59316 | ghrelin precursor |
| 3 | 88.5 | 14.5 | 115 | 1 A33323 | motilin precursor |
| 4 | 86 | 14.1 | 119 | 1 MSPG | motilin precursor |
| 5 | 79 | 12.9 | 1234 | 2 T30160 | hypothetical prote |
| 6 | 75.5 | 12.4 | 410 | 2 C84205 | hypothetical prote |
| 7 | 73.5 | 12.0 | 709 | 2 D82825 | conserved hypothet |
| 8 | 72.5 | 11.9 | 115 | 2 J05511 | motilin precursor |
| 9 | 72.5 | 11.9 | 482 | 1 S03904 | platelet-derived e |
| 10 | 72.5 | 11.9 | 922 | 2 G83109 | probable two-compo |
| 11 | 72 | 11.8 | 147 | 2 T09722 | histone H2B1 - upl |
| 12 | 71 | 11.6 | 299 | 2 B36134 | RepC protein - Esc |
| 13 | 70 | 11.5 | 840 | 2 F90788 | probable outer mem |
| 14 | 70 | 11.5 | 840 | 2 G85648 | probable usher pro |
| 15 | 69 | 11.3 | 411 | 2 S47436 | flagellar antigen |
| 16 | 69 | 11.3 | 792 | 2 JC7122 | protein kinase (EC |
| 17 | 69 | 11.3 | 2273 | 2 I46477 | calcium channel BI |
| 18 | 69 | 11.3 | 2424 | 2 I46480 | calcium channel BI |
| 19 | 68.5 | 11.2 | 133 | 1 S24315 | motilin precursor |
| 20 | 68.5 | 11.2 | 340 | 2 S63763 | homeotic protein H |
| 21 | 68.5 | 11.2 | 533 | 2 AC0414 | probable exported |
| 22 | 68 | 11.1 | 330 | 2 A82292 | beta-hexosaminidas |
| 23 | 68 | 11.1 | 409 | 2 D87426 | cyclopropane-fatty |
| 24 | 67.5 | 11.0 | 270 | 2 E87408 | hypothetical prote |
| 25 | 67.5 | 11.0 | 416 | 2 I38428 | T-complex protein |
| 26 | 67.5 | 11.0 | 938 | 2 A13417 | [glutamate-ammonia |
| 27 | 67 | 11.0 | 233 | 2 T41263 | hypothetical prote |
| 28 | 67 | 11.0 | 2212 | 2 A41098 | calcium channel pr |
| 29 | 66.5 | 10.9 | 385 | 2 F70591 | probable kefB prot |

ALIGNMENTS

RESULT 1

A59316

ghrelin precursor - human

N:Alternate names: preproghrelin

C:Species: Homo sapiens (man)

C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000

C:Accession: A59316

R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

Nature 402, 656-660, 1999

A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A:Reference number: A59316; MUID:20067959; PMID:10604470

A:Accession: A59316

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-117 <KOJ>

A:Cross-references: GB:AB029434; NID:g6691571; PIDN:BA089371.1; PID:g6691572

A:Experimental source: tissue stomach endocrine cells

A:Note: submitted to Genbank, June 1999

C:Comment: Ghrelin secreted by the stomach stimulates the release of spmatotropin (gr

C:Superfamily: motilin

C:Keywords: hormone; lipoprotein; stomach

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-51/Product: ghrelin #status predicted <MAT>

F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 611; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 9.1e-55;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPTVCSLLLLGLMLDLAMAGSFLSPHQRVQQRKESKPPAKLPRLAGWLRLPE 60

Db 1 MPSPTVCSLLLLGLMLDLAMAGSFLSPHQRVQQRKESKPPAKLPRLAGWLRLPE 60

QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117

Db 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 2

B59316

ghrelin precursor - rat

N:Alternate names: preproghrelin

C:Species: Rattus norvegicus (Norway rat)

C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000

C:Accession: B59316

R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

Nature 402, 656-660, 1999

A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A:Reference number: A59316; MUID:20067959; PMID:10604470

A:Accession: B59316

A:Status: not compared with conceptual translation

hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
DNA-directed DNA p
myelin/oligodendro
ISGF3 p91-related
DNA-binding protol
exonuclease ABC c
probable pseudouri
transaldolase (EC
protein containing
hypothetical prote
flagellar biosynth
flagellar biosynth
acriflavin resista

30 66.5 10.9 485 2 C75460
31 66.5 10.9 575 2 F86639
32 66.5 10.9 992 2 T08772
33 66.5 10.9 1018 2 T43168
34 66.5 10.9 1171 2 AB0130
35 66 10.8 247 2 S38394
36 66 10.8 770 2 I49508
37 66 10.8 770 2 A54444
38 66 10.8 922 2 D75615
39 65.5 10.7 262 2 D71068
40 65.5 10.7 334 2 S39870
41 65.5 10.7 491 2 H97088
42 65.5 10.7 627 2 T19542
43 65.5 10.7 692 2 B55546
44 65.5 10.7 692 2 AE0745
45 65.5 10.7 1065 2 E69795

C:Superfamily: motilin

```
Query Match          11.9%; Score 72.5; DB 2; Length 115;
Best Local Similarity 25.0%; Pred. No. 2.9;
Matches 21; Conservative 21; Mismatches 33; Indels 9; Gaps 2;

Qy 27 FLSPHORVQQRKSKPPAKLPALAGWLRPEDGQAEGADELE----VRFNAPFDV 82
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30 FTYGEVQMQRKERYKG-----QKSLSVQQRSEVGPVDPAPRPEEKQEVKITAPVEI 84
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 83 GIKLSGVQYQHSQAIGKFLQDIL 106
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 85 GMRNRSQLEKYQATLEGLLRKAL 108
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
S03904
platelet-derived endothelial cell growth factor precursor [validated] - human
N:Contains: thymidine phosphorylase (EC 2.4.2.4)
C:Species: Homo sapiens (man)
C:Date: 23-Oct-1998 #sequence_revision 23-Oct-1998 #text_change 23-Dec-2002
C:Accession: S03904; JX0275; A60966
R:Ishikawa, F.; Miyazono, K.; Hellman, U.; Drexler, H.; Wernstedt, C.; Hagiwara, K.; Usui,
  Nature 338, 557-562, 1989
A:Title: Identification of angiogenic activity and the cloning and expression of platelet
A:Reference number: S03904; MUID:89181955; PMID:2467210
A:Accession: S03904
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-482 <ISH>
A>Note: part of this sequence, including the amino end of the mature protein, was confirmed
R:Sumizawa, T.; Furukawa, T.; Harauchi, M.; Yoshimura, A.; Takeyasu, A.; Ishizawa, M.;
  J. Biochem. 114, 9-14, 1993
A:Title: Thymidine phosphorylase activity associated with platelet-derived endothelial cell
A:Reference number: JX0275; MUID:94012588; PMID:8407883
A:Accession: JX0275
A:Molecule type: mRNA
A:Residues: 125-244 <SUM>
A:Experimental source: placenta
R:Usuki, K.; Norberg, L.; Larsson, E.; Miyazono, K.; Hellman, U.; Wernstedt, C.; Rubin,
  Cell Regul. 1, 577-596, 1990
A:Title: Localization of platelet-derived endothelial cell growth factor in human placenta
A:Reference number: A60966; MUID:91175877; PMID:2078568
A:Accession: A60966
A:Molecule type: protein
A:Residues: 6-14 <USU>
C:Genetics:
A:Gene: GDB:ECGF1
A:Cross-references: GDB:127754; OMIM:131222
A:Map position: 22q13-22q13
C:Superfamily: thymidine phosphorylase/pyrimidine-nucleoside phosphorylase
C:Keywords: angiogenesis; glycosyltransferase; growth factor; mitogen; pentosyltransferase
F:6-482/Product: platelet-derived endothelial cell growth factor, placental form #status
F:11-482/Product: platelet-derived endothelial cell growth factor, platelet form #status
F:63/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match          11.9%; Score 72.5; DB 1; Length 482;
Best Local Similarity 24.4%; Pred. No. 14;
Matches 30; Conservative 23; Mismatches 43; Indels 27; Gaps 5;

Qy 2 PSPCTVCSLLLLGLMLDLAMAGSSFL--SPEHORVQQRKSKPPAKLPALAGWLR 58
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 13 PAFG-----DFGEGSQGLPDPSPKQQLPELIRMKRQDGRLEADIRGFVA 59
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 59 PEDGGQAEGADELEVRNAPFDVGIKLSGVQYQHS----QALGKFLQDILWEA-KEAP 114
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 AVVNGSAQGAQIGAML-----MAIRLGMGLETSVLTQAALQAQSQQLPEWPAWQQQL 112
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 115 ADK 117
    ||
Db 113 VDK 115
```

RESULT 10

```
G83109
Probable two-component sensor PA4293 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83109
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Miziochui, S.D.; Warrenner, P.; Hickey, M.J.;
  adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.
  Lory, S.; Olson, M.V.
  Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83109
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-922 <STO>
A:Cross-references: GB:AF004845; GB:AF004091; NID:g9950507; PIDN:AAG07681.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4293

Query Match          11.9%; Score 72.5; DB 2; Length 922;
Best Local Similarity 28.7%; Pred. No. 30;
Matches 25; Conservative 8; Mismatches 29; Indels 25; Gaps 3;

Qy 3 SPGTVCSSLL-LGLMLDLAMAGSSFLSPHORVQQRKSKPPAKLPALAGWLRPED 61
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 570 SPALICRYTADLVITYVNRFTADSLATSPE-----RLVGRRLDEWLAED 614
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 62 -----GQAEGADELEVRNAP 79
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 615 ASALRRLGSPREGASEVPELRNLP 641
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
T09722
histone H2B1 - upland cotton
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
C:Accession: T09722
R:Turley, R.B.; Parker, S.M.
  Submitted to the EMBL Data Library, September 1997
A:Reference number: Z16835
A:Accession: T09722
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-147 <TUR>
A:Cross-references: EMBL:AF025667; NID:g2558961; PID:g2558962
A:Experimental source: strain DPL 62; etiolated cotyledon
C:Superfamily: histone H2B
C:Keywords: DNA binding; nucleus

Query Match          11.8%; Score 72; DB 2; Length 147;
Best Local Similarity 25.2%; Pred. No. 4.3;
Matches 28; Conservative 22; Mismatches 31; Indels 30; Gaps 5;

Qy 22 MAGSSFLSPHORVQQRKE--SKKPPAKLPALAGWLRPEDGQAEGADELEVRNAP 79
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MAPKAERKPAEKPAEKKAVAERKPK--AGKKLPKEGAAAGDKKKRVKKSVE 58
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 80 F-----DVGIKLSGVQYQHSQALG---KFLQDILWEAEKA 113
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 59 TYKIYIPKVLQVHPDIGIS-----SKAMGIMNSFINDFEKLQAQEA 100
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
B36134
RepC protein - Escherichia coli plasmid TF-FC2
C:Species: Escherichia coli
C:Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 08-Oct-1999
C:Accession: B36134
R:Dorrington, R.A.; Rawlings, D.E.
```

J. Bacteriol. 172, 5697-5705, 1990
A:Title: Characterization of the minimum replicon of the broad-host-range plasmid pTF-FC
A:Reference number: A36134; MUID:91008941; PMID:2120189
A:Accession: B36134
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <DOR>
A:Cross-references: GB:M73777; GB:M35249; NID:g154646; PIDN:AAA27382.1; PID:g154648
C:Genetics:
C:Genome: plasmid

Query Match 11.6%; Score 71; DB 2; Length 299;
Best Local Similarity 25.8%; Pred. No. 12;
Matches 25; Conservative 15; Mismatches 37; Indels 20; Gaps 4;
QY 32 HORVOORRESK--KPPAKLQPRALAGWLRPEGGQAE-----GAEDE-LEVRPN 77
DB 200 HTRINNAEVRKLETPARLLHRLCGWIDPGSGKAEIDTLCGYVMPDAANDAMKKRRQ 259
QY 78 APFDVGIKLSGVYQOQHSQALGKFLQDILWEEAKEAP 114
DB 260 TARKALVELAAVGTWVNEYAKCK-----WEISRPNP 290

RESULT 13
F90788
probable outer membrane usher protein ECs1278 [imported] - Escherichia coli (strain O157
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: F90788
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90788
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-840 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA034701.1; PID:g13360738; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs1278
C:Superfamily: outer membrane usher protein fimD

Query Match 11.5%; Score 70; DB 2; Length 840;
Best Local Similarity 25.9%; Pred. No. 48;
Matches 30; Conservative 15; Mismatches 43; Indels 28; Gaps 5;
QY 3 SPGTVCSSLLGLMLDLAMAGSFLSPHQVRQORRESKPPAKLQPRPRA-----LAG 55
DB 127 APG-ITSQTQLSQLRLDLSPQSLIS-----RPRGYVPPSELDTGASLAFMYNIAN 177

QY 56 WLRPEDGGQAEAELEVRFNAPFDVGIKLSGVYQOQHSQALGKFLQDILWEEAK 111
DB 178 YYNVAYSGONAHQSRLWASFNQ-----GINLGAWQYRQ-----LSNMTWDNDK 221

RESULT 14
G85648
probable usher protein 21536 [imported] - Escherichia coli (strain O157:H7, substrain ED
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: G85648
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouasis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85648
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-840 <STO>

A:Cross-references: GB:AE005174; NID:g12514401; PIDN:AAG55651.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z1536
C:Superfamily: outer membrane usher protein fimD

Query Match 11.5%; Score 70; DB 2; Length 840;
Best Local Similarity 25.9%; Pred. No. 48;
Matches 30; Conservative 15; Mismatches 43; Indels 28; Gaps 5;
QY 3 SPGTVCSSLLGLMLDLAMAGSFLSPHQVRQORRESKPPAKLQPRPRA-----LAG 55
DB 127 APG-ITSQTQLSQLRLDLSPQSLIS-----RPRGYVPPSELDTGASLAFMYNIAN 177

QY 56 WLRPEDGGQAEAELEVRFNAPFDVGIKLSGVYQOQHSQALGKFLQDILWEEAK 111
DB 178 YYNVAYSGONAHQSRLWASFNQ-----GINLGAWQYRQ-----LSNMTWDNDK 221

RESULT 15
S47436
flagellar antigen - Trypanosoma brucei (fragment)
C:Species: Trypanosoma brucei
C:Date: 13-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 03-Nov-2000
C:Accession: S47436
R:Imboden, M.; Mueller, N.; Hemphill, A.; Mattioli, X.Y.Z.; Seebeck, T.
submitted to the EMBL Data Library, August 1994
A:Description: Repetitive proteins from the flagellar cytoskeleton of African Trypano
A:Reference number: S47436
A:Accession: S47436
A:Molecule type: mRNA
A:Residues: 1-411 <IMB>
A:Cross-references: EMBL:Z36281; NID:g530358; PID:g530359
A:Experimental source: strain stock TREU 1285
C:Superfamily: cytoadherence-accessory protein hmw1

Query Match 11.3%; Score 69; DB 2; Length 411;
Best Local Similarity 30.2%; Pred. No. 27;
Matches 26; Conservative 16; Mismatches 28; Indels 16; Gaps 4;
QY 33 QRVOQRRESKPPAKLQPRALAGWLRPEDGGQAEAELEVRFNAPFDVGIKLSGVYQY 92
DB 317 EALEELEEPQQAPEAQPEAVA-----PE-GDIAVEALEELEEPQQAPE-----AEAQ 362

QY 93 QHSQALGKFLQDIL--WEEAKEAPAD 116
DB 363 PEAQPEGDIAVEALEELEEPQQAPE 388

Search completed: September 11, 2003, 17:26:21
Job time : 46.7968 secs

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; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (23)...(23)
US-09-853-253-6

Query Match 100.0%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 9e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
Db 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 3
US-09-853-253-4
; Sequence 4, Application US/09853253
; Patent No. US2002005156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-4

Query Match 100.0%; Score 23; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
Db 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 4
US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. US20010041791A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East

; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

Query Match 100.0%; Score 23; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
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Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 5
US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. US2002005156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-2

Query Match 100.0%; Score 23; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
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DB 52 ALAGWLRPEDGQAEAEDEV 74

RESULT 6

US-09-989-722-268

Sequence 268, Application US/09989722

Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gunney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC63

CURRENT APPLICATION NUMBER: US/09/989.722

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

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PRIOR APPLICATION NUMBER: 60/087827

PRIOR FILING DATE: 1998-06-03

PRIOR APPLICATION NUMBER: 60/088021

PRIOR FILING DATE: 1998-06-04

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Query Match 100.0%; Score 23; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.5e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGAEGAELEV 23
 Db 52 ALAGWLRPEDGGAEGAELEV 74
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RESULT 7
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 ; Sequence 268, Application US/09989723
 ; Patent No. US20020072092A1

; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: KJavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC62
 ; CURRENT APPLICATION NUMBER: US/09/989,723
 ; PRIOR FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

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Query Match      100.0%; Score 23; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      52 ALAGWLRPEDGGQAGAEDELEV 74

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RESULT 8
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; Sequence 268, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

```

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonl, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 23; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 52 ALAGWLRPEDGGQAGAEDELEV 74

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; Sequence 268, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.5e-15; Mismatches 0; Indels 0; Gaps 0;
 Matches 23; Conservative 0;

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 Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 10

US-09-989-731-268
 ; Sequence 268, Application US/09989731
 ; Patent No. US20020103125A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
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 ; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
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Query Match 100.0%; Score 23; DB 10; Length 117;
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RESULT 12
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 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
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 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC15
 ; CURRENT FILING DATE: 2001-11-14
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
DB 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 13

US-09-990-442-268
Sequence 268, Application US/09990442
Patent No. US20020132252A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC8
;; CURRENT APPLICATION NUMBER: US/09/990,442
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25

;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
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;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
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;; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.08; Score 23; DB 10; Length 117;
Best Local Similarity 100.08; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 ALAGWLRPDGGQAGAEDELEV 23
        |||||
Db      52 ALAGWLRPDGGQAGAEDELEV 74

RESULT 15
US-09-993-604-268
; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993.604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:37 ; Search time 8.73262 Seconds
(without alignments)
253.289 Million cell updates/sec

Title: US-09-853-253-5

Perfect score: 23

Sequence: 1 ALAGWLRPEDGGQAEAGAEDEV 23

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 23 | 100.0 | 117 | 1 A59316 | ghrelin precursor |
| 2 | 8 | 34.8 | 483 | 2 T04453 | hypothetical prote |
| 3 | 7 | 30.4 | 302 | 2 JH0572 | hypothetical prote |
| 4 | 7 | 30.4 | 344 | 2 A48990 | transcription regu |
| 5 | 7 | 30.4 | 910 | 2 B83451 | aconitine hydratas |
| 6 | 7 | 30.4 | 1239 | 1 Q0BE10 | BOLFI protein - hu |
| 7 | 6 | 26.1 | 69 | 2 C87574 | cold-shock domain |
| 8 | 6 | 26.1 | 142 | 2 AB0401 | probable membrane |
| 9 | 6 | 26.1 | 175 | 2 E82118 | conserved hypothet |
| 10 | 6 | 26.1 | 178 | 2 A30230 | quiescence-specifi |
| 11 | 6 | 26.1 | 180 | 2 T46695 | hypothetical prote |
| 12 | 6 | 26.1 | 189 | 2 A91082 | hypothetical prote |
| 13 | 6 | 26.1 | 189 | 2 B85927 | hypothetical prote |
| 14 | 6 | 26.1 | 198 | 2 D69070 | imidazoleglycerol- |
| 15 | 6 | 26.1 | 223 | 2 A40866 | HL-60-induced diff |
| 16 | 6 | 26.1 | 237 | 2 T30002 | hypothetical prote |
| 17 | 6 | 26.1 | 265 | 2 A95298 | hypothetical prote |
| 18 | 6 | 26.1 | 267 | 1 CTPGP | corticotropin / li |
| 19 | 6 | 26.1 | 284 | 2 B25624 | tropomyosin I, tho |
| 20 | 6 | 26.1 | 284 | 2 A25624 | tropomyosin I, emb |
| 21 | 6 | 26.1 | 288 | 2 A55737 | PD-1 protein - hum |
| 22 | 6 | 26.1 | 289 | 2 T48894 | lipoprotein mtsA, |
| 23 | 6 | 26.1 | 289 | 2 H83433 | hypothetical prote |
| 24 | 6 | 26.1 | 290 | 2 H71852 | hypothetical prote |
| 25 | 6 | 26.1 | 299 | 2 T35144 | glutamate transpor |
| 26 | 6 | 26.1 | 302 | 2 T48871 | catechol 1,2-dioxy |
| 27 | 6 | 26.1 | 308 | 2 F72508 | probable hydrogena |
| 28 | 6 | 26.1 | 313 | 2 E82762 | conserved hypothet |
| 29 | 6 | 26.1 | 315 | 2 F64129 | probable phosphogl |

ALIGNMENTS

RESULT 1

A59316

ghrelin precursor - human

N:Alternate names: preproghrelin

C:Species: Homo sapiens (man)

C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000

C:Accession: A59316

R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A:Reference number: A59316; MUID:20067959; PMID:10604470

A:Accession: A59316

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-117 <KO>

A:Cross-references: GB:AB029434; NID:g6691571; PIDN:BAH89371.1; PID:g6691572

A:Experimental source: tissue stomach endocrine cells

A:Note: submitted to GenBank, June 1999

C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (gr

C:Superfamily: motilin

C:Keywords: hormone; lipoprotein; stomach

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-51/Product: ghrelin #status predicted <MAT>

F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match

Best Local Similarity 100.0%; Score 23; DB 1; Length 117;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAEAGAEDEV 23

DB 52 ALAGWLRPEDGGQAEAGAEDEV 74

RESULT 2

T04453

hypothetical protein F4D11.80 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999

C:Accession: T04453

R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Anson, W.; Hohnsels, J.; Mewes,

submitted to the Protein Sequence Database, April 1998

A:Reference number: Z15360

A:Accession: T04453

A:Molecule type: DNA

A:Residues: 1-483 <BEV>

A:Cross-references: EMBL:AL022537

A:Experimental source: cultivar Columbia; BAC clone F4D11

C:Genetics:

A:Map position: 4

A:Introns: 17/3; 44/1; 94/1; 141/3; 206/2; 247/2; 345/3; 395/1; 434/2

transcription repr
30S ribosomal prot
probable prolipopr
hypothetical prote
sam-dependent meth
cysteine proteinas
hypothetical prote
alcohol dehydrogen
cysteine proteinas
phosphoribosylamin
molybdopterin bios
hypothetical prote
hypothetical prote
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hypothetical prote
hypothetical membr

A;Note: F4D11.80

Query Match 34.8%; Score 8; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAED 20
Db 302 QAEGAED 309
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RESULT 3

JH0572
hypothetical protein - Streptomyces lividans (fragment)
C;Species: Streptomyces lividans
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-1999
C;Accession: JH0572
R;Lichenstein, H.S.; Busse, L.A.; Smith, G.A.; Narhi, L.O.; McGinley, M.O.; Rohde, M.F.;
Gene 111, 125-130, 1992
A;Title: Cloning and characterization of a gene encoding extracellular metalloprotease f
A;Reference number: JH0571; MUID:92192468; PMID:1547948
A;Accession: JH0572
A;Molecule type: DNA
A;Residues: 1-302 <LIC>
A;Cross-references: GB:M89476; NID:g153411; PIDN:AAA26804.1; PID:g153412
A;Experimental source: strain TK24
A;Note: the authors translated the codon GTA for residue 260 as Asp
C;Superfamily: Pseudomonas putida regulatory protein catR

Query Match 30.4%; Score 7; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
Db 100 ALAGWLR 106
|||||

RESULT 4

A48990
transcription regulator LysR family homolog SnpR - Streptomyces lividans
C;Species: Streptomyces lividans
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C;Accession: A48990
R;Butler, M.J.; Davey, C.C.; Krygsmann, P.; Walczyk, E.; Malek, L.T.
Can. J. Microbiol. 38, 912-920, 1992
A;Title: Cloning of genetic loci involved in endoprotease activity in Streptomyces livid
A;Reference number: A48990; MUID:93099553; PMID:1464066
A;Contents: 66
A;Accession: A48990
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-344 <BUT>
A;Note: sequence extracted from NCBI backbone (NCBIN:121210, NCBI:121213)
C;Superfamily: Pseudomonas putida regulatory protein catR

Query Match 30.4%; Score 7; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
Db 104 ALAGWLR 110
|||||

RESULT 5

B83451
aconitate hydratase 1 PA1562 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83451
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bf

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83451
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-910 <STO>
A;Cross-references: GB:AE004584; GB:AE004091; NID:99947516; PIDN:AA04951.1; GSPDB:GN
A;Experimental source: strain PA01
C;Genetics:
A;Gene: acnA; PA1562
C;Superfamily: iron-responsive element-binding protein

Query Match 30.4%; Score 7; DB 2; Length 910;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
Db 65 ALAGWLR 71
|||||

RESULT 6

Q0BE10
BOLFI protein - human herpesvirus 4 (strain B95-8)
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
C;Accession: A43041; A03752; S32995
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi
A;Reference number: A93065; MUID:85035713; PMID:6092825
A;Accession: A43041
A;Molecule type: DNA
A;Residues: 1-1239 <BAN>
A;Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24841.1; PID:g1334855
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.
Nature 310, 207-211, 1984

A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A03794; MUID:84270667; PMID:6087149
A;Contents: annotation; protein coding region
C;Superfamily: human herpesvirus 4 BOLFI protein

Query Match 30.4%; Score 7; DB 1; Length 1239;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AEGAED 20
Db 696 AEGAED 702
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RESULT 7

C87574
cold-shock domain family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C;Accession: C87574
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87574
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <STO>
A;Cross-references: GB:AE005673; NID:g13424199; PIDN:AAK24591.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC2623

C:Superfamily: major cold shock protein; cold shock domain homology

Query Match 26.1%; Score 6; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PEDGGQ 13
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Db 20 PEDGGQ 25

RESULT 8

AB0401
Probable membrane protein YPO3302 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0401
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; et al., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0401
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92534.1; PID:gl5981232; GSPDB:GN00175
C:Genetics:
A:Gene: YPO3302
C:Superfamily: hypothetical protein HI0489

Query Match 26.1%; Score 6; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAGWLR 7
|||||
Db 104 LAGWLR 109

RESULT 9

E82118
conserved hypothetical protein VC2111 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82118
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; et al., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301
A:Accession: E82118
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-175 <HEI>
A:Cross-references: GB:AE004284; GB:AE003852; NID:g9656649; PIDN:AAF95256.1; GSPDB:GN00175
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2111
A:Map position: 1

Query Match 26.1%; Score 6; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GOAEGA 17
|||||
Db 54 GOAEGA 59

RESULT 10

C:Superfamily: Lactobacillus helveticus plasmid pLH1 hypothetical protein ORF-180

A30230

quiescence-specific protein precursor - chicken
N:Alternate names: Ch21 protein
C:Species: Gallus gallus (Chicken)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 15-Nov-1996
C:Accession: A30230; A42581; A36595; A35491
R:Bedard, P.A.; Yannoni, Y.; Simmons, D.L.; Erikson, R.L.
Mol. Cell. Biol. 9, 1371-1375, 1989
A:Title: Rapid repression of quiescence-specific gene expression by epidermal growth factor.
A:Reference number: A30230; MUID:89261749; PMID:2498647
A:Accession: A30230
A:Molecule type: mRNA
A:Residues: 1-178 <BED>
R:Dozin, B.; Descalzi, F.; Briata, L.; Hayashi, M.; Gentili, C.; Hayashi, K.; Quarto, J. Biol. Chem. 267, 2979-2985, 1992
A:Title: Expression, regulation, and tissue distribution of the Ch21 protein during cell growth.
A:Reference number: A42581; MUID:92147639; PMID:17377754
A:Accession: A42581
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-95, 'L', 97-178 <DOZ>
A:Experimental source: tibia hypertrophic cartilage
A:Note: Sequence extracted from NCBI backbone (NCBI:80796, NCBI:80797)
R:Cancedda, F.D.; Dozin, B.; Rossi, F.; Molina, F.; Cancedda, R.; Negri, A.; Ronchi, J. Biol. Chem. 265, 19060-19064, 1990
A:Title: The Ch21 protein, developmentally regulated in chick embryo, belongs to the chondrin family.
A:Reference number: A36595; MUID:91035433; PMID:2229062
A:Accession: A36595
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 21-95, 'L', 97-178 <CAN>
A:Cross-references: GB:M37611

R:Cancedda, F.D.; Asaro, D.; Molina, F.; Cancedda, R.; Caruso, C.; Camardella, L.; Negri, A.; Ronchi, J. Biochem. Biophys. Res. Commun. 168, 933-938, 1990

A:Title: The amino terminal sequence of the developmentally regulated CH21 protein sh

F:22-178/Product: quiescence-specific protein #status predicted <MAT>

F:25-173/Domain: lipocalin homology <LIP>

Query Match 26.1%; Score 6; DB 2; Length 178;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EDELEV 23

Db 65 EDELEV 70

RESULT 11

T46695

hypothetical protein ORF-180 [imported] - Lactobacillus helveticus plasmid pLH1

C:Species: Lactobacillus helveticus

C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 04-Mar-2000

C:Accession: T46695

R:Thompson, K.; McConville, K.J.; McReynolds, C.; Foley, S.

submitted to the EMBL Data Library, December 1997

A:Description: Complete sequence of plasmid pLH1 from Lactobacillus helveticus ATCC15

A:Reference number: 223135

A:Accession: T46695

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-180 <THO>

A:Cross-references: EMBL:AJ222725; PIDN:CAA10962.1

A:Experimental source: ATCC 15009

C:Genetics:

A:Genome: plasmid pLH1

C:Superfamily: Lactobacillus helveticus plasmid pLH1 hypothetical protein ORF-180

```

Query Match      26.1% Score 6; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWL 6
Db 31 ALAGWL 36

RESULT 12
A:Accession: D69070
A:Title: Complete genome sequence of Escherichia coli (strain O157:H7, substrain R1)
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA037048.1; PID:g13363096; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs3625

Query Match      26.1% Score 6; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWL 6
Db 14 ALAGWL 19

RESULT 13
A:Accession: B85927
A:Title: Complete genome sequence of Escherichia coli (strain O157:H7, substrain EDL5)
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <STO>
A:Cross-references: GB:AE005174; NID:g12517231; PIDN:AGS57878.1; GSPDB:GN00145; UWGP:240
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: 24080

Query Match      26.1% Score 6; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWL 6
Db 14 ALAGWL 19

RESULT 14
A:Accession: D69070
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum (strain Delta H)
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-198 <MTH>
A:Cross-references: GB:AE000912; GB:AE000666; NID:g2622632; PIDN:AAB85999.1; PID:g262
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1524
A:Start codon: TTG
C:Superfamily: amidotransferase h1sh; trpG homology

Query Match      26.1% Score 6; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 EGAEDE 20
Db 130 EGAEDE 135

RESULT 15
A:Accession: A40866
A:Title: HL-60-induced differentiation immediate-early protein ETR101 - human
A:Reference number: A40866; MUID:91286224; PMID:2061303
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-223 <SHI>
A:Cross-references: GB:M62831; NID:g182260; PIDN:AAA35814.1; PID:g182261

Query Match      26.1% Score 6; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GQAEGA 17
Db 165 GQAEGA 170

Search completed: September 11, 2003, 17:57:06
Job time : 9.73262 secs

```

```

C:Accession: D69070
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: D69070
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-198 <MTH>
A:Cross-references: GB:AE000912; GB:AE000666; NID:g2622632; PIDN:AAB85999.1; PID:g262
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1524
A:Start codon: TTG
C:Superfamily: amidotransferase h1sh; trpG homology

Query Match      26.1% Score 6; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 EGAEDE 20
Db 130 EGAEDE 135

RESULT 15
A:Accession: A40866
A:Title: HL-60-induced differentiation immediate-early protein ETR101 - human
A:Reference number: A40866; MUID:91286224; PMID:2061303
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-223 <SHI>
A:Cross-references: GB:M62831; NID:g182260; PIDN:AAA35814.1; PID:g182261

Query Match      26.1% Score 6; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GQAEGA 17
Db 165 GQAEGA 170

Search completed: September 11, 2003, 17:57:06
Job time : 9.73262 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:30:37 ; Search time 4.42781 Seconds
(without alignments)
244.278 Million cell updates/sec

Title: US-09-853-253-5
Perfect score: 23
Sequence: 1 ALAGWLRPEDGGQAGAEDELEV 23

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 23 | 100.0 | 117 | 1 | GHRL_HUMAN |
| 2 | 10 | 43.5 | 116 | 1 | GHRL_BOVIN |
| 3 | 7 | 30.4 | 328 | 1 | MPR2_STRCO |
| 4 | 7 | 30.4 | 344 | 1 | MPR2_STRLI |
| 5 | 7 | 30.4 | 1239 | 1 | V120_EBV |
| 6 | 6 | 26.1 | 117 | 1 | GHRL_CANFA |
| 7 | 6 | 26.1 | 178 | 1 | EFAB_CHICK |
| 8 | 6 | 26.1 | 198 | 1 | HIS5_METTH |
| 9 | 6 | 26.1 | 267 | 1 | COLI_PIG |
| 10 | 6 | 26.1 | 284 | 1 | TPW2_DROME |
| 11 | 6 | 26.1 | 288 | 1 | PCD1_HUMAN |
| 12 | 6 | 26.1 | 289 | 1 | OPSD_LIMPA |
| 13 | 6 | 26.1 | 290 | 1 | PARB_HELPJ |
| 14 | 6 | 26.1 | 310 | 1 | MTSA_STRP8 |
| 15 | 6 | 26.1 | 310 | 1 | MTSA_STRPY |
| 16 | 6 | 26.1 | 313 | 1 | MRW_XYLEFA |
| 17 | 6 | 26.1 | 315 | 1 | YF56_HAEIN |
| 18 | 6 | 26.1 | 326 | 1 | RBRB_BACSU |
| 19 | 6 | 26.1 | 346 | 1 | MRW_BRUME |
| 20 | 6 | 26.1 | 360 | 1 | CYS2_MAIZE |
| 21 | 6 | 26.1 | 379 | 1 | PURK_BACSU |
| 22 | 6 | 26.1 | 395 | 1 | IF5_SCHPO |
| 23 | 6 | 26.1 | 433 | 1 | TIG_STAAM |
| 24 | 6 | 26.1 | 436 | 1 | CUS1_YEAST |
| 25 | 6 | 26.1 | 497 | 1 | RPSD_MYCGE |
| 26 | 6 | 26.1 | 499 | 1 | RPSD_MYCPN |
| 27 | 6 | 26.1 | 511 | 1 | SYS_MOUSE |
| 28 | 6 | 26.1 | 513 | 1 | SYS_BOVIN |
| 29 | 6 | 26.1 | 513 | 1 | SYS_HUMAN |
| 30 | 6 | 26.1 | 535 | 1 | AMYB_HORVU |
| 31 | 6 | 26.1 | 539 | 1 | Z173_HUMAN |
| 32 | 6 | 26.1 | 547 | 1 | CH60_BUCTC |
| 33 | 6 | 26.1 | 566 | 1 | HS60_CANAL |

RESULT 1

| ID | GHRL_HUMAN | STANDARD; | PRT; | 117 AA. |
|-----|--|-----------|------|---------|
| AC | Q9UBU3; Q8TAT9; Q9H3R3; | | | |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) | | | |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein). | | | |
| DE | GhRL OR MTLRP. | | | |
| GN | Homo sapiens (Human). | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| [1] | | | | |
| RN | SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26. | | | |
| RP | MEDLINE=20067959; PubMed=10604470; | | | |
| RX | Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.; | | | |
| RA | "Ghrelin is a growth-hormone-releasing acylated peptide from stomach." | | | |
| RT | | | | |
| RL | Nature 402:656-660(1999). | | | |
| [2] | | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). | | | |
| RA | Kojima M.; | | | |
| RL | Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases. | | | |
| [3] | | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). | | | |
| RC | TISSUE=Stomach; | | | |
| RA | Tomasetto C., Karam S.M., Rio M.-C.; | | | |
| RT | "Identification of a novel gastric protein m46." | | | |
| RL | Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases. | | | |
| [4] | | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). | | | |
| RA | Wajraich M.P., Ten I.S., Gertner J.M., Leibell R.L.; | | | |
| RT | "Genomic organization of the human Ghrelin gene." | | | |
| RL | J. Endocrinol. Genet. 1:231-233(2000). | | | |
| [5] | | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). | | | |
| RC | TISSUE=Blood; | | | |
| RX | MEDLINE=22388257; PubMed=12477932; | | | |
| RA | Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., | | | |

ALIGNMENTS

| | | | | | | |
|----|---|------|-----|---|------------|--------------------|
| 34 | 6 | 26.1 | 572 | 1 | HS60_YEAST | P19882 saccharomyc |
| 35 | 6 | 26.1 | 590 | 1 | HS60_AJECA | P50142 ajellomyc |
| 36 | 6 | 26.1 | 620 | 1 | SMP_COTJA | Q92154 coturnix co |
| 37 | 6 | 26.1 | 641 | 1 | DXS_RHOCA | P26242 rhodobacter |
| 38 | 6 | 26.1 | 650 | 1 | APPL_HUMAN | P51693 homo sapien |
| 39 | 6 | 26.1 | 657 | 1 | HUTH_MOUSE | P35492 mus musculu |
| 40 | 6 | 26.1 | 683 | 1 | Z263_HUMAN | O14978 homo sapien |
| 41 | 6 | 26.1 | 702 | 1 | HELS_AERPE | Q9Vfg8 aeropyrum p |
| 42 | 6 | 26.1 | 728 | 1 | UVRG_STRCO | Q92512 streptomyce |
| 43 | 6 | 26.1 | 886 | 1 | SM6B_MOUSE | O54951 mus musculu |
| 44 | 6 | 26.1 | 887 | 1 | SM6B_RAT | O70141 rattus norv |
| 45 | 6 | 26.1 | 890 | 1 | ACOL_ECOLI | P25516 escherichia |

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.:
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [6]
 RC SEQUENCE OF 24-33.
 RX TISSUE=Stomach;
 RA MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.:
 RT "Identification and characterization of a novel gastric peptide
 hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [7]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.:
 RA "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -|- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -|- PTM: O-n-octanoylation is essential for activity.
 CC -|- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -|- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.fr/services/chromancer/Genes/GhrelinID327.html".
 CC -----
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 DR EMBL; AB029434; BAA89371.1; -;
 DR EMBL; AB035700; BAB19045.1; -;
 DR EMBL; AJ252278; CAB65733.1; -;
 DR EMBL; AF296558; AAG10300.1; -;
 DR EMBL; BC025791; AAH25791.1; -;
 DR PIR; A59316; A59316.
 DR MI; 605353; -;
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005131; F:growth hormone receptor ligand activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaling. . .; TAS.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc; 1.
 DR Pfam; PF04644; motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 KW SIGNAL 1 23
 FT PEPTIDE 24 51 GHRELIN.
 FT PROPEP 52 117 REMOVED IN MATURE FORM.
 FT LIPID 26 26 N-OCTANOATE.
 FT VARSPPLIC 37 37 Missing (in Isoform 2).
 FT FTId=VSP_003245.
 FT CONFLICT 72 72 L -> M (IN REF. 5).

SO SEQUENCE 117 AA; 12911 MW; 39C0572BECA2755 CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGGAEGAEDELEV 23
 Db 52 ALAGWLRPEDGGGAEGAEDELEV 74
 RESULT 2
 GHRL_BOVIN STANDARD; PRT; 116 AA.
 ID GHRL_BOVIN
 AC Q9BDJ6; Q9GKY6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ghrelin precursor (growth hormone secretagogue) (Growth hormone
 GN releasing peptide).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kita K., Harada K., Yokota H.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 24-99 FROM N.A.
 RA Kojima M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -|- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation (By similarity).
 CC -|- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -|- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -|- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF350329; AAK18612.1; -;
 DR EMBL; AB035702; BAB19047.1; -;
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc; 1.
 DR Pfam; PF04644; motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 KW SIGNAL 1 23 BY SIMILARITY.
 FT PEPTIDE 24 50 GHRELIN (BY SIMILARITY).
 FT PROPEP 51 116 REMOVED IN MATURE FORM (BY SIMILARITY).
 FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
 FT CONFLICT 34 34 K -> E (IN REF. 2).
 SQ SEQUENCE 116 AA; 12792 MW; F553536DAC5FA59B6 CRC64;
 Query Match 43.5%; Score 10; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 QAEGAEDELE 22

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Db 63 QAEGADELE 72
|||||
RESULT 3
MPR2_STRCO STANDARD; PRT; 328 AA.
AC Q9L127;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Small neutral protease regulatory protein.
GN MPRR2 OR MPRR2 OR SCO7433 OR SC6D11.29.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RA "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- FUNCTION: TRANSCRIPTIONAL TRANS-ACTIVATOR OF THE GENE (MPRA) FOR
CC THE SMALL NEUTRAL PROTEASE.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AL939131; CAB76352.1; -
CC InterPro: IPR000847; HTH_LysR.
CC Pfam: PF00126; HTH_1; 1.
CC PRINTS: PR00039; HTHLYSR.
CC PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
CC DNA-binding; Protease; Transcription regulation; Complete proteome.
FT DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 328 AA; 35885 MW; 2BA97730AE4FA16B CRC64;
Query Match 30.4%; Score 7; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLR 7
Db 104 ALAGWLR 110
|||||
RESULT 4
MPR2_STRLI STANDARD; PRT; 344 AA.
AC P43161;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
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DE Small neutral protease regulatory protein.
GN MPRR OR SNPR.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=66 / 1326;
RX MEDLINE=93099553; PubMed=14540866;
RA Butler M.J., Davey C.C., Krygsmann P., Walczyk E., Malek L.T.;
RT "Cloning of genetic loci involved in endoprotease activity in
RT Streptomyces lividans 66: a novel neutral protease gene with an
RT adjacent divergent putative regulatory gene.";
RL Can. J. Microbiol. 38:912-920(1992).
RN [2]
RP SEQUENCE OF 1-305 FROM N.A.
RC STRAIN=TK24;
RX MEDLINE=92192468; PubMed=1547948;
RA Lichenstein H.S., Busse L.A., Smith G.A., Narhi L.O.,
RA McGinley M.O., Rohde M.F., Katowitz J.L., Zukowski M.M.;
RT "Cloning and characterization of a gene encoding extracellular
RT metalloprotease from Streptomyces lividans.";
RL Gene 111:125-130(1992).
CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE GENE (SNPA) FOR THE
CC SMALL NEUTRAL PROTEASE.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M81703; AAA26739.1; -
CC EMBL: M89476; AAA26804.1; ALT_INIT.
CC InterPro: IPR000847; HTH_LysR.
CC InterPro: IPR005119; LysR_subst.
CC Pfam: PF00126; HTH_1; 1.
CC Pfam: PF03466; LysR_substrate; 1.
CC PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
CC Transcription regulation; DNA-binding; Activator.
FT DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
FT CONFLICT 270 270 G -> AR (IN REF. 2).
SQ SEQUENCE 344 AA; 37415 MW; 485C82C813B52312 CRC64;
Query Match 30.4%; Score 7; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLR 7
Db 104 ALAGWLR 110
|||||
RESULT 5
V120_EBV
ID V120_EBV STANDARD; PRT; 1239 AA.
AC P03189;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Capsid assembly protein BOLF1.
GN BOLF1.
OS Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Sequin C.,
RA Tufnell P.S., Barrall B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,
CC EHv-1 23, EBV BOLE1, VZV 21, HVS-1 63, AND HCMV UL47.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; V01555; CAA24841.1; -.
CC PIR; A43041; Q0BE10.
CC Capsid assembly.
CC SEQUENCE 1239 AA; 132748 MW; 6C5DBFC55F2FF729 CRC64;

Query Match 30.48; Score 7; DB 1; Length 1239;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AEGAEDE 20
Db 696 AEGAEDE 702
|||||

RESULT 6
GHRL CANFA
ID GHRL CANFA STANDARD; PRT; 117 AA.
AC Q9BEF8; Q9BEF7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide).
DE GHRL OR MTLRP.
GN Canis familiaris (Dog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Gastric fundus;
RA Tomasetto C., Wendling C., Rio M.-C., Poltras P.;
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
RT fundus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms-2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9BEF8-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9BEF8-2; Sequence=VSP_003244;
CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
CC EMBL; AJ298295; CAC29155.1; -.
CC EMBL; AJ298296; CAC29156.1; -.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin-ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin-ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD33216; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPIC 37 37 Missing (in isoform 2).
FT FTID=VSP_003244.
SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;

Query Match 26.18; Score 6; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 AEDELE 22
Db 68 AEDELE 73
|||||

RESULT 7
EFAB CHICK
ID EFAB CHICK STANDARD; PRT; 178 AA.
AC P21760; P21928; Q9PWN9;
DT 01-MAY-1991 (Rel. 18, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Extracellular fatty acid binding protein precursor (Ex-FABP)
DE Quiescence-specific protein (p20K) (Ch21 protein).
DE EXFABP.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89261749; PubMed=2498647;
RA Bedard P.-A., Yannoni Y., Simmons D.L., Erikson R.L.;
RT "Rapid repression of quiescence-specific gene expression by epidermal
RT growth factor, insulin, and pp60v-src.";
RL Mol. Cell. Biol. 9:1371-1375(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92147639; PubMed=1737754;
RA Dozin B., Descalzi F., Briata L., Hayashi M., Gentili C.,
RA Hayashi K., Quarto R., Cancedda R.;
RT "Expression, regulation, and tissue distribution of the Ch21 protein
RT during chicken embryogenesis.";
RL J. Biol. Chem. 267:2979-2985(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Leghorn;
RA Giannoni P., Dozin B., Zambotti A., Neri M., Cancedda R.;
RT "Differentiation-dependent activation of the extracellular fatty acid
RT binding protein (EXFABP) gene in chicken embryo chondrocytes.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 25-178 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91035433; PubMed=2229062;
RA Cancedda F.D., Dozin B., Rossi F., Molina F., Cancedda R.,
RA Negri A., Ronchi S.;
RT "The Ch21 protein, developmentally regulated in chick embryo, belongs

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to the superfamily of lipophilic molecule carrier proteins.";
 J. Biol. Chem. 265:19060-19064(1990).
 [5]
 RN SEQUENCE OF 21-48.
 RP MEDLINE=90267487; PubMed=2346493;
 RA Cancedda F.D., Asaro D., Molina F., Cancedda R., Caruso C.,
 RA Camardella L., Negri A., Ronchi S.;
 RT "The amino terminal sequence of the developmentally regulated Ch21
 RT protein shows homology with amino terminal sequences of low molecular
 RT weight proteins binding hydrophobic molecules.";
 RL Biochem. Biophys. Res. Commun. 168:933-938(1990).
 RN [6]
 RN SEQUENCE OF 103-178 FROM N.A.
 RP STRAIN=White leghorn; TISSUE=Bone marrow;
 RX MEDLINE=92195690; PubMed=1549365;
 RA Nakano T., Graf T.;
 RT "Identification of genes differentially expressed in two types of
 RT v-myb-transformed avian myelomonocytic cells.";
 RL Oncogene 7:527-534(1992).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE=96355330; PubMed=8702740;
 RA Cancedda F.D., Malpeli M., Gentili C., Di Marzo V., Bet P.,
 RA Carlevaro M., Cermelli S., Cancedda R.;
 RT "The developmentally regulated avian Ch21 lipocalin is an
 RT extracellular fatty acid-binding protein.";
 RL J. Biol. Chem. 271:20163-20169(1996).
 RN [8]
 RP CHARACTERIZATION.
 RX MEDLINE=20513977; PubMed=11058755;
 RA Descalzi Cancedda F., Dozin B., Zerega B., Cermelli S., Cancedda R.;
 RT "Ex-FABP: a fatty acid binding lipocalin developmentally regulated in
 RT chicken endochondral bone formation and myogenesis.";
 RL Biochim. Biophys. Acta 1482:127-135(2000).
 CC -!- FUNCTION: Preferentially binds long-chain unsaturated fatty acids
 CC such as linoleic acid, oleic acid, arachidonic acid. Also binds
 CC with a lower affinity long chain saturated fatty acids such as
 CC stearic acid. May act as survival protein by playing a role in
 CC maintaining cell viability.
 CC -!- SUBUNIT: Monomer.
 CC -!- TISSUE SPECIFICITY: PREFERENTIALLY SYNTHESIZED IN NONPROLIFERATING
 CC CELLS.
 CC -!- PTM: Does not seem to be glycosylated.
 CC -!- MISCELLANEOUS: Developmentally regulated in chick embryo.
 CC -!- SIMILARITY: Belongs to the lipocalin family.
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 CC -----
 CC EMBL: M25784; AAA53371.1; -;
 CC EMBL: M55644; AAA48677.1; -;
 CC EMBL: AF121346; AAD23569.1; -;
 CC EMBL: X61199; -; NOT_ANNOTATED_CDS.
 CC PIR: A30230; A30230.
 CC InterPro: IPR002345; Lipocalin.
 CC InterPro: IPR000566; Lipocalin_cytFABP.
 CC Pfam: PF00061; Lipocalin; 1.
 CC PRINTS: PR00179; LIPOCALIN.
 CC PROSITE: PS00213; LIPOCALIN; 1.
 CC Lipocalin; Transport; Signal.
 CC SIGNAL 1 20 EXTRACELLULAR FATTY ACID BINDING PROTEIN.
 CC CHAIN 21 178 BLOCKED.
 CC MOD_RES 21 21 BY SIMILARITY.
 CC DISULFID 80 173 L -> S (IN REF. 2).
 CC CONFLICT 4 4 L -> S (IN REF. 2).
 CC CONFLICT 27 27 R -> S (IN REF. 2 AND 4).
 CC CONFLICT 45 45 F -> S (IN REF. 2 AND 4).
 CC FT

FT CONFLICT 62 62 F -> S (IN REF. 1).
 FT CONFLICT 96 96 L -> V (IN REF. 1).
 SQ SEQUENCE 178 AA; 20201 MW; 0DDBD333C1A0C6B8 CRC64;
 Query Match 26.1%; Score 6; DB 1; Length 178;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 EDELEV 23
 DB 65 EDELEV 70
 RESULT 8
 HIS5_METH STANDARD; PRT; 198 AA.
 ID HIS5_METH
 AC 027568;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Imidazole glycerol phosphate synthase subunit hsh (EC 2.4.2.-) (IGP
 DE synthase glutamine amidotransferase subunit) (IGP synthase subunit
 DE hsh) (IMGF synthase subunit hsh) (IGPS subunit hsh).
 GN HSH OR MTH1524.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhekar S.,
 RA McDougall S., Shiner G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -!- FUNCTION: IGP catalyzes the conversion of PRFAR and glutamine to
 CC IGP, AICAR and glutamate. The hsh subunit provides the glutamine
 CC amidotransferase activity that produces the ammonia necessary to
 CC hsh for the synthesis of IGP and AICAR (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulos-1-
 CC ylamino)methylideneamino]-1-(5-phospho-1-deoxyribulos-1-
 CC carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-
 CC aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
 CC -!- PATHWAY: Histidine biosynthesis; fifth step.
 CC -!- SUBUNIT: Heterodimer of hsh and hsf (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
 CC -----
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 CC -----
 CC EMBL: AE000912; AAB85999.1; -;
 CC PIR: D69070; D69070.
 CC HAMAP: MF_00278; -; 1.
 CC InterPro: IPR000991; GATase_1.
 CC Pfam: PF00117; GATase; 1.
 CC PROSITE: PS00442; GATASE_TYPE_I; 1.
 CC Histidine biosynthesis; Transferase; Glutamine amidotransferase;
 CC Complete proteome.
 CC ACT_SITE 77 77 BY SIMILARITY.
 CC ACT_SITE 177 177 BY SIMILARITY.
 CC FT

CC GLAND.
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
CC THE DIFFERENT ACTIVE PEPTIDES.
CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X03561; CAA27248.1; -
CC EMBL: X00135; CAA24968.1; -
CC EMBL: S73519; AAB32312.1; -
CC EMBL: K01879; AAB31104.1; -
CC PIR: A93496; CTPGP.
CC InterPro: IPR001941; Mcoitin_ACTH.
CC Pfam: PF00976; ACTH_domain; 1.
CC PRINTS: PR00383; MELANOCORTIN.
CC Endorphin; Hormone; Cleavage on pair of basic residues; Amidation;
CC Glycoprotein; Signal.
CC SIGNAL 1 26
CC PEPTIDE 27 106 BY SIMILARITY.
CC NPP.
CC MELANOTROPIN GAMMA.
CC CORTICOTROPIN.
CC MELANOTROPIN ALPHA.
CC CORTICOTROPIN-LIKE INTERMEDIARY PEPTIDE.
CC LIPOTRONIN BETA.
CC MELANOTROPIN GAMMA.
CC MELANOTROPIN BETA.
CC BETA-ENDORPHIN.
CC MET-ENKEPHALIN.
CC AMIDATION (G-88 PROVIDE AMIDE GROUP).
CC AMIDATION (G-149 PROVIDE AMIDE GROUP).
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC R -> T.
CC G -> S (IN REF. 3 AND 4).
CC T -> A (IN REF. 3 AND 4).
CC G -> E (IN REF. 3 AND 4).
CC A -> S (IN REF. 4).
CC SEQUENCE 267 AA; 28894 MW; A6DB487A5032B648 CRC64;

CC Query Match 26.1%; Score 6; DB 1; Length 267;
CC Best Local Similarity 100.0%; Pred.No. 36;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GAEDEL 21
DB 161 GAEDEL 166

RESULT 10
TPM2_DROME STANDARD; PRT: 284 AA.
AC P09491; P09490; Q24408; Q24427; Q24428; Q8S265; Q9VF95;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tropomyosin 2 (Tropomyosin I).
GN TM2 OR TM1 OR CG4843.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
RC TISSUE=Embryo. Larva, and Pupae;
RX MEDLINE=84205681; PubMed=6202423;
RA Karlik C.C., Mahaffey J.W., Coutu M.D., Fyrberg E.A.;
RT "Organization of contractile protein genes within the 88F subdivision

RT of the D. melanogaster third chromosome.";
RL Cell 37:469-481(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
RX MEDLINE=86085920; PubMed=3079761;
RA Basi G.S., Storti R.V.;
RT "Structure and DNA sequence of the tropomyosin I gene from Drosophila
RT melanogaster.";
RL J. Biol. Chem. 261:817-827(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [4]
RP REVISIONS.
RC STRAIN=Berkley;
RX MEDLINE=22426069; PubMed=12537572;
RA Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM EMBRYONIC).
RC STRAIN=Berkley; TISSUE=Embryo;
RX PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";

```
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
RN [6]
RP SEQUENCE OF 258-284 FROM N.A. (ISOFORM EMBRYONIC).
RX MEDLINE=85215579; PubMed=4000944.
RA Boardman M., Basi G.S., Storti R.V.;
RT "Multiple polyadenylation sites in a Drosophila tropomyosin gene are
RT used to generate functional mRNAs.";
RL Nucleic Acids Res. 13:1763-1776(1985).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Thoracic; Synonyms=127, t;
CC Isoid=P09491-1; Sequence=Displayed;
CC Name=Embryonic; Synonyms=129, A, B, e;
CC Isoid=P09491-2; Sequence=VSP_006616;
CC -1- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE
CC EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
CC -1- SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY.
CC -1- CAUTION: Ref.6 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: K02622; AAA28970.1; -
CC EMBL: K02623; AAA28971.1; -
CC EMBL: K02622; AAA28971.1; JOINED.
CC EMBL: K03277; AAA28973.1; -
CC EMBL: K03277; AAA28974.1; -
CC EMBL: AE003708; AAI13652.1; -
CC EMBL: AY071087; AAL48709.1; -
CC EMBL: X02220; CAA26142.1; ALT_SEQ.
CC PIR: A25624; A25624.
CC PIR: B25624; B25624.
CC FlyBase: FBgn0004117; Tm2.
CC InterPro: IPR000533; Tropomyosin.
CC Pfam: PF00261; Tropomyosin.1.
CC PRINTS: PR00194; TROPOMYOSIN.
CC PROSITE: PS00326; TROPOMYOSIN; 1.
CC Muscle protein; Coiled coil; Repeat; Alternative splicing;
CC Multigene family.
CC VARSPLIC 259 284 RLFNEKEKYKAICDDLQDTFAELTGY -> ELGINKORYKS
CC LADMDSTFAELAGY (in isoform Embryonic).
CC /FTid=VSP_006616.
CC M -> V (IN REF. 1).
CC Q -> L (IN REF. 1).
CC I -> T (IN REF. 1).
CC R -> D (IN REF. 1).
CC SEQUENCE 284 AA; 32981 MW; 07AD03FDD304EA5F CRC64;
CC -----
CC Query Match 26.1%; Score 6; DB 1; Length 284;
CC Best Local Similarity 100.0%; Pred. No. 38;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 18 EDELEV 23
CC Db 173 EDELEV 178
CC RESULT 11
CC PCD1_HUMAN STANDARD; PRT; 288 AA.
CC AC Q15116; Q00517;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Programmed cell death protein 1 precursor (Protein PD-1) (hpd-1).
CC GN PCD1 OR PDL.
CC OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95154844; PubMed=7851902;
RA Shinohara T., Taniwaki M., Ishida Y., Kawaich M., Honjo T.;
RT "Structure and chromosomal localization of the human PD-1 gene
RT (PCD1)".
RL Genomics 23:704-706(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97473511; PubMed=9332365;
RA Finger L.R., Pu J., Wasserman R., Vibhakhar R., Louie E., Hardy R.R.,
RA Burrows P.D., Billips L.D.;
RA Burrows P.D., Billips L.D.;
RT "The human PD-1 gene: complete cDNA, genomic organization, and
RT developmentally regulated expression in B cell progenitors.";
RL Gene 197:177-187(1997).
RN [3]
RP ERRATUM.
RA Finger L.R., Pu J., Wasserman R., Vibhakhar R., Louie E., Hardy R.R.,
RA Burrows P.D., Billips L.D.;
RL Gene 203:253-253(1997).
CC -1- FUNCTION: POSSIBLE CELL DEATH INDUCER, IN ASSOCIATION WITH
CC OTHER FACTORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DEVELOPMENTAL STAGE: INDUCED AT PROGRAMMED CELL DEATH.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L27440; AAC41700.1; -
CC EMBL: U64863; AAC51773.1; -
CC PIR: A55737; A55737.
CC HSP: P01607; IREI.
CC Genew: HGNC:8760; PDCD1.
CC MIN: 600244; -
CC GO: GO:0004871; F:signal transducer activity; TAS.
CC GO: GO:0006915; P:apoptosis; TAS.
CC GO: GO:0007275; P:development; TAS.
CC GO: GO:0006959; P:humoral immune response; TAS.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003006; Ig_MHC.
CC Pfam: PF00047; Ig_V.
CC SMART: SM00406; IgV; 1.
CC PROSITE: PS50835; IG_LIKE; 1.
CC Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; Apoptosis.
KW SIGNAL 1 20
FT CHAIN 21 288 PROGRAMMED CELL DEATH PROTEIN 1.
FT DOMAIN 21 170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 171 191 POTENTIAL.
FT DOMAIN 192 288 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 35 145 IG-LIKE V-TYPE.
FT DISULFID 54 123 POTENTIAL.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 38 38 F -> S (IN REF. 1).
FT CONFLICT 162 162 P -> S (IN REF. 1).
SQ SEQUENCE 288 AA; 31707 MW; A5210AD50C3046C7 CRC64;
CC -----
CC Query Match 26.1%; Score 6; DB 1; Length 288;
CC Best Local Similarity 100.0%; Pred. No. 39;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 6 LRPEDG 11
Db 277 LRPEDG 282

RESULT 12
OPSD_LIMPA STANDARD; PRT; 289 AA.
AC 042431;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Rhodopsin (Fragment).
GN RHO.
OS Limnocottus pallidus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidae; Abyssocottidae; Limnocottus.
OX NCBI_TaxID=61634;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98086781; PubMed=9417898;
RA Hunt D.M., Fitzgibbon J., Slobodyanyuk S.J., Bowmaker J.K.,
RA Dulai K.S.;
RT "Molecular evolution of the cottoid fish endemic to Lake Baikal
RT deduced from nuclear DNA evidence.";
RL Mol. Phylogenet. Evol. 8:415-422(1997).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES
CC VISION IN DIM LIGHT.
CC -!- PH: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC -----
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CC -----
DR EMBL: U97271; AAB61725.1; -.
DR HSSP: P02699; IBOJ.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR001760; Opsin.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PS00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_FL1; FALSE_NEG.
DR PROSITE: PS00262; G-PROTEIN_RECEPTOR_FL2; 1.
DR PROSITE: PS00238; OPSIN; 1.
KW Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.
FT NON_TER 1 1
FT DOMAIN <1 7 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 8 32 1 (POTENTIAL).
FT DOMAIN 33 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 69 2 (POTENTIAL).
FT DOMAIN 70 84 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 85 104 3 (POTENTIAL).
FT DOMAIN 105 123 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 124 147 4 (POTENTIAL).
FT DOMAIN 148 173 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 174 201 5 (POTENTIAL).
FT DOMAIN 202 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 247 6 (POTENTIAL).
FT DOMAIN 248 255 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 256 280 7 (POTENTIAL).

FT DOMAIN 281 >289 CYTOPLASMIC (POTENTIAL).
FT DISULFID 81 158 BY SIMILARITY.
FT BINDING 267 267 RETINAL CHROMOPHORE (BY SIMILARITY).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 289 289
SQ SEQUENCE 289 AA; 32715 MW; 160D08E17E5E1280 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LAGWLR 7
Db 143 LAGWLR 148

RESULT 13
PARB_HELPJ STANDARD; PRT; 290 AA.
AC 092K75;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable chromosome partitioning protein parB.
GN PARB OR JHP1066.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Gullid B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- FUNCTION: INVOLVED IN CHROMOSOME PARTITION. LOCALIZE TO BOTH POLES
CC OF THE PREDIVISIONAL CELL FOLLOWING COMPLETION OF DNA REPLICATION.
CC BINDS TO THE DNA ORIGIN OF REPLICATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARB FAMILY.
CC -----
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CC -----
DR EMBL: AE001534; AAD06646.1; -.
DR PIR: H71852; H71852.
DR InterPro: IPR004437; ParB_part.
DR InterPro: IPR003115; ParBc.
DR Pfam: PF02195; ParBc; 1.
DR SMART: SM00470; ParB; 1.
DR TIGRFAMs: TIGR00180; parB_part; 1.
KW Chromosome partition; DNA-binding; Complete proteome.
SQ SEQUENCE 290 AA; 33405 MW; 6709BA0547A55A4F CRC64;

Query Match 26.1%; Score 6; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 AEDELE 22
Db 245 AEDELE 250

RESULT 14
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MTSA_STRP8      STANDARD;      PRT;      310 AA.
ID  QBP280;
AC  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Metal ABC transporter substrate-binding lipoprotein precursor.
GN  MTSA OR SPYM18_0494.
OS  Streptococcus pyogenes (serotype M18).
OC  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC  Streptococcus
OX  NCBI_TaxID=186103;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-MGAS8232 / Serotype M18;
RX  MEDLINE=21927593; PubMed=11917108;
RA  Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA  Sylva G.B., Sturdevant D.E., Rickles S.M., Porcella S.F.,
RA  Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA  Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT  "Genome sequence and comparative microarray analysis of serotype M18
RT  group A Streptococcus strains associated with acute rheumatic fever
RT  outbreaks.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC  -1- FUNCTION: Part of an ATP-driven transport system for a metal; this
CC  protein has affinity for Zn(II), Fe(III) and Cu(II).
CC  -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC  -1- SIMILARITY: Belongs to the bacterial solute-binding protein family
CC  9. Lipoprotein receptor antigen (Lral) subfamily.
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CC  EMBL; AEO09988; AAL97215.1; -
CC  InterPro: IPR006128; Lipoprotein_4.
CC  InterPro: IPR006127; SBP_bac_9.
CC  Pfam; PF01297; SBP_bac_9; 1.
CC  PRINTS; PR00690; ADHESNFAMILY.
CC  PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
CC  Transport; Zinc transport; Iron transport; Copper; Membrane;
CC  Lipoprotein; Signal; Complete proteome.
CC  SIGNAL 1 20 PROBABLE.
CC  CHAIN 21 310 METAL ABC TRANSPORTER SUBSTRATE-
CC  BINDING LIPOPROTEIN.
CC  LIPID 21 21 N-ACYL DIGLYCERIDE (PROBABLE).
CC  SQ SEQUENCE. 310 AA; 34330 MW; 40F613659AAD1768 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 EDGGQA 14
      |||||
Db 94 EDGGQA 99

RESULT 15
MTSA_STRP8      STANDARD;      PRT;      310 AA.
ID  Q9A157; Q9RN17; Q9RNJ0;
AC  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Metal ABC transporter substrate-binding lipoprotein precursor.
GN  MTSA OR SPY0453 OR SPYM3_0318 OR SPS1539.
OS  Streptococcus pyogenes, and
OS  Streptococcus pyogenes (serotype M3).
OC  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

Streptococcus.
NCBI_TaxID=1314, 198466;
[1]
SEQUENCE FROM N.A., SEQUENCE OF 30-39, AND CHARACTERIZATION.
STRAIN-SF370 / ATCC 700294 / Serotype M1, and API / Serotype M1;
MEDLINE=20032372; PubMed=10564500;
Janutczyk R., Fallon J., Bjoerck L.;
"Identification and characterization of a Streptococcus pyogenes ABC
transporter with multiple specificity for metal cations.";
Mol. Microbiol. 34:596-606(1999).
[2]
SEQUENCE FROM N.A.
STRAIN-SF370 / ATCC 700294 / Serotype M1;
MEDLINE=21192684; PubMed=11296296;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
[3]
SEQUENCE FROM N.A.
STRAIN-MGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
emergence.";
Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
[4]
SEQUENCE FROM N.A.
STRAIN-SSI-1 / Serotype M3;
Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
Hayashi H., Hamada S.;
"The genome of invasive Streptococcus pyogenes; a comparative analysis
of S. pyogenes SSI-1, SF370 and MGAS8232.";
Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Part of an ATP-driven transport system for a metal; this
protein has affinity for Zn(II), Fe(III) and Cu(II).
-1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
-1- SIMILARITY: Belongs to the bacterial solute-binding protein family
9. Lipoprotein receptor antigen (Lral) subfamily.
-----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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-----
CC  EMBL; AF180520; AAD56936.1; -
CC  EMBL; AF180521; AAD56939.1; -
CC  EMBL; AE006505; AAK33468.1; -
CC  EMBL; AE014143; AAM78925.1; ALT_INIT.
CC  EMBL; AF005145; BAC64634.1; ALT_INIT.
CC  HSSP; P96116; 1TOA.
CC  InterPro: IPR006128; Lipoprotein_4.
CC  InterPro: IPR006127; SBP_bac_9.
CC  Pfam; PF01297; SBP_bac_9; 1.
CC  PRINTS; PR00690; ADHESNFAMILY.
CC  PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
CC  Transport; Zinc transport; Iron transport; Copper; Membrane;
CC  Lipoprotein; Signal; Complete proteome.
CC  SIGNAL 1 20 PROBABLE.
CC  CHAIN 21 310 METAL ABC TRANSPORTER SUBSTRATE-
CC  BINDING LIPOPROTEIN.
CC  LIPID 21 21 N-ACYL DIGLYCERIDE (PROBABLE).
CC  V 21 V -> A (IN STRAIN API).
CC  VARIANT 77

```

FT CONFLICT 26 26 T -> A (IN REF. 1).
 FT CONFLICT 30 30 K -> E (IN REF. 1).
 FT CONFLICT 44 44 A -> G (IN REF. 1).
 FT CONFLICT 49 50 AI -> VM (IN REF. 1).
 SQ SEQUENCE 310 AA: 34358 MW: B0F829EF1C72CADC CRC64;

 Query Match 26.1%; Score 6; DB 1; Length 310;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 9 EDGGOA 14
 Db 94 EDGGOA 99
 |||||

Search completed: September 11, 2003, 17:52:41
 Job time : 5.42781 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: September 11, 2003, 17:46:02 ; Search time 22.016 seconds
(without alignments)
269.586 Million cell updates/sec

Title: US-09-853-253-5
Perfect score: 23
Sequence: 1 ALAGWLRPEDGGQAEDELEV 23

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | | | |
|------------|-------|-------------|--------|-----------|---------------------|
| Result No. | Score | Query Match | Length | ID | Description |
| 1 | 20 | 87.0 | 117 | 08TAT9 | Q8TAT9 homo sapien |
| 2 | 11 | 47.8 | 117 | 08CH53 | Q8CH53 meriones un |
| 3 | 8 | 34.8 | 433 | 10 Q932V7 | Q932V7 arabidopsis |
| 4 | 8 | 34.8 | 433 | 10 Q8L7E4 | Q8L7E4 arabidopsis |
| 5 | 8 | 34.8 | 483 | 10 Q85529 | Q85529 arabidopsis |
| 6 | 7 | 30.4 | 103 | 16 Q9L063 | Q9L063 streptomyce |
| 7 | 7 | 30.4 | 313 | 2 Q8VP52 | Q8VP52 streptomyce |
| 8 | 7 | 30.4 | 433 | 16 Q8CNY4 | Q8CNY4 staphylococ |
| 9 | 7 | 30.4 | 887 | 16 Q8XY49 | Q8XY49 raltstonia s |
| 10 | 7 | 30.4 | 910 | 16 Q913F5 | Q913F5 pseudomonas |
| 11 | 7 | 30.4 | 2376 | 5 Q9V5J0 | Q9V5J0 drosophila |
| 12 | 7 | 30.4 | 2376 | 5 Q966V1 | Q966V1 drosophila |
| 13 | 6 | 26.1 | 69 | 16 Q9A542 | Q9A542 caulobacter |
| 14 | 6 | 26.1 | 88 | 17 Q8ZZR1 | Q8ZZR1 pyrobaculum |
| 15 | 6 | 26.1 | 98 | 5 P91785 | P91785 onchocerca |
| 16 | 6 | 26.1 | 100 | 16 Q8PBN4 | Q8PBN4 xanthomonas |

| | | | | | |
|----|---|------|-----|-----------|---------------------|
| 17 | 6 | 26.1 | 106 | 10 P93359 | P93359 nicotiana t |
| 18 | 6 | 26.1 | 110 | 2 087801 | 087801 pseudomonas |
| 19 | 6 | 26.1 | 112 | 5 Q26847 | Q26847 trypanosoma |
| 20 | 6 | 26.1 | 113 | 16 Q8G7N5 | Q8G7N5 blifidobacte |
| 21 | 6 | 26.1 | 117 | 12 Q65548 | Q65548 bovine herp |
| 22 | 6 | 26.1 | 129 | 4 Q43180 | Q43180 homo sapien |
| 23 | 6 | 26.1 | 133 | 13 Q8JFY6 | Q8JFY6 litoria cae |
| 24 | 6 | 26.1 | 137 | 4 Q8N8H9 | Q8N8H9 homo sapien |
| 25 | 6 | 26.1 | 138 | 16 Q9RD30 | Q9RD30 streptomyce |
| 26 | 6 | 26.1 | 142 | 16 Q8ZBU1 | Q8ZBU1 yersinia pe |
| 27 | 6 | 26.1 | 147 | 5 Q25622 | Q25622 onchocerca |
| 28 | 6 | 26.1 | 148 | 5 Q8WT59 | Q8WT59 onchocerca |
| 29 | 6 | 26.1 | 154 | 5 Q8WT58 | Q8WT58 onchocerca |
| 30 | 6 | 26.1 | 154 | 5 Q8WT56 | Q8WT56 litomosoid |
| 31 | 6 | 26.1 | 154 | 5 Q8WT57 | Q8WT57 onchocerca |
| 32 | 6 | 26.1 | 159 | 3 Q05697 | Q05697 saccharomyc |
| 33 | 6 | 26.1 | 159 | 4 Q8N9A4 | Q8N9A4 homo sapien |
| 34 | 6 | 26.1 | 161 | 10 Q9LWY4 | Q9LWY4 oryza sativ |
| 35 | 6 | 26.1 | 165 | 2 Q9RNJ3 | Q9RNJ3 zymomonas m |
| 36 | 6 | 26.1 | 165 | 16 Q8XXY6 | Q8XXY6 raltstonia s |
| 37 | 6 | 26.1 | 171 | 5 Q25624 | Q25624 onchocerca |
| 38 | 6 | 26.1 | 175 | 13 Q8JFY7 | Q8JFY7 litoria cae |
| 39 | 6 | 26.1 | 175 | 16 Q9KQ90 | Q9KQ90 vibrio chol |
| 40 | 6 | 26.1 | 177 | 11 Q8CIQ8 | Q8CIQ8 rattus norv |
| 41 | 6 | 26.1 | 178 | 5 Q25619 | Q25619 onchocerca |
| 42 | 6 | 26.1 | 178 | 5 Q8WZJ8 | Q8WZJ8 acanthochei |
| 43 | 6 | 26.1 | 178 | 16 Q98IM5 | Q98IM5 rhizobium l |
| 44 | 6 | 26.1 | 180 | 2 Q50344 | Q50344 lactobacilli |
| 45 | 6 | 26.1 | 186 | 5 Q9UIY0 | Q9UIY0 caenorhabdi |

ALIGNMENTS

RESULT 1
Q8TAT9 PRELIMINARY; PRT; 117 AA.
AC 08TAT9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Ghrelin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025791; AAH25791.1; -
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_assoc.1.
DR Pfam; PF04644; motilin_ghrelin.1.
SQ SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;
Query Match 87.0%; Score 20; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.4e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDGGQAEDE 20
|||||
DB 52 ALAGWLRPEDGGQAEDE 71
RESULT 2
Q8CH53 PRELIMINARY; PRT; 117 AA.
AC Q8CH53;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)

```

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AAO06965.1; -;
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 47.8%; Score 11; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GOAEGAEDELE 22
Db 63 GOAEGAEDELE 73

RESULT 3
Q932V7 PRELIMINARY; PRT; 433 AA.
ID Q932V7;
AC Q932V7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative RNA-binding protein LAHI.
GN AT4G32720
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene AT4g32720 (GI:7270219).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY056237; AAL07086.1; -;
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 433 AA; 48095 MW; E58EBAF51C35A8F7 CRC64;

Query Match 34.8%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAEDE 20
Db 287 QAEGAEDE 294

RESULT 4
Q8L7E4 PRELIMINARY; PRT; 433 AA.
ID Q8L7E4;
AC Q8L7E4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN AT4G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Shinn P., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
RA Theologis A., Davis R.W.;
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY136302; AAM96968.1; -;
DR EMBL; BT000396; AAN15715.1; -;
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 433 AA; 48126 MW; CFF611A29AA0318 CRC64;

Query Match 34.8%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAEDE 20
Db 287 QAEGAEDE 294

RESULT 5
O65529 PRELIMINARY; PRT; 483 AA.
ID O65529;
AC O65529;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 54.1 kDa protein.
GN F4D11.80 OR AT4G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoorge W., Hohseisel J.,
RA Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]

```

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RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoorge W., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.:
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022537; CAAL8589.1; -.
DR EMBL; AL161582; CAB79989.1; -.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 483 AA; 54125 MW; 20840B34A0BC94E2 CRC64;

Query Match 34.8%; Score 8; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAED 20
DB 302 QAEGAED 309
|||||||

RESULT 6
Q9L063
ID Q9L063 PRELIMINARY; PRT; 103 AA.
AC Q9L063:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein SC02791.
GN SC02791 OR SCCL05_22C
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939114; CAB87228.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 103 AA; 10639 MW; 9316F1F38C1BD492 CRC64;

Query Match 30.4%; Score 7; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAE 16
DB 48 DGGQAE 54
|||||||

RESULT 7
Q8Y49
ID Q8Y49 PRELIMINARY; PRT; 887 AA.

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Q8VP52
ID Q8VP52 PRELIMINARY; PRT; 313 AA.
AC Q8VP52:
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE LysR-like transcriptional activator Snpr.
OS Streptomyces sp. C5.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=45212;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C5;
RA DeSanti C.L., Strohl W.R.;
RT "Characterization of the Streptomyces sp. strain C5 snp locus and
RT development of an snp-derived expression vector family.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AY072041; AAL61992.1; -.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; Transcription; Transcription regulation.
SQ SEQUENCE 313 AA; 34258 MW; C907C8AF51C3FA13 CRC64;

Query Match 30.4%; Score 7; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
DB 103 ALAGWLR 109
|||||||

RESULT 8
Q8CNY4
ID Q8CNY4 PRELIMINARY; PRT; 433 AA.
AC Q8CNY4:
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Trigger factor.
GN SEI350.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
RA Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016748; AAO04949.1; -.
KW Complete proteome.
SQ SEQUENCE 433 AA; 48732 MW; FF2490AD097F437D CRC64;

Query Match 30.4%; Score 7; DB 16; Length 433;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAE 16
DB 180 DGGQAE 186
|||||||

RESULT 9
Q8XY49
ID Q8XY49 PRELIMINARY; PRT; 887 AA.

```

AC Q8XY49;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Probable phage-related tail transmembrane protein..
 GN RSC1914 OR R503483.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottiler P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502(2002).
 DR EMBL: AL646067; CAD15616.1; ..
 KW Complete proteome.
 SQ SEQUENCE 887 AA; 94105 MW; 9A8840E5362E740E CRC64;
 Query Match 30.4%; Score 7; DB 16; Length 887;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 QOAGAE 18
 Db 290 QOAGAE 296
 RESULT 10
 Q913F5 PRELIMINARY; PRT; 910 AA.
 ID Q913F5
 AC Q913F5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE Aconitate hydratase 1.
 GN ACNA OR PA1562.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Slover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RL Nature 406:959-964(2000).
 DR EMBL: AE004584; AAC04951.1; ..
 DR HSP; P20004; IACO.
 DR InterPro: IPR006249; Aconitase_1.
 DR InterPro: IPR000573; Aconitase_C.
 DR InterPro: IPR001030; Aconitase_N.
 DR Pfam: PF00330; aconitase; 1.
 DR Pfam: PF00694; Aconitase_C; 1.
 DR PRINTS: PR00415; ACONITASE.
 DR ProDom: PD000511; Aconitase_N; 1.
 DR TIGRFAMS: TIGR01341; aconitase_1; 1.
 DR PROSITE: PS00450; ACONITASE_1; 1.
 DR PROSITE: PS01244; ACONITASE_2; 1.

KW Complete proteome.
 SQ SEQUENCE 910 AA; 99147 MW; C65F23CDB6FA0E1C CRC64;
 Query Match 30.4%; Score 7; DB 16; Length 910;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLR 7
 Db 65 ALAGWLR 71
 RESULT 11
 Q9V5J0 PRELIMINARY; PRT; 2376 AA.
 ID Q9V5J0
 AC Q9V5J0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE CG18408 protein.
 GN REXIN OR CG3451 OR CG18408 OR CG18409.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkelley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottiler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mklukov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Gallie R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Bernan B., Carlson J.W., Celniker S.E.,
 RA Clump M., Brysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003830; AAF58816.2; -
 DR FlyBase: FBgn0033504; rexin.
 DR InterPro: IPR001452; SH3.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR ProDom: PD000066; SH3; 3.
 DR SMART: SM00326; SH3; 3.
 DR PROSITE: PS50002; SH3; 3.
 SQ SEQUENCE 2376 AA; 267666 MW; A5F2D0589B8B695C CRC64;
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 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 QAEGAEAD 19
 Db 37 QAEGAEAD 43
 RESULT 12
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 ID Q966V1
 AC Q966V1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Rexin L1.
 GN REXIN OR RXN OR CG3451 OR CG18408 OR CG18409.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidae; Drosophilidae; *Drosophila*.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamazaki H.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamazaki H., Willert K., Fish M., Nusse R.;
 RT "Drosophila Rexin, a Novel SH3 Adaptor Protein of Axin and Arrow that
 RT is Essential for Living in Late Stage Embryo.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: CONTAINS 3 SH3 DOMAINS.
 DR EMBL: AB053478; BAB62017.1; -
 DR FlyBase: FBgn0033504; rexin.
 DR InterPro: IPR002965; P-rich_extensn.
 DR IPfam: PF00018; SH3; 3.
 DR PRINTS: PR01217; PRICHEXTENS.
 DR ProDom: PD000066; SH3; 3.
 DR SMART: SM00326; SH3; 3.
 DR PROSITE: PS50002; SH3; 3.
 KW SH3 domain.
 SQ SEQUENCE 2376 AA; 267657 MW; 9C7BD6C7A705C888 CRC64;
 Query Match 30.4%; Score 7; DB 5; Length 2376;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 QAEGAEAD 19
 Db 37 QAEGAEAD 43
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 ID Q9A542
 AC Q9A542;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Cold-shock domain family protein.
 GN CC2623.
 OS *Caulobacter crescentus*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteraceae; *Caulobacter*.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of *Caulobacter crescentus*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
 DR EMBL: AE005930; AAK24591.1; -
 DR HSPF: F15277; IMJC.
 DR TIGR: CC2623; -
 DR InterPro: IPR002059; Cold_shock.
 DR Pfam: PF00313; CSD; 1.
 DR PRINTS: PR00050; COLDSHOCK.
 DR ProDom: PD000821; Cold_shock; 1.
 DR SMART: SM00357; Csp; 1.
 KW Activator; DNA-binding; Transcription regulation; Complete proteome.
 SQ SEQUENCE 69 AA; 7450 MW; 8EA80BE9EE56853C CRC64;
 Query Match 26.1%; Score 6; DB 16; Length 69;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 PEDGGQ 13
 Db 20 PEDGGQ 25
 RESULT 14
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 ID Q8ZZR1

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AC Q82ZRI;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PAE0124.
GN PAE0124.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009752; AAL62578.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 88 AA; 9492 MW; 22091651B45CADD1 CRC64;

Query Match 26.1%; Score 6; DB 17; Length 88;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
DB 45 ALAGWL 50

RESULT 15
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ID P91785 PRELIMINARY; PRT; 98 AA.
AC P91785;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Antigen maltose binding protein (Fragment).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94336252; PubMed=8058358;
RA Trenholme K.R., Tree T.I., Gillespie A.J., Guderian R., Maizels R.M.,
RA Bradley J.E.;
RT "Heterogeneity of IgG antibody responses to cloned Onchocerca volvulus
RT antigens in microfilaremia positive individuals from Esmeraldas
RT Province, Ecuador."
RL Parasite Immunol. 16:201-209(1994).
DR EMBL; S71371; AAC60510.2; -.
FT NON_TER 1
FT NON_TER 98
SQ SEQUENCE 98 AA; 11165 MW; 221BEFEFE14DC76 CRC64;

Query Match 26.1%; Score 6; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LRPEDG 11
DB 51 LRPEDG 56

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Search completed: September 11, 2003, 17:55:49
Job time : 23.016 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 : Search time 23.984 Seconds
(without alignments)
152.215 Million cell updates/sec

Title: US-09-853-253-5

Perfect score: 121

Sequence: 1 ALAGWLRPEDGGQAGAEDELEV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 121 | 100.0 | 23 | AAE23840 | Human zsig33-linker |
| 2 | 121 | 100.0 | 23 | AAE23841 | Human zsig33-linker |
| 3 | 121 | 100.0 | 23 | AAE15885 | Human zsig33-linker |
| 4 | 121 | 100.0 | 23 | AAE15886 | Human zsig33-linker |
| 5 | 121 | 100.0 | 24 | AAE23839 | Human zsig33-linker |
| 6 | 121 | 100.0 | 24 | AAE15884 | Human zsig33-linker |
| 7 | 121 | 100.0 | 91 | AAE33410 | Human exon 3-delet |
| 8 | 121 | 100.0 | 116 | AAE60517 | Human des-Gln14-gh |
| 9 | 121 | 100.0 | 117 | AAW87991 | Protein designated |

| | | | | | | |
|----|------|-------|------|----|----------|---------------------|
| 10 | 121 | 100.0 | 117 | 21 | AAV87236 | Human signal pepti |
| 11 | 121 | 100.0 | 117 | 22 | AAW38890 | Human polypeptide |
| 12 | 121 | 100.0 | 117 | 22 | AAE62649 | Human zsig33 poly |
| 13 | 121 | 100.0 | 117 | 22 | AAE20101 | Human zsig33 protei |
| 14 | 121 | 100.0 | 117 | 22 | AAE60511 | Human ghrelin prep |
| 15 | 121 | 100.0 | 117 | 23 | ABW78319 | Amino acid sequenc |
| 16 | 121 | 100.0 | 117 | 23 | AAE23838 | Human zsig33 prote |
| 17 | 121 | 100.0 | 117 | 23 | AAE15883 | Human zsig33 prote |
| 18 | 121 | 100.0 | 117 | 24 | ABW66790 | Human PRO polypept |
| 19 | 121 | 100.0 | 117 | 24 | ABW67066 | Human secreted/tr |
| 20 | 121 | 100.0 | 117 | 24 | ABW59871 | Novel secreted and |
| 21 | 121 | 100.0 | 117 | 24 | ABU59124 | Novel human secret |
| 22 | 121 | 100.0 | 117 | 24 | ABU59271 | Human secreted/tr |
| 23 | 121 | 100.0 | 117 | 24 | ABU59420 | Novel human secret |
| 24 | 121 | 100.0 | 117 | 24 | ABU60555 | Human secreted/tr |
| 25 | 121 | 100.0 | 117 | 24 | ABU58046 | Human PRO polypept |
| 26 | 121 | 100.0 | 117 | 24 | ABU58977 | Human secreted/tr |
| 27 | 121 | 100.0 | 117 | 24 | AAE33409 | Human preproghreli |
| 28 | 121 | 100.0 | 117 | 24 | ABU13937 | Human PRO1066 poly |
| 29 | 121 | 100.0 | 117 | 24 | ABU10892 | Human PRO polypept |
| 30 | 121 | 100.0 | 118 | 21 | AAV66708 | Membrane-bound pro |
| 31 | 121 | 100.0 | 118 | 22 | AAU12392 | Human PRO1066 poly |
| 32 | 121 | 100.0 | 118 | 22 | AAE65231 | Human PRO1066 (UNQ |
| 33 | 121 | 100.0 | 126 | 22 | AAW40676 | Human polypeptide |
| 34 | 90 | 74.4 | 90 | 23 | ABP08975 | Human OREF protein |
| 35 | 90 | 74.4 | 116 | 22 | AAE60516 | Rat des-Gln14-ghre |
| 36 | 90 | 74.4 | 117 | 22 | AAE60510 | Rat ghrelin prepro |
| 37 | 87 | 71.9 | 117 | 22 | AAE60521 | Porcine des-Gln14- |
| 38 | 87 | 71.9 | 118 | 22 | AAE60520 | Porcine ghrelin pr |
| 39 | 62.5 | 51.7 | 89 | 22 | AAE60523 | Bovine ghrelin pre |
| 40 | 54 | 44.6 | 200 | 24 | ABP58240 | Xenopus laevis nuc |
| 41 | 50 | 41.3 | 653 | 17 | AAE98903 | Murine AP1. Mus |
| 42 | 48 | 39.7 | 82 | 22 | AAE73526 | Human colon cancer |
| 43 | 48 | 39.7 | 287 | 22 | ABE15575 | Novel human diagno |
| 44 | 48 | 39.7 | 570 | 22 | ABE20671 | Novel human diagno |
| 45 | 48 | 39.7 | 2836 | 22 | ABE62719 | Drosophila melanog |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | AAE23840 |
| ID | AAE23840 standard; peptide; 23 AA. |
| AC | AAE23840; |
| XX | |
| DT | 10-SEP-2002 (first entry) |
| DE | Human zsig33-linker peptide #2. |
| XX | |
| KW | Human; zsig33-like peptide; gastric contractility; nutrient uptake; |
| KW | growth hormone; digestive enzyme; restorative therapy; gene therapy; |
| KW | protein therapy; gastrointestinal; endocrine; anabolic. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | US2002055156-A1. |
| XX | |
| PD | 09-MAY-2002. |
| XX | |
| PF | 10-MAY-2001; 2001US-0853253. |
| XX | |
| PR | 11-MAY-2000; 2000US-203300P. |
| XX | |
| PA | {JASP/} JASPERS S R. |
| PA | {SHEP/} SHEPPARD P O. |
| PA | {DEIS/} DEISHER T A. |
| PA | {BISH/} BISHOP P D. |
| XX | |
| PI | Jaspers SR, Sheppard PO, Deisher TA, Bishop PD; |
| XX | |
| DR | WPI; 2002-443750/47. |

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones -
XX
XX Claim 1; Page 28; 34pp; English.
XX
CC The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 121; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALAGWLRPEDGGQAEDELEV 23
DB 1 ALAGWLRPEDGGQAEDELEV 23

RESULT 2
AAE23841
ID AAE23841 standard; peptide; 23 AA.
XX
AC AAE23841;
XX
XX 10-SEP-2002 (first entry)
XX
XX Human zsig33-linker peptide #3.
XX
XX Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.
XX
XX Homo sapiens.
OS
XX US2002055156-A1.
PN
XX 09-MAY-2002.
XX
XX 10-MAY-2001; 2001US-0853253.
XX
XX 11-MAY-2000; 2000US-203300P.
XX
XX (JASP/) JASPERS S R.
PA (SHEP/) SHEPPARD P O.
PA (DEIS/) DEISHER T A.
PA (BISH/) BISHOP P D.
XX
XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
PI WPI; 2002-443750/47.
XX
XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

PT contractility, nutrient uptake, growth hormones and/or secretion of
XX digestive/pancreatic enzymes and hormones -
XX Claim 1; Page 28; 34pp; English.
XX
CC The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 121; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALAGWLRPEDGGQAEDELEV 23
DB 1 ALAGWLRPEDGGQAEDELEV 23

RESULT 3
AAE15885
ID AAE15885 standard; peptide; 23 AA.
XX
AC AAE15885;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human zsig33-linker peptide #2.
XX
XX Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycemic;
KW adsorption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33-linker peptide.
XX
XX Homo sapiens.
OS
XX WO200187933-A2.
PN
XX 22-NOV-2001.
XX
XX 10-MAY-2001; 2001WO-US15091.
PF
XX 11-MAY-2000; 2000US-0569271.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
PI WPI; 2002-082982/11.
XX
XX N-PSDB; AAD25760.
XX
XX New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and
PT treating gastrointestinal and growth related diseases, comprises

PN W09842840-A1.
 XX 01-OCT-1998.
 XX 23-MAR-1998; 98WO-US05620.
 XX 24-MAR-1997; 97US-0822897.
 XX 24-MAR-1997; 97US-0041102.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Delsher TA, Sheppard PO;
 PI WPI: 1999-070071/06.
 DR N-PSDB: AAX04550.
 XX Human polypeptide having homology to motilin, zsig33 - useful e.g.
 PT to treat gastrointestinal motility disorders, obesity etc. and to
 PT identify antagonists to treat gastrointestinal hypermotility
 XX Claim 13; Page 55-56; 69pp; English.
 XX The present sequence represents a protein designated zsig33. The nucleic
 CC acids are strongly expressed in stomach tissue. The polypeptide (or
 CC allelic variants/orthologs) can be used to stimulate gastric motility,
 CC measured as increased transit time or gastric emptying of an ingested
 CC substance in mammals. The products are used to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes/acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
 CC absorption regulation. Zsig33 polypeptides may also be important
 CC neurologically, since the family of gut-brain peptides to which the
 CC homologous protein motilin belongs has been associated with neurological
 CC or CNS functions. They may therefore be used e.g. to regulate satiety
 CC or treat obesity and other metabolic disorders where neurological
 CC feedback modulates nutritional absorption. They are useful to identify
 CC zsig33 agonists, antagonists and ligands and to produce antibodies.
 XX SQ Sequence 117 AA;
 Query Match 100.0%; Score 121; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. NO. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 |||||
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 10
 AAY87236
 ID AAY87236 standard; Protein; 117 AA.
 XX AC AAY87236;
 XX 11-MAY-2000 (first entry)
 XX Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
 XX Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's disease; ovulatory defect;
 KW muscular dystrophy.
 XX Homo sapiens.
 OS W0200000610-A2.
 XX PN
 XX

PD 06-JAN-2000.
 XX 25-JUN-1999; 99WO-US14484.
 XX 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX (INCY-) INCYTE PHARM INC.
 PA Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 XX Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 PI WPI: 2000-160673/14.
 DR N-PSDB: AAZ98121.
 XX New human signal peptide-containing proteins useful in treatment,
 XX prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease
 PT Claim 1; Page 168-169; 327pp; English.
 PS AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 XX human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
 CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can
 CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPP. Antagonists of
 CC HSPP are used to treat or prevent disorders associated with increased
 CC activity or function of HSPP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
 CC nucleic acids can be used for the recombinant production of HSPP, for
 CC detecting HSPP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPP-related diseases (in usual immunoassays) as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPP
 CC from natural sources.
 XX SQ Sequence 117 AA;
 Query Match 100.0%; Score 121; DB 21; Length 117;
 Best Local Similarity 100.0%; Pred. NO. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 |||||
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 11
 AAM38890
 ID AAM38890 standard; Protein; 117 AA.
 XX AC AAM38890;
 XX 22-OCT-2001 (first entry)
 XX Human polypeptide SEQ ID NO 2035.
 DE Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 XX peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

PN 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

PF 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI: 2001-442253/47.

DR N-PSDB; AAI58046.

XX Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -

PS Example 3; SEQ ID NO 2035; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and

CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: Immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed

CC specification.

XX Sequence 117 AA;

KW amytrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

PN 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

PF 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI: 2001-442253/47.

DR N-PSDB; AAI58046.

XX Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -

PS Example 3; SEQ ID NO 2035; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and

CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: Immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed

CC specification.

XX Sequence 117 AA;

KW zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
 KW G-protein coupled receptor.

XX Homo sapiens.

OS Key

XX Location/Qualifiers

FT 24..37

FT /note= "specifically claimed fragment that binds to

XX the GHS-R"

XX WO200138355-A2.

XX 31-MAY-2001.

PF 22-NOV-2000; 2000WO-US32074.

XX 22-NOV-1999; 99US-0166765.

PR (ZYMO) ZYMOGENETICS INC.

PA Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

XX WPI: 2001-355879/37.

DR N-PSDB; AAF83678.

XX Forming reversible peptide receptor complex for purifying cell and

PT peptides, stimulating signal transduction and modulating hormone

PT secretion, involves contacting a receptor with zsig33 polypeptide -

XX Claim 1; Page 93-94; 111pp; English.

PS The invention relates to a method of forming a reversible peptide-

XX receptor complex that involves providing an immobilized receptor, and

CC contacting the receptor with a zsig33 peptide (comprising residues 24-37

CC of AAB62649), where the receptor binds to the zsig33 peptide. The method

CC is useful for purifying cells, purifying a peptide, stimulating signal

CC transduction in a cell expressing a receptor. It is also useful for

CC modulating secretion of hormones, neural development and/or utilization,

CC gastric contractility, nutrient uptake, secretion of digestive and

CC pancreatic enzymes and hormones, secretion of insulin-like growth factor

CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth

CC hormone secretion in a mammal having a disease associated with abnormal

CC levels of growth hormone, such as osteoporosis, bone repair, bone

CC remodeling, low osteoblast levels, cartilage repair and remodeling,

CC skeletal dysplasia, immune suppression, obesity, growth retardation,

CC protein catabolic responses after surgery, cachexia, protein loss,

CC dwarfism, wound healing and ovulation induction, treating a mammal having

CC a metabolic disorder requiring neurological feedback, such as satiety

CC regulation, glucose absorption and metabolism and neuropathy-associated

CC gastrointestinal disorders, and stimulating glucose-induced insulin

CC release in a mammal. The present sequence represents the human zsig33

XX polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.

XX Sequence 117 AA;

XX Query Match 100.0%; Score 121; DB 22; Length 117;

XX Best Local Similarity 100.0%; Pred. No. 2.2e-10;

XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23

DB 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 13

AAB20101

ID AAB20101 standard; Protein; 117 AA.

XX AC AAB20101;

XX

| Key | Location/Qualifiers |
|---|---------------------|
| 1..23 | |
| /note= "signal peptide" | |
| 24..119 | |
| /note= "mature protein" | |
| US6420521-B1. | |
| 16-JUL-2002. | |
| 30-JUN-2000; 2000US-0608810. | |
| 30-JUN-1999; 99US-141592p. | |
| (ZYMO) ZYMOGENETICS INC. | |
| Sheppard PO, Jaspers SR, Deisher TA, Bishop PD; | |
| WPI; 2002-634794/68. | |
| N-PSDB; ABV72214. | |
| New Short Gastrointestinal Peptide, which has homology to motilin, useful for preventing, diagnosing and treating gastrointestinal disorders | |
| Disclosure; Columns 39-40; 23pp; English. | |
| The present sequence represents human zsig33. The specification describes a short gastrointestinal peptide (SGIP), which is derived from zsig33. SGIP has homology to motilin. The SGIP peptide may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SGIP expression. For example, SGIP may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of SGIP by expressing inactive proteins or to supplement the patients own production of SGIP. SGIP may also be used as an antigen in the production of antibodies against SGIP and in assays to identify modulators of SGIP expression and activity. The anti-SGIP antibodies, agonists and antagonists may also be used to regulate expression and activity. The anti-SGIP antibodies may also be used as diagnostic agents for detecting the presence of SGIP in samples. | |
| Sequence 117 AA; | |
| Query Match 100.0%; Score 121; DB 23; Length 117; | |
| Best Local Similarity 100.0%; Pred. No. 2.2e-10; | |
| Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| 1 ALAGWLRPDGGQAGAEDELEV 23 | |
| 52 ALAGWLRPDGGQAGAEDELEV 74 | |

Search completed: September 11, 2003, 17:25:03
Job time : 24.984 secs

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 6.14973 Seconds
(without alignments)
158.243 Million cell updates/sec

Title: US-09-853-253-5

Perfect score: 121

Sequence: 1 ALAGWLRPEDGGQAGAEDELEV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 121 | 100.0 | 117 | 3 | US-09-046-479-2 |
| 2 | 121 | 100.0 | 117 | 4 | US-08-822-897C-2 |
| 3 | 121 | 100.0 | 117 | 4 | US-09-608-810A-4 |
| 4 | 121 | 100.0 | 117 | 4 | US-09-996-243-268 |
| 5 | 52 | 43.0 | 233 | 4 | US-09-252-991A-27758 |
| 6 | 50 | 41.3 | 634 | 1 | US-08-339-152A-17 |
| 7 | 50 | 41.3 | 653 | 1 | US-08-339-152A-16 |
| 8 | 50 | 41.3 | 653 | 2 | US-08-007-999B-3 |
| 9 | 50 | 41.3 | 653 | 2 | US-08-689-276A-3 |
| 10 | 49 | 40.5 | 139 | 2 | US-08-039-198B-10 |
| 11 | 48 | 39.7 | 518 | 4 | US-09-252-991A-23604 |
| 12 | 47 | 38.8 | 283 | 4 | US-09-252-991A-29700 |
| 13 | 46 | 38.0 | 341 | 4 | US-09-252-991A-27327 |
| 14 | 46 | 38.0 | 428 | 4 | US-09-252-991A-19723 |
| 15 | 46 | 38.0 | 517 | 4 | US-09-252-991A-25921 |
| 16 | 46 | 38.0 | 1049 | 4 | US-09-252-991A-18853 |
| 17 | 45.5 | 37.6 | 579 | 3 | US-08-704-711A-1 |
| 18 | 45.5 | 37.6 | 579 | 4 | US-09-521-220-1 |
| 19 | 45.5 | 37.6 | 582 | 3 | US-08-704-711A-2 |
| 20 | 45.5 | 37.6 | 582 | 3 | US-08-448-489-1 |
| 21 | 45.5 | 37.6 | 582 | 3 | US-09-211-704A-9 |
| 22 | 45.5 | 37.6 | 582 | 4 | US-09-521-220-2 |
| 23 | 45.5 | 37.6 | 582 | 4 | US-09-391-104-28 |
| 24 | 45.5 | 37.6 | 591 | 2 | US-08-889-402-1 |
| 25 | 45 | 37.2 | 174 | 4 | US-09-252-991A-18600 |
| 26 | 45 | 37.2 | 494 | 1 | US-08-464-340A-4 |
| 27 | 45 | 37.2 | 494 | 5 | PCT-US94-08449A-4 |

| | | | | | | |
|----|----|------|------|---|----------------------|-------------------|
| 28 | 45 | 37.2 | 1059 | 4 | US-09-394-272-5 | Sequence 5, Appli |
| 29 | 44 | 36.4 | 405 | 4 | US-09-252-991A-20326 | Sequence 20326, A |
| 30 | 43 | 35.5 | 118 | 3 | US-08-482-304-12 | Sequence 12, Appl |
| 31 | 43 | 35.5 | 118 | 3 | US-08-483-474-12 | Sequence 12, Appl |
| 32 | 43 | 35.5 | 140 | 3 | US-08-483-304-9 | Sequence 9, Appli |
| 33 | 43 | 35.5 | 140 | 3 | US-08-483-474-9 | Sequence 9, Appli |
| 34 | 43 | 35.5 | 162 | 4 | US-09-252-991A-24838 | Sequence 24838, A |
| 35 | 43 | 35.5 | 191 | 4 | US-09-252-991A-21437 | Sequence 21437, A |
| 36 | 43 | 35.5 | 212 | 3 | US-09-154-083-4 | Sequence 4, Appli |
| 37 | 43 | 35.5 | 247 | 4 | US-09-252-991A-27419 | Sequence 27419, A |
| 38 | 43 | 35.5 | 268 | 4 | US-09-252-991A-27950 | Sequence 27950, A |
| 39 | 43 | 35.5 | 311 | 4 | US-09-252-991A-28068 | Sequence 28068, A |
| 40 | 43 | 35.5 | 380 | 3 | US-08-765-743-2 | Sequence 2, Appli |
| 41 | 43 | 35.5 | 380 | 4 | US-09-341-446B-2 | Sequence 2, Appli |
| 42 | 43 | 35.5 | 424 | 4 | US-09-341-446B-6 | Sequence 6, Appli |
| 43 | 43 | 35.5 | 424 | 4 | US-09-341-446B-8 | Sequence 8, Appli |
| 44 | 43 | 35.5 | 427 | 4 | US-09-341-446B-4 | Sequence 4, Appli |
| 45 | 43 | 35.5 | 450 | 4 | US-09-252-991A-25523 | Sequence 25523, A |

ALIGNMENTS

RESULT 1

US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 100.0%; Score 121; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches .23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGADELEV 23
|||||
Db 52 ALAGWLRPEDGGGAEGADELEV 74

RESULT 2

US-08-822-897C-2
; Sequence 2, Application US/08822897C
; Patent No. 6380158
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,897C
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-822-897C-2

Query Match 100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGADELEV 23
|||||
Db 52 ALAGWLRPEDGGGAEGADELEV 74

RESULT 3

US-09-608-810A-4
; Sequence 4, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608,810A
; CURRENT FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4

Query Match 100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGADELEV 23
|||||
Db 52 ALAGWLRPEDGGGAEGADELEV 74

RESULT 4

US-09-996-243-268
; Sequence 268, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC13
; CURRENT APPLICATION NUMBER: US/09/996,243
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 5

US-09-252-991A-27758
; Sequence 27758, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27758
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27758

Query Match 43.0%; Score 52; DB 4; Length 233;
Best Local Similarity 72.7%; Pred. No. 2.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GWRPDDGQA 14
|||||
Db 203 GWRPDDGSA 213

RESULT 6

US-08-339-152A-17
; Sequence 17, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-152A-16

Query Match 41.3%; Score 50; DB 1; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGOAEGAEDELEV 23
|||||
Db 233 GGOAEGAEDELEV 245

; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-339-152A-17

Query Match 41.3%; Score 50; DB 1; Length 634;
Best Local Similarity 76.9%; Pred. No. 16;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGOAEGAEDELEV 23
|||||
Db 213 GGOAEGAEDELEV 225

RESULT 7

US-08-339-152A-16
; Sequence 16, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-152A-16

Query Match 41.3%; Score 50; DB 1; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGOAEGAEDELEV 23
|||||
Db 233 GGOAEGAEDELEV 245

RESULT 8
US-08-007-999B-3
; Sequence 3, Application US/08007999B
; Patent No. 5851787
; GENERAL INFORMATION:
; APPLICANT: Wasco, Wilma
; APPLICANT: Bupp, Keith
; APPLICANT: Magendantz, Margaret
; APPLICANT: Tanzi, Rudolph
; APPLICANT: Solomon, Frank
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/007,999B
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,642
; FILING DATE: 20-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,022
; FILING DATE: 17-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: 0609.3520002/JAG/GKT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2571
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-007-999B-3
Query Match 41.3%; Score 50; DB 2; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 11 GGQAGGADELEV 23
||:|||||
Db 233 GGRAEGGEDEEV 245
RESULT 9
US-08-689-276A-3
; Sequence 3, Application US/08689276A
; Patent No. 5891991
; GENERAL INFORMATION:
; APPLICANT: Wasco, Wilma
; APPLICANT: Bupp, Keith
; APPLICANT: Magendantz, Margaret
; APPLICANT: Tanzi, Rudolph
; APPLICANT: Solomon, Frank
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,276A
; FILING DATE: 06-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/007,999
; FILING DATE: 21-JAN-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,642
; FILING DATE: 20-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,022
; FILING DATE: 17-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.3520003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2571
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-689-276A-3
Query Match 41.3%; Score 50; DB 2; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 11 GGQAGGADELEV 23
||:|||||
Db 233 GGRAEGGEDEEV 245
RESULT 10
US-08-039-198B-10
; Sequence 10, Application US/08039198B
; Patent No. 5858725
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PREPARATION OF CHIMAERIC ANTIBODIES
; TITLE OF INVENTION: RECOMBINANT PCR STRATEGY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/039,198B
; FILING DATE: 29-JUL-1993
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01744
; FILING DATE: 08-OCT-91
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-86
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-039-198B-10

Query Match 40.5%; Score 49; DB 2; Length 139;
Best Local Similarity 61.5%; Pred. No. 4.4;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGQAEQ 16
||: ||||| |
Db 68 GWIDPEDGGTKYG 80

RESULT 11

US-09-252-991A-23604
; Sequence 23604, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23604
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23604

Query Match 39.7%; Score 48; DB 4; Length 518;
Best Local Similarity 47.4%; Pred. No. 26;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 3 AGWLRPEDGGQAEQDEL 21
||: ||| | |
Db 412 AGWAQPEPGCGGAAERL 430

RESULT 12

US-09-252-991A-29700
; Sequence 29700, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29700
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29700

Query Match 38.8%; Score 47; DB 4; Length 283;
Best Local Similarity 58.8%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 AGWLRPEDGGQAEQ 19
| ||||| |
Db 86 AAGLRQEDGADGTGAED 102

RESULT 13

US-09-252-991A-27327
; Sequence 27327, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27327
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27327

Query Match 38.0%; Score 46; DB 4; Length 341;
Best Local Similarity 52.4%; Pred. No. 33;
Matches 11; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

Qy 7 RPEDGGQAEQAE---DELEV 23
: || ||| | |
Db 181 QPEOGGQGEHAQADRPDPLEV 201

RESULT 14

US-09-252-991A-19723
; Sequence 19723, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19723
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19723

Query Match 38.0%; Score 46; DB 4; Length 428;
Best Local Similarity 55.0%; Pred. No. 42;
Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQGAEGAEDEL 21
 || | || | : | || |
 Db 293 LALWSLPEDPRPADWADEL 312

RESULT 15

US-09-252-991A-25921
 ; Sequence 25921, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25921
 ; LENGTH: 517
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25921

Query Match 38.0%; Score 46; DB 4; Length 517;
 Best Local Similarity 47.6%; Pred. No. 52;
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQGAEGAEDEL 22
 || | | | | : | | : | :
 Db 338 LAGQLDPHPGIAOGPHQQLQ 358

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:26:32 ; Search time 14.0214 Seconds
(without alignments)
239.348 Million cell updates/sec

Title: US-09-853-253-5

Perfect score: 121

Sequence: 1 ALAGWLRPDGGQAGAEDELEV 23

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Gapop 10.0 , Gapext 0.5

Searched: 541936 segs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------------|-------------------|
| 1 | 121 | 100.0 | 23 | US-09-853-253-5 | Sequence 5, Appli |
| 2 | 121 | 100.0 | 23 | US-09-853-253-6 | Sequence 6, Appli |
| 3 | 121 | 100.0 | 24 | US-09-853-253-4 | Sequence 4, Appli |
| 4 | 121 | 100.0 | 117 | US-09-794-987-2 | Sequence 2, Appli |
| 5 | 121 | 100.0 | 117 | US-09-853-253-2 | Sequence 2, Appli |
| 6 | 121 | 100.0 | 117 | US-09-989-723-268 | Sequence 268, App |
| 7 | 121 | 100.0 | 117 | US-09-989-723-268 | Sequence 268, App |
| 8 | 121 | 100.0 | 117 | US-09-989-279-268 | Sequence 268, App |
| 9 | 121 | 100.0 | 117 | US-09-989-727-268 | Sequence 268, App |
| 10 | 121 | 100.0 | 117 | US-09-989-731-268 | Sequence 268, App |
| 11 | 121 | 100.0 | 117 | US-09-989-732-268 | Sequence 268, App |
| 12 | 121 | 100.0 | 117 | US-09-991-073-268 | Sequence 268, App |
| 13 | 121 | 100.0 | 117 | US-09-990-442-268 | Sequence 268, App |
| 14 | 121 | 100.0 | 117 | US-09-991-163-268 | Sequence 268, App |
| 15 | 121 | 100.0 | 117 | US-09-993-604-268 | Sequence 268, App |

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| 16 | 121 | 100.0 | 117 | 10 | US-09-990-456-268 | Sequence 268, App |
| 17 | 121 | 100.0 | 117 | 10 | US-09-989-721-268 | Sequence 268, App |
| 18 | 121 | 100.0 | 117 | 10 | US-09-992-598-268 | Sequence 268, App |
| 19 | 121 | 100.0 | 117 | 10 | US-09-989-293A-268 | Sequence 268, App |
| 20 | 121 | 100.0 | 117 | 10 | US-09-989-735-268 | Sequence 268, App |
| 21 | 121 | 100.0 | 117 | 10 | US-09-990-444-268 | Sequence 268, App |
| 22 | 121 | 100.0 | 117 | 10 | US-09-991-181-268 | Sequence 268, App |
| 23 | 121 | 100.0 | 117 | 10 | US-09-989-730-268 | Sequence 268, App |
| 24 | 121 | 100.0 | 117 | 10 | US-09-990-436-268 | Sequence 268, App |
| 25 | 121 | 100.0 | 117 | 10 | US-09-993-687-268 | Sequence 268, App |
| 26 | 121 | 100.0 | 117 | 11 | US-09-989-734-268 | Sequence 268, App |
| 27 | 121 | 100.0 | 117 | 11 | US-09-997-653-268 | Sequence 268, App |
| 28 | 121 | 100.0 | 117 | 11 | US-09-993-667-268 | Sequence 268, App |
| 29 | 121 | 100.0 | 117 | 11 | US-09-997-428-268 | Sequence 268, App |
| 30 | 121 | 100.0 | 117 | 11 | US-09-997-666-268 | Sequence 268, App |
| 31 | 121 | 100.0 | 117 | 11 | US-09-990-438-268 | Sequence 268, App |
| 32 | 121 | 100.0 | 117 | 11 | US-09-990-562-268 | Sequence 268, App |
| 33 | 121 | 100.0 | 117 | 11 | US-09-990-711-268 | Sequence 268, App |
| 34 | 121 | 100.0 | 117 | 11 | US-09-989-726-268 | Sequence 268, App |
| 35 | 121 | 100.0 | 117 | 11 | US-09-998-156-268 | Sequence 268, App |
| 36 | 121 | 100.0 | 117 | 11 | US-09-990-437-268 | Sequence 268, App |
| 37 | 121 | 100.0 | 117 | 11 | US-09-991-157-268 | Sequence 268, App |
| 38 | 121 | 100.0 | 117 | 11 | US-09-997-514-268 | Sequence 268, App |
| 39 | 121 | 100.0 | 117 | 11 | US-09-997-573-268 | Sequence 268, App |
| 40 | 121 | 100.0 | 117 | 11 | US-09-991-172-268 | Sequence 268, App |
| 41 | 121 | 100.0 | 117 | 11 | US-09-990-726-268 | Sequence 268, App |
| 42 | 121 | 100.0 | 117 | 11 | US-09-997-559-268 | Sequence 268, App |
| 43 | 121 | 100.0 | 117 | 11 | US-09-997-601-268 | Sequence 268, App |
| 44 | 121 | 100.0 | 117 | 11 | US-09-990-443-268 | Sequence 268, App |
| 45 | 121 | 100.0 | 117 | 11 | US-09-991-854-268 | Sequence 268, App |

ALIGNMENTS

RESULT 1
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; Sequence 5, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-5

Query Match 100.0%; Score 121; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
DB 1 ALAGWLRPDGGQAGAEDELEV 23

RESULT 2
US-09-853-253-6
; Sequence 6, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN

Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 6

US-09-989-722-268

Sequence 268, Application US/09989722

Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC63

CURRENT APPLICATION NUMBER: US/09/989,722

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

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PRIOR APPLICATION NUMBER: 60/083322

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PRIOR FILING DATE: 1998-06-03

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 52 ALAGWLRLPDGGGAEGAEDELEV 74
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; Sequence 268, Application US/09989723
; Patent No. US20020072092A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLG62
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US/09/989,723
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
DB 52 ALAGWLRPEDGGQAGAEDELEV 74
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RESULT 8
US-09-989-279-268
; Sequence 268, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGADELEV 23
Db 52 ALAGWLRPEDGGGAEGADELEV 74

RESULT 9

US-09-989-727-268

Sequence 268, Application US/09989727

Patent No. US20020072497A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
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Query Match 100.0%; Score 121; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09; Mismatches 0; Indels 0; Gaps 0; Matches 23; Conservative 0;

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 Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 10

US-09-989-731-268
 ; Sequence 268, Application US/09989731
 ; Patent No. US20020103125A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
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 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC70
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Qy 1 ALAGWLRPDGGGAEGAEDELEV 23
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RESULT 11

US-09-989-732-268
 ; Sequence 268, Application US/09989732
 ; Patent No. US20020123463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
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 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
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 ; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730P1C57

; CURRENT APPLICATION NUMBER: US/09/989,732
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; PRIOR FILING DATE: 1998-07-01
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 121; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09; Mismatches 0; Caps 0;

Matches 23; Conservative 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23

Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 12

US-09-991-073-268

Sequence 268, Application US/09991073

Patent No. US20020127576A1

GENERAL INFORMATION:

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; APPLICANT: ASHENAZI, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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[illegible]

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Query Match          100.0%; Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ALAGWLRPDGQGAEGADELVEV 23
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Db 52 ALAGWLRPDGQGAEGADELVEV 74

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RESULT 13

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US-09-990-442-268
Sequence 268, Application US/09990442
Patent No. US20020132252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC8
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. NO. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGMLRPEDGGQGAEGAEDEV 23
Db 52 ALAGMLRPEDGGQGAEGAEDEV 74

RESULT 14
US-09-991-163-268
; Sequence 268, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; PRIOR FILING DATE: 2001-11-14
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; PRIOR APPLICATION NUMBER: 60/087106

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; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
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Oy 1 ALAGWLRPEDGGQGAEGAEDELEV 23
Db 52 ALAGWLRPEDGGQGAEGAEDELEV 74

RESULT 15
US-09-993-604-268
; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Aclods Encoding the Same
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALAGWLRPEDGGQAEDELEV 23
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Db 52 ALAGWLRPEDGGQAEDELEV 74

Search completed: September 11, 2003, 17:48:32
Job time : 15.0214 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 8.60963 Seconds
(without alignments)
256.908 Million cell updates/sec

Title: US-09-853-253-5
Perfect score: 121

Sequence: 1 ALAGWLRPEDGGQAEDELEV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

- 1: pir1:*
- 2: pir2:*
- 3: pir3:*
- 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 121 | 100.0 | 117 | 1 A59316 | ghrelin precursor |
| 2 | 90 | 74.4 | 117 | 1 B59316 | ghrelin precursor |
| 3 | 54 | 44.6 | 200 | 2 A26169 | nucleoplasm - Af |
| 4 | 52 | 43.0 | 232 | 2 G83609 | probable transcrip |
| 5 | 51.5 | 42.6 | 249 | 2 T21920 | hypothetical prote |
| 6 | 51 | 42.1 | 91 | 2 B69811 | conserved hypothet |
| 7 | 51 | 42.1 | 604 | 2 A82760 | chloride channel p |
| 8 | 51 | 42.1 | 604 | 2 C97541 | hypothetical prote |
| 9 | 50 | 41.3 | 131 | 2 B75433 | hypothetical prote |
| 10 | 50 | 41.3 | 653 | 2 A46362 | amyloid precursor- |
| 11 | 49.5 | 40.9 | 484 | 2 C75609 | amino acid ABC tra |
| 12 | 49 | 40.5 | 274 | 2 A26050 | exfoliative toxin |
| 13 | 48 | 39.7 | 114 | 2 T49338 | hypothetical prote |
| 14 | 48 | 39.7 | 1199 | 2 S20969 | Na+/Ca2+,K+-exchan |
| 15 | 47 | 38.8 | 355 | 2 T09738 | protein kinase PK1 |
| 16 | 47 | 38.8 | 380 | 2 A52529 | kappa opioid recep |
| 17 | 47 | 38.8 | 1273 | 2 C96767 | unknown protein F2 |
| 18 | 46.5 | 38.4 | 80 | 2 T26398 | hypothetical prote |
| 19 | 46 | 38.0 | 259 | 2 A87377 | hypothetical prote |
| 20 | 46 | 38.0 | 287 | 2 C82965 | hypothetical prote |
| 21 | 46 | 38.0 | 491 | 2 H97088 | protein containing |
| 22 | 46 | 38.0 | 528 | 2 C84110 | xylan beta-1,4-xy |
| 23 | 46 | 38.0 | 871 | 2 B71039 | hypothetical prote |
| 24 | 45.5 | 37.6 | 582 | 2 I38028 | matrix metalloprot |
| 25 | 45.5 | 37.6 | 582 | 2 I48673 | matrix metalloprot |
| 26 | 45.5 | 37.6 | 582 | 2 I84771 | matrix metalloprot |
| 27 | 45 | 37.2 | 69 | 2 C87574 | cold-shock domain |
| 28 | 45 | 37.2 | 184 | 2 T43321 | ribosomal protein |
| 29 | 45 | 37.2 | 191 | 2 S62409 | 40s ribosomal prot |

| | | | | | |
|----|------|------|------|----------|--------------------|
| 30 | 45 | 37.2 | 242 | 2 S67270 | CCAAT-binding fact |
| 31 | 45 | 37.2 | 296 | 2 T15550 | hypothetical prote |
| 32 | 45 | 37.2 | 297 | 2 G71446 | hypothetical prote |
| 33 | 45 | 37.2 | 494 | 2 JC5919 | potassium channel |
| 34 | 45 | 37.2 | 544 | 2 B75379 | CTP synthase - Del |
| 35 | 45 | 37.2 | 600 | 2 T17436 | ATP-binding protei |
| 36 | 45 | 37.2 | 600 | 2 AF0233 | inner membrane ABC |
| 37 | 45 | 37.2 | 1059 | 2 T12195 | sucrose-phosphate |
| 38 | 44.5 | 36.8 | 777 | 2 T08659 | ral guanine nucleo |
| 39 | 44.5 | 36.8 | 1233 | 1 P3XR03 | major core protein |
| 40 | 44 | 36.4 | 102 | 2 T44994 | probable tryptopha |
| 41 | 44 | 36.4 | 273 | 2 JC4634 | vertebrate NK-2 ho |
| 42 | 44 | 36.4 | 358 | 2 AC2960 | hypothetical prote |
| 43 | 44 | 36.4 | 413 | 2 C98323 | algS protein (AB01 |
| 44 | 44 | 36.4 | 449 | 1 A41520 | chromogranin A pre |
| 45 | 44 | 36.4 | 479 | 2 A75353 | mock protein - Del |

ALIGNMENTS

RESULT 1

A59316
ghrelin precursor - human
N:Alternate names: preproghrelin
C:Species: Homo sapiens (man)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C:Accession: A59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: A59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-117 <KOJ>
A:Cross-references: GB:AB029434; NID:g6691571; PIDN:BAA89371.1; PID:g6691572
A:Experimental source: tissue stomach endocrine cells
A:Note: submitted to GenBank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (gr
C:Superfamily: motilin
C:Keywords: hormone; lipoprotein; stomach
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <MAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 121; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAEDELEV 23
DB 52 ALAGWLRPEDGGQAEDELEV 74

RESULT 2

B59316
ghrelin precursor - rat
N:Alternate names: preproghrelin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C:Accession: B59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: B59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA; protein
A:Residues: 1-117 <KOJ>
A:Cross-references: GB:AB029433; NID:g6691569; PIDN:BAA89370.1; PID:g6691570
A:Experimental source: strain SD; tissue stomach endocrine cells

A;Note: submitted to GenBank, June 1999
C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth hormone) from the hypothalamus.
C;Superfamily: motilin
C;Keywords: hormone; lipoprotein; stomach
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-51/Product: ghrelin #status predicted <MAT>
F;52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 74.4%; Score 90; DB 1; Length 117;
Best Local Similarity 73.9%; Pred. No. 1.1e-05;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ALAGWLRLPEDGGGAEGAEDELEV 23
II III III III III III III III
DB 52 ALEGWLHPDRGQAEEAELEI 74

RESULT 3
A26169
nucleoplasmin - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 13-Aug-1999
C;Accession: A26169
R;Dingwall, C.; Dillworth, S.M.; Black, S.J.; Kearsley, S.E.; Cox, L.S.; Laskey, R.A.
EMBO J. 6, 69-74, 1987
A;Title: Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and a cluster of serine residues.
A;Reference number: A26169; MUID:87218476; PMID:2884102
A;Accession: A26169
A;Molecule type: mRNA
A;Residues: 1-200 <DIN>
A;Cross-references: GB:X04766; NID:g64939; PIDN:CAA28460.1; PID:g64940
C;Superfamily: nucleophosmin
C;Keywords: molecular chaperone; nucleus

Query Match 44.6%; Score 54; DB 2; Length 200;
Best Local Similarity 55.6%; Pred. No. 2.4;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 WLRPE-DGGGAEGAEDELE 22
II III III III III III III III
DB 126 WAEEDGEAGEGEEEE 143

RESULT 4
G83609
probable transcription regulator PA0279 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83609
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brinkman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83609
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-232 <STO>
A;Cross-references: GB:AE004466; GB:AE004091; NID:g9946120; PIDN:AAG03668.1; GSPDB:GN001019
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0279

Query Match 43.0%; Score 52; DB 2; Length 232;
Best Local Similarity 72.7%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GWLRPEDGGOA 14
II III III III III III III III
DB 202 GWLRPDGGSRA 212

RESULT 5

T21920

hypothetical protein F37D6.7 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T21920

R;McMurray, A.

submitted to the EMBL Data Library, June 1996

A;Reference number: Z19487

A;Accession: T21920

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-249 <WIL>

A;Cross-references: EMBL:Z75540; PIDN:CAA99852.1; GSPDB:GN00019; CESP:F37D6.7

A;Experimental source: clone F37D6

C;Genetics:

A;Gene: CESP:F37D6.7

A;Map position: 1

A;Introns: 41/1; 62/1; 115/1; 176/1; 209/1

Query Match 42.6%; Score 51.5; DB 2; Length 249;
Best Local Similarity 52.9%; Pred. No. 6.9;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 5 WLRPE-DGGGAEGAEDE 20

II III III III III III III III

DB 73 WIRPETNGDDGSEDK 89

RESULT 6

B69811

conserved hypothetical protein yfil - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C;Accession: B69811

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gal

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshi

A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: B69811

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-91 <KUN>

A;Cross-references: GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12593.1; PID:g36330

A;Experimental source: strain 168

C;Genetics:

A;Gene: yfil

C;Superfamily: acylphosphatase

Query Match 42.1%; Score 51; DB 2; Length 91;
Best Local Similarity 44.0%; Pred. No. 2.9;
Matches 11; Conservative 5; Mismatches 5; Indels 4; Gaps 1;

QY 2 LAGWLRLPEDGGQ----AEGAEDELE 22

II III III III III III III III

DB 30 LAGWVRNDRDGRVEILAEQSPENALQ 54

RESULT 7

AE2760

chloride channel protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AE2760
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, S.; Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AE2760
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <KUR>
 A:Cross-references: GB:AE008688; PIDN:AAI42499.1; PID:g17739917; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: clc
 A:Map position: circular chromosome

Query Match 42.1%; Score 51; DB 2; Length 604;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAGWLRPDDGGQAG 16
 I: ||||| ||| I
 Db 288 AIPGWLRLPLGGVAVG 303

RESULT 8
 C97541
 chloride channel, clc (AE005067) [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C:Accession: C97541
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: C97541
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK87284.1; PID:g15156576; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C2753
 A:Map position: circular chromosome

Query Match 42.1%; Score 51; DB 2; Length 604;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAGWLRPDDGGQAG 16
 I: ||||| ||| I
 Db 288 AIPGWLRLPLGGVAVG 303

RESULT 9
 B75433
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
 C:Accession: B75433
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: B75433

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-131 <WHI>
 A:Cross-references: GB:AE001963; GB:AE000513; NID:g6458869; PIDN:AAF10714.1; PID:g6458869
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1139
 A:Map position: 1
 C:Superfamily: Deinococcus radiodurans hypothetical protein DR1139

Query Match 41.3%; Score 50; DB 2; Length 131;
 Best Local Similarity 47.4%; Pred. No. 5.9;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 ALAGWLRPDDGGQAG 19
 I: ||| ||| ||| I
 Db 101 ALLANFPFPPGGAQVGGAAE 119

RESULT 10
 A46362
 amyloid precursor-like protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
 C:Accession: A46362
 R:Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F. Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
 A:Title: Identification of a mouse brain cDNA that encodes a protein related to the A:Reference number: A46362; MUID:93066322; PMID:1279693
 A:Accession: A46362
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-653 <WAS>
 A:Experimental source: brain
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBI:118683, NCBI:118684)
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinases
 C:Keywords: transmembrane protein

Query Match 41.3%; Score 50; DB 2; Length 653;
 Best Local Similarity 76.9%; Pred. No. 29;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGQAGGAEDELEV 23
 I: ||| ||| ||| I
 Db 233 GGRAEGGEDEEV 245

RESULT 11
 C75609
 amino acid ABC transporter, permease protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: C75609
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: C75609
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <WHI>
 A:Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF12224.1; PID:g6460468
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DRA0136
 A:Map position: 2

Query Match 40.9%; Score 49.5; DB 2; Length 484;
 Best Local Similarity 61.1%; Pred. No. 26;
 Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 2 LAGWLRPEDGGQAGAEDE 19
 ||||| | | : || | | :
 Db 468 LAGWLTFR-GLRAEGEE 484

RESULT 12

A26050
 exfoliative toxin B precursor - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 18-Nov-2002
 C:Accession: A26050
 R:Jackson, M.P.; Iandolo, J.J.
 J. Bacteriol. 167, 726-728, 1986
 A:Title: Sequence of the exfoliative toxin B gene of Staphylococcus aureus.
 A:Reference number: A26050; MUID:86277939; PMID:3733674
 A:Accession: A26050
 A:Molecule type: DNA
 A:Residues: 1-274 <JAC>
 C:Superfamily: staphylococcal serine proteinase
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-274/Product: exfoliative toxin B #status predicted <NAT>

Query Match 40.5%; Score 49; DB 2; Length 274;
 Best Local Similarity 44.4%; Pred. No. 17;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 WLRPEDGGQAGAEDELE 22
 ||: |||| | ||: |
 Db 86 WLKIQDGGDTTQGEQPE 103

RESULT 13

T49338
 hypothetical protein B13N20.230 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
 C:Accession: T49338
 R:Schulte, U.; Algn, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, May 2000
 A:Reference number: Z25022
 A:Accession: T49338
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-114 <SCH>
 A:Cross-references: EMBL:AL355925; GSPDB:GND0116; NCSP:B13N20.230
 A:Experimental source: BAC clone B13N20; strain OR74A
 C:Genetics:
 A:Gene: NCSP:B13N20.230
 A:Map position: 6
 C:Superfamily: Neurospora crassa hypothetical protein B13N20.230

Query Match 39.7%; Score 48; DB 2; Length 114;
 Best Local Similarity 66.7%; Pred. No. 9.9;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 EDGGQAGAEDELEV 23
 |||| | | |||||
 Db 44 EDGFDEGKEDQLEV 58

RESULT 14

S20969
 Na/Ca2+,K+-exchanging protein - bovine
 N:Alternate names: Na/Ca2+,K+ antiporter; Na/Ca,K-exchanger
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S20969
 R:Reilander, H.; Achilles, A.; Friedel, U.; Maul, G.; Lottspeich, F.; Cook, N.J.
 EMBO J. 11, 1689-1695, 1992
 A:Title: Primary structure and functional expression of the Na/Ca,K-exchanger from bovin
 A:Reference number: S20969; MUID:92258377; PMID:1582405
 A:Accession: S20969

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1199 <REI>
 A:Cross-references: GB:X66481; NID:g505578; PIDN:CAA47108.1; PID:g505579

Query Match 39.7%; Score 48; DB 2; Length 1199;
 Best Local Similarity 45.0%; Pred. No. 1e+02;
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 GWLRPEDGGQAGAEDELEV 23
 | : | : || | || | :
 Db 816 GETQAGEGGEVEGEDEGEI 835

RESULT 15

T09738
 protein kinase PK1 (EC 2.7.1.1) - Craterostigma plantagineum
 C:Species: Craterostigma plantagineum
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
 C:Accession: T09738
 R:Heino, P.; Nylander, M.; Palva, T.; Bartels, D.
 submitted to the EMBL data library, April 1998
 A:Description: Isolation of a cDNA corresponding to a protein kinase differentially e
 A:Reference number: Z16839
 A:Accession: T09738
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-355 <HEI>
 A:Cross-references: EMBL:AJ005373
 C:Genetics:
 A:Gene: pk1
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase; protein kinase
 F:2-260/Domain: protein kinase homology <KIN>

Query Match 38.8%; Score 47; DB 2; Length 355;
 Best Local Similarity 37.0%; Pred. No. 43;
 Matches 10; Conservative 4; Mismatches 5; Indels 8; Gaps 1;

QY 4 GW-----LRPEDGGQAGAEDELE 22
 || : | : || || |
 Db 313 GWGTEEDENVEEVEEGEGEDEV 339

Search completed: September 11, 2003, 17:26:24
 Job time : 9.60963 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 3.32086 Seconds
(without alignments)
325.703 Million cell updates/sec

Title: US-09-853-253-5
Perfect score: 121
Sequence: 1 ALAGWLPRPDGQAGAEDELEV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result NO. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|------------|---------------------|
| 1 | 121 | 100.0 | 117 | GHRL_HUMAN | Q9ub33 homo sapien |
| 2 | 90 | 74.4 | 117 | GHRL_RAT | Q9qyh7 rattus norv |
| 3 | 87 | 71.9 | 118 | GHRL_PIG | Q9gky5 sus scrofa |
| 4 | 86 | 71.1 | 117 | GHRL_MOUSE | Q9eqx0 mus musculus |
| 5 | 72 | 59.5 | 116 | GHRL_BOVIN | Q9bdj6 bos taurus |
| 6 | 68 | 56.2 | 117 | GHRL_CANFA | Q9bef8 canis fami |
| 7 | 54 | 44.6 | 200 | NUP1_XENLA | P05221 xenopus lae |
| 8 | 51 | 42.1 | 91 | ACIP_BACSU | Q03031 bacillus su |
| 9 | 50 | 41.3 | 653 | APPI_MOUSE | Q03157 mus musculus |
| 10 | 48 | 39.7 | 300 | NRX1_BISBI | Q46383 bison bison |
| 11 | 48 | 39.7 | 668 | SYM_METKA | Q8tx28 methanopyru |
| 12 | 48 | 39.7 | 1216 | NRX1_BOVIN | Q28139 bos taurus |
| 13 | 47 | 38.8 | 380 | OPRK_CAVPO | P41144 cavia porce |
| 14 | 47 | 38.8 | 1168 | DDX8_ARATH | Q38953 arabidopsis |
| 15 | 45.5 | 37.6 | 580 | MM14_PIG | Q9xt90 sus scrofa |
| 16 | 45.5 | 37.6 | 582 | MM14_HUMAN | P50281 homo sapien |
| 17 | 45.5 | 37.6 | 582 | MM14_MOUSE | P53690 mus musculus |
| 18 | 45.5 | 37.6 | 582 | MM14_RAT | Q10739 rattus norv |
| 19 | 45.5 | 37.6 | 591 | PAX1_HUMAN | P49023 homo sapien |
| 20 | 45 | 37.2 | 190 | RS9A_SCHPO | Q09757 schizosacch |
| 21 | 45 | 37.2 | 242 | HAP5_YEAST | Q02516 saccharomyc |
| 22 | 45 | 37.2 | 494 | KCF1_HUMAN | Q9rh30 homo sapien |
| 23 | 45 | 37.2 | 544 | PYRG_DEIRA | Q9ru23 deinococcus |
| 24 | 45 | 37.2 | 992 | SNX1_HUMAN | Q92543 homo sapien |
| 25 | 45 | 37.2 | 1059 | SPS_VICFA | Q34876 vicla faba |
| 26 | 44.5 | 36.8 | 777 | RLG2_HUMAN | O15211 homo sapien |
| 27 | 44.5 | 36.8 | 1233 | VLJ1_REOVD | P15024 verovirus (t |
| 28 | 44 | 36.4 | 115 | INS_VERMO | Q9w7r2 verasper mo |
| 29 | 44 | 36.4 | 168 | TKTP_BRAOL | Q944w6 brassica ol |
| 30 | 44 | 36.4 | 273 | NC22_MOUSE | P42586 mus musculus |
| 31 | 44 | 36.4 | 449 | CMGA_BOVIN | P05059 bos taurus |
| 32 | 44 | 36.4 | 4447 | PKSK_BACSU | P40803 bacillus su |
| 33 | 43.5 | 36.0 | 525 | SYK_DEIRA | Q9rxel deinococcus |

| | | | | | | |
|----|------|------|------|---|------------|--------------------|
| 34 | 43.5 | 36.0 | 582 | 1 | MM14_RABIT | Q95220 oryctolagus |
| 35 | 43 | 35.5 | 365 | 1 | SVAP_MOUSE | Q9d5v6 mus musculu |
| 36 | 43 | 35.5 | 380 | 1 | OPRK_HUMAN | P41145 homo sapien |
| 37 | 43 | 35.5 | 579 | 1 | SYQ_XANAC | Q8pn25 xanthomonas |
| 38 | 43 | 35.5 | 852 | 1 | SRCH_RABIT | P16230 oryctolagus |
| 39 | 43 | 35.5 | 862 | 1 | SYV_THETH | P96142 thermus the |
| 40 | 43 | 35.5 | 864 | 1 | KLTK_HUMAN | P29376 homo sapien |
| 41 | 43 | 35.5 | 894 | 1 | WPRK_BACSU | P54423 bacillus su |
| 42 | 43 | 35.5 | 1876 | 1 | GLS1_YEAST | P38631 saccharomyc |
| 43 | 42.5 | 35.1 | 116 | 1 | INS_LOPPI | P01341 lophius pls |
| 44 | 42.5 | 35.1 | 195 | 1 | IGFB_HUMAN | P05019 homo sapien |
| 45 | 42.5 | 35.1 | 214 | 1 | GRP2_NICSY | P27484 nicotiana s |

ALIGNMENTS

RESULT 1
GHRL_HUMAN
ID GHRL_HUMAN STANDARD; PRT; 117 AA.
AC Q9UBU3: Q8TAT9; Q9H3R3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
GN GHRL OR MLRP
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
RX MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach."
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Stomach;
RA Tomasetto C., Karam S.M., Rio M.-C.;
RT "Identification of a novel gastric protein m46."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Wajhrach M.P., Ten I.S., Gertner J.M., Leibel R.L.;
RT "Genomic organization of the human Ghrelin gene."
RL J. Endocrinol. Genet. 1:231-233(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=2388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.M., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 24-33.
 RC TISSUE-Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RT hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [7]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -1- PTM: O-n-octanoylation is essential for activity.
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/GhrelinID327.html".
 CC -----
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 DR EMBL; AB029434; BAB89371.1; -
 DR EMBL; AB035700; BAB19045.1; -
 DR EMBL; AJ252278; CAB65733.1; -
 DR EMBL; AF296558; AAG10300.1; -
 DR EMBL; BC025791; AAH25791.1; -
 DR PIR; A59316; A59316.
 DR MIM; 605353; -
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005131; F:growth hormone receptor ligand activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007186; P:g-protein coupled receptor protein signalin. . . ; TAS.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006736; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc; 1.
 DR Pfam; PF04644; motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 23
 FT PEPTIDE 24 51 GHRELIN.
 FT PROPEP 52 117 REMOVED IN MATURE FORM.
 FT LIPID 26 26 N-OCTANOATE.
 FT VARSPIC 37 37 Missing (in isoform 2).
 FT /FTID=VSP_003245.
 FT CONFLICT 72 72 L -> M (IN REF. 5).

SQ SEQUENCE 117 AA; 12911 MW; 39C0572BECA2755 CRC64;
 Query Match 100.0%; Score 121; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
 Db 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 2
 GHRL_RAT
 ID GHRL_RAT STANDARD; PRT; 117 AA.
 AC QSQYH7; Q9ET69;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide).
 GN GHRL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,
 RP AND ACYLATION OF SER-26.
 RC STRAIN-Sprague-Dawley; TISSUE-Stomach;
 RX MEDLINE=20067959; PubMed=10604470;
 RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
 RT "Ghrelin is a growth-hormone-releasing acylated peptide from
 RT stomach.";
 RL Nature 402:656-660(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS
 RP SPECTROMETRY, AND ACYLATION OF SER-26.
 RC STRAIN-Sprague-Dawley; TISSUE-Stomach;
 RX MEDLINE=20357315; PubMed=10801861;
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
 RT "Purification and characterization of rat des-Gln14-ghrelin, a second
 RT endogenous ligand for the growth hormone secretagogue receptor.";
 RL J. Biol. Chem. 275:21995-22000(2000).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=21092536; PubMed=11162448;
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
 RT "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
 RT in gastrointestinal tissue.";
 RL Biochem. Biophys. Res. Commun. 279:909-913(2000).
 RN [4]
 RP STRUCTURE-ACTIVITY RELATIONSHIP.
 RX MEDLINE=21433488; PubMed=11549267;
 RA Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
 RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
 RT "Structure-activity relationship of ghrelin: pharmacological study of
 RT ghrelin peptides.";
 RL Biochem. Biophys. Res. Commun. 287:142-146(2001).
 RN [5]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;


```

CC Name=1; Synonyms=Ghrelin;
CC IsoID=Q9GYH7-1; Sequence-Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoID=Q9GYH7-2; Sequence=VSP_003248;
CC TISSUE SPECIFICITY: Broadly expressed with higher expression in
CC the stomach. Very low levels are detected in the hypothalamus,
CC heart, lung, pancreas, intestine and adipose tissue.
CC -1- PTM: O-n-octanoylation is essential for activity. The replacement
CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.
CC -1- MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;
CC RANGE=24-51.
CC -1- MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;
CC RANGE=24-36, 38-51.
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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CC -----
CC EMBL; AB029433; BAA89370.1; -
CC EMBL; AB035699; BAB11956.1; -
CC PIR; B59316; B59316.
CC InterPro: IPR006737; motilin_assoc.
CC InterPro: IPR006738; motilin_ghrelin.
CC InterPro: IPR005441; Preproghrelin.
CC Pfam; PF04643; motilin_assoc; 1.
CC Pfam; PF04644; motilin_ghrelin; 1.
CC PRINTS; PR01624; GHRELIN.
CC ProDom; PD332162; preproghrelin; 1.
CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
CC Alternative splicing.
CC SIGNAL 1 23 GHRELIN.
CC PEPTIDE 24 51 REMOVED IN MATURE FORM.
CC PROPEP 52 117 N-OCTANOATE.
CC LIPID 26 26 Missing (in isoform 2).
CC VARSPLIC 37 37 /FTID=VSP_003248.
CC SEQUENCE 117 AA; 13176 MW; 8857546FES1A7691 CRC64;

Query Match 74.4%; Score 90; DB 1; Length 117;
Best Local Similarity 73.9%; Pred. No. 4.1e-06;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ALAGWLRLPEDGGQAGAEDELEV 23
Db || ||| ||| ||| ||| ||| |||
52 ALEGWLRLPEDGGQAGAEDELEI 74

RESULT 3
GHRL_PIG STANDARD; PRT; 118 AA.
AC Q9GKY5; Q9BDG8; Q9GKY4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide).
DE GHRL.
GN Sus scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Stomach;

RA Rousselle J., Lacroix D., Dubreuil P.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoID=Q9GKY5-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoID=Q9GKY5-2; Sequence=VSP_003247;
CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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CC -----
CC EMBL; AB035703; BAB19048.1; -
CC EMBL; AB035704; BAB19049.1; -
CC EMBL; AF308930; AAK19243.1; -
CC EMBL; AY028942; AAK30002.1; -
CC InterPro: IPR006737; motilin_assoc.
CC InterPro: IPR006738; motilin_ghrelin.
CC InterPro: IPR005441; Preproghrelin.
CC Pfam; PF04643; motilin_assoc; 1.
CC Pfam; PF04644; motilin_ghrelin; 1.
CC PRINTS; PR01624; GHRELIN.
CC ProDom; PD332162; Preproghrelin; 1.
CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
CC Alternative splicing.
CC SIGNAL 1 24 BY SIMILARITY.
CC PEPTIDE 25 52 GHRELIN.
CC PROPEP 53 118 REMOVED IN MATURE FORM (BY SIMILARITY).
CC LIPID 27 27 N-OCTANOATE (BY SIMILARITY).
CC VARSPLIC 38 38 Missing (in isoform 2).
CC /FTID=VSP_003247.
CC CONFLICT 17 17 L -> P (IN REF. 2; AAK30002).
CC CONFLICT 72 72 K -> E (IN REF. 2; AAK30002).
CC SEQUENCE 118 AA; 12795 MW; 856D3E1D6DAB1A76 CRC64;

Query Match 71.9%; Score 87; DB 1; Length 118;
Best Local Similarity 65.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAGWLRLPEDGGQAGAEDELEV 23
Db || ||| ||| ||| ||| ||| |||
53 ALEGWLRLPEDSGVEGETDKLEI 75

RESULT 4
GHRL_MOUSE STANDARD; PRT; 117 AA.
AC Q9EQX0; Q9WUZ1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide) (M46 protein).
DE GHRL OR MTLRP.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.

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RC RX TISSUE=Stomach;
RA MEDLINE=20389976; PubMed=10930375;
RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT "Identification and characterization of a novel gastric peptide
RL hormone: the motilin-related peptide.";
RL Gastroenterology 119:395-405(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Kojima M.;
RA "Mouse mRNA for preproghrelin.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Ozaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata I., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=09EQX0-1; Sequence=Displayed;
CC IsoId=09EQX0-2; Sequence=Vsp_003246;
CC -1- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
CC with higher levels in the stomach, medium levels in the duodenum,
CC jejunum, ileum and colon. Low expression in the testis and brain.
CC Not detected in the salivary gland, pancreas, liver and lung.
CC -1- PFM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC EMBL; AJ243503; CAB46500.1; -
DR EMBL; AB035701; BAB19046.1; -
DR EMBL; AB060078; BAB69857.1; -
DR EMBL; AK008658; BAB25814.1; -
DR EMBL; AK008860; BAB25934.1; -
DR MGD; MGI:1930008; Ghrl.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005576; C:extracellular; IDA.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin-ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin-ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23
FT PEPTIDE 24 51
FT PROPEP 52 117
FT LIPID 26 26
FT VANSPLIC 37 37
FT SQ SEQUENCE 117 AA; 13207 MW; EACB49D2E3CA7203 CRC64;
Query Match 71.18; Score 86; DB 1; Length 117;
Best Local Similarity 69.68; Pred. No. 1.5e-05;
Matches 16; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Oy 1 ALAGWLRPEDGGQGAEGAEDELEV 23
Db 52 ALGGLHPEDRGQAEEETEELEI 74
RESULT 5
GHRL_BOVIN STANDARD; PRT; 116 AA.
ID GHRL_BOVIN
AC O9BDJ6; O9GKY6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide).
GN GHRL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Kita K., Harada K., Yokota H.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 24-99 FROM N.A.
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- PFM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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EMBL: AJ298296; CAC29156.1; -.
InterPro: IPR006737; motilin_assoc.
InterPro: IPR006738; motilin_ghrelin.
InterPro: IPR005441; Preproghrelin.
Pfam: PF04643; motilin_assoc. 1.
Pfam: PF04644; motilin_ghrelin; 1.
PRINTS: PR01624; GHRELIN.
PRODOM: PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
Alternative splicing.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPLIC 37 37 Missing (in isoform 2).
FT FTID=VSP_003244.
SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;
Query Match 56.2%; Score 68; DB 1; Length 117;
Best Local Similarity 65.2%; Pred. No. 0.0058;
Matches 15; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDSGOAGAEDELEV 23
||| ||||| |||||
DB 52 ALGSLGPDTSQVEEADELEI 74

RESULT 7
NUPL_XENLA STANDARD; PRT; 200 AA.
AC P05221;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nucleoplasmin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=87218476; PubMed=2884102;
RA Dingwall C., Dillworth S.M., Black S.J., Kearsey S.E., Cox L.S.,
RT Laskey R.A.;
RT "Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and a
RT cluster of sequences homologous to putative nuclear localization
RT signals.";
RL EMBO J. 6:69-74(1987).
[2]
RN SEQUENCE OF 7-200 FROM N.A.
RX MEDLINE=88112783; PubMed=3428591;
RA Buerglin T.R., Mattaj I.W., Newmeyer D.D., Zeller R.,
RA de Robertis E.M.;
RT "Cloning of nucleoplasmin from Xenopus laevis oocytes and analysis of
RT its developmental expression.";
RL Genes Dev. 1:97-107(1987).
CC -1- FUNCTION: NUCLEOPLASMIN IS AN ACIDIC, PENTAMERIC, THERMOSTABLE
CC PROTEIN WHICH IS ABLE TO ASSEMBLE NUCLEOSOMES BY BINDING HISTONES
CC AND TRANSFERRING THEM TO DNA.
CC -1- SUBUNIT: Homopentamer.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.

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DB EMBL: X04766; CAA28460.1; -.

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DR EMBL; Y00204; CAA68363.1; -.
DR PIR; A26169; A26169.
DR PDB; 1EE5; 26-SEP-01.
DR PDB; 1EJY; 24-APR-00.
DR PDB; 1K5J; 21-NOV-01.
DR InterPro; IPR004301; Nucleoplasm.
DR Pfam; PF03066; Nucleoplasm.
KW Nuclear protein; Phosphorylation; 3D-structure.
FT DOMAIN 138 145 POLY-GLU (PROBABLE HISTONE BINDING SITE).
FT CONFLICT 11 11 L -> V (IN REF. 2).
FT CONFLICT 27 27 D -> N (IN REF. 2).
FT CONFLICT 31 31 E -> A (IN REF. 2).
FT CONFLICT 34 34 V -> I (IN REF. 2).
FT CONFLICT 61 61 N -> H (IN REF. 2).
FT CONFLICT 72 72 A -> K (IN REF. 2).
FT CONFLICT 75 75 S -> P (IN REF. 2).
FT CONFLICT 80 80 T -> S (IN REF. 2).
FT CONFLICT 111 111 L -> V (IN REF. 2).
FT CONFLICT 134 137 MISSING (IN REF. 2).
FT CONFLICT 147 147 Q -> P (IN REF. 2).
SQ SEQUENCE 200 AA; 22023 MW; A91DD110F2965812 CRC64;

Query Match 44.6%; Score 54; DB 1; Length 200;
Best Local Similarity 55.6%; Pred. No. 1;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 WLRPEDGGQAGAEDELE 22
D 126 WABEEDEGEAGEEEEE 143

RESULT 8
ID ACYP-BACSU STANDARD; PRT; 91 AA.
AC O35031;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative acylphosphatase (EC 3.6.1.7) (Acylphosphate
DE phosphohydrolase).
GN YFLL.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AC327;
RX MEDLINE=97417488; PubMed=9272861;
RA Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;
RT "Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region
RT of the Bacillus subtilis genome reveal genes for a new two-component
RT system, three spore germination proteins, an iron uptake system and a
RT general stress response protein.";
RL Gene 194:191-199(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertolo M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Brusch C.V., Brans A., Braun M., Brignell S.C., Bron S.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel N.M.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karanata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

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RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Portwollik S., Prescott A.M.,
RA Presecan E., Pujić P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche D., Rose M., Sadale F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -1- CATALYTIC ACTIVITY: An acyl phosphate + H(2)O -> a fatty acid anion
CC + phosphate.
CC -1- SIMILARITY: BELONGS TO THE ACYLPHOSPHATASE FAMILY.
CC -----
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CC -----
DR EMBL; D86417; BAA22305.1; -.
DR EMBL; Z99108; CAB12593.1; -.
DR PIR; B69811; B69811.
DR HSP; P00818; IAPS.
DR Subtilist; BG12947; yfll.
DR InterPro; IPR001792; Acylphosphatase.
DR Pfam; PF00708; Acylphosphatase; 1.
DR PRINTS; PR00112; ACYLPHPTASE.
DR ProDom; PD001884; Acylphosphatase; 1.
DR PROSITE; PS00150; ACYLPHOSPHATASE_1; 1.
DR PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.
KW Hypothetical protein; Hydrolase; Complete proteome.
SQ SEQUENCE 91 AA; 10318 MW; 50795631BF310F4 CRC64;

Query Match 42.1%; Score 51; DB 1; Length 91;
Best Local Similarity 44.0%; Pred. No. 1;
Matches 11; Conservative 5; Mismatches 5; Indels 4; Gaps 1;

Qy 2 LAGWLRPEDGGQ---AEGAEDELE 22
D 30 LAGWVRNRDDGRVEIIAEGPENALQ 54

RESULT 9
ID APPI_MOUSE STANDARD; PRT; 653 AA.
AC Q03137; Q8VC38;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
GN APLP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93066322; PubMed=1279693;
RA Wasco W., Bupp K., Magendanz M., Guseella J.F., Tanzi R.E.,
RA Solomon F.;
RT "Identification of a mouse brain cDNA that encodes a protein related
RT to the Alzheimer disease-associated amyloid beta protein precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).

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RN [2]
RP SEQUENCE FROM M.A.
RC TISSUE=Retina;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RX COLLAGEN-BINDING.
RP MEDLINE=96139497; PubMed=8576160;
RA Behr D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RL mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [4]
RX INTERACTION WITH DAB1.
RP MEDLINE=99389880; PubMed=10460257;
RA Homayouni R., Rice D.S., Sheldon M., Curran T.;
RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
RL protein 1.";
RL J. Neurosci. 19:7507-7515(1999).
RN [5]
RX INTERACTION WITH MAPR81P1.
RP MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/isllet-brain-1
RL scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
RN [6]
RX GAMMA-SECRETASE PROCESSING, INTERACTION WITH APPB1, AND MUTAGENESIS OF
RP TYR-641.
RX MEDLINE=22313598; PubMed=12228233;
RA Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.;
RT "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
RL secretase regulates transcription.";
RL J. Biol. Chem. 277:44195-44201(2002).
CC -1- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC gamma-secretase processed fragment, ALIDI, activates transcription
CC activation through APPB1 (Fe65) binding. Couples to JIP signal
CC transduction through C-terminal binding. May interact with
CC cellular G-protein signaling pathways. Can regulate neurite
CC outgrowth through binding to components of the extracellular
CC matrix such as heparin and collagen I.
CC -1- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC neuronal apoptosis (By similarity).
CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APPB and APBA family members,
CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC serine phosphorylation.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC processed in the Golgi complex.
CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-

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CC terminal to the NPXY motif are often required for complete
CC interaction. The NPXY site is also involved in clatherin-mediated
CC endocytosis.
CC -1- PTM: Proteolytically cleaved by caspases during neuronal
CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
CC similarity).
CC -1- PTM: N-glycosylated.
CC -1- PTM: O-glycosylated.
CC -1- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC Zinc-binding increases heparin binding. No Cu(II) reducing
CC activity with copper-binding.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L04538; AAA37247.1; -.
CC EMBL; BC021877; AAH21877.1; -.
CC PIR; A46362; A46362.
CC HSSP; P05067; 1MWP.
CC MGD; MGI:88046; Aplp1.
CC InterPro; IPR001868; A4_APP.
CC Pfam; PF02177; A4_EXTRA; 1.
CC PRINTS; PR00203; AMYLOIDA4.
CC SMART; SM00006; A4_EXTRA; 1.
CC PROSITE; PS00319; A4_INTRA; 1.
CC PROSITE; PS00320; A4_INTRA; 1.
CC Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
CC Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
CC Glycoprotein.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 653 AMYLOID-LIKE PROTEIN 1.
FT CHAIN 624 653 C30 (BY SIMILARITY).
FT DOMAIN 38 583 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 584 606 POTENTIAL.
FT DOMAIN 607 653 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 157 177 COPPER-BINDING.
FT DOMAIN 203 210 ZINC-BINDING (BY SIMILARITY).
FT DOMAIN 313 345 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 413 444 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 445 462 COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN 263 271 POLY-GLU.
FT DOMAIN 535 538 POLY-SER.
FT DOMAIN 601 606 POLY-LEU.
FT SITE 166 166 REQUIRED FOR COPPER(II) REDUCTION (BY
FT SIMILARITY).
FT SITE 607 618 BASOLATERAL SORTING SIGNAL (BY
FT SIMILARITY).
FT SITE 623 624 CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT SITE 641 644 ENDOCYTOSIS SIGNAL.
FT SITE 643 646 NPXY MOTIF.
FT CARBOHYD 464 464 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 554 554 N-LINKED (GLCNAC...) (POTENTIAL).
FT MUTAGEN 641 641 Y->G: REDUCED BINDING OF APPB1.
FT CONFLICT 17 17 P -> PP (IN REF. 2).
SQ SEQUENCE 653 AA; 72750 MW; 56516DC3EA40E4B0 CRC64;
Query Match 41.3%; Score 50; DB 1; Length 653;
Best Local Similarity 76.9%; Pred. No. 12;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 11 GGOAEGADELEV 23
11:11111111
Db 233 GGRAEGGEDEEV 245
RESULT 10
NKX1_BISBI

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ID NKX1_BISBI STANDARD; PRT; 300 AA.
AC O46383;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 (Na(+)/K(+)/Ca(2+)-
DE exchange protein 1) (Retinal rod Na-Ca+K exchanger) (Fragment).
CN SLC24A1 OR NCKX1.
OS Bison bison (American bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bison.
OC NCBI_TaxID=9901;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98138491; PubMed=9478004;
RA Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.;
RT "cDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison
RT with a revised bovine sequence.";
RL Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
CC -1- FUNCTION: Critical component of the visual transduction cascade,
CC controlling the calcium concentration of outer segments during
CC light and darkness. Light causes a rapid lowering of cytosolic
CC free calcium in the outer segment of both retinal rod and cone
CC photoreceptors and the light-induced lowering of calcium is caused
CC by extrusion via this protein which plays a key role in the
CC process of light adaptation. Transports one Ca(2+) and one K(+) in
CC exchange for four Na(+) (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC -----
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CC -----
DR EMBL; AF025480; AAC13320.1;
DR Vision; Transport; Antiport; Symport; Calcium transport;
KW Potassium transport; Sodium transport; Transmembrane.
FT NON_TER 1
FT TRANSMEM 259 275 POTENTIAL.
FT DOMAIN 218 242 POLY-GLU.
FT NON_TER 300 300
SQ SEQUENCE 300 AA; 31671 MW; 2BE592DA5AB9781E CRC64;

Query Match 39.7%; Score 48; DB 1; Length 300;
Best Local Similarity 45.0%; Pred. No. 11;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 4 GWRPDEGGQAEDELEV 23
I::: :||: ||| :|
DB 84 GEIQAGEGGEDEGEI 103

RESULT 11
SYM_METKA
ID SYM_METKA STANDARD; PRT; 668 AA.
AC Q8TX28;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
DE (MetRS).
DE METG OR MK0850.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OC NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natile D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozayavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC -1- FUNCTION: Is required not only for elongation of protein synthesis
CC but also for the initiation of all mRNA translation through
CC initiator tRNA(fMet) aminoacylation (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) -> AMP +
CC diphosphate + L-methionyl-tRNA(Met).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC MetG subfamily 1.
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
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CC -----
DR EMBL; AE010375; AM02063.1;
DR HAMAP; MF_00098; fused; 1.
DR InterPro; IPR004495; MetG_Cterm.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002304; tRNA-synt_met.
DR InterPro; IPR002347; tRNA_bind.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR Pfam; PF01588; tRNA_bind; 1.
DR PIRSF; PIRSF001528; METRS_dimerising; 1.
DR TIGRFAMS; TIGR00398; metG; 1.
DR TIGRFAMS; TIGR00399; metG_Cterm; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
DR PROSITE; PS50886; TRBD; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW RNA-binding; tRNA-binding; Metal-binding; Zinc; Complete proteome.
FT SITE 11 21 "HIGH" REGION.
FT SITE 332 336 "KWSKS" REGION.
FT DOMAIN 567 668 tRNA-BINDING.
FT METAL 146 146 ZINC (BY SIMILARITY).
FT METAL 149 149 ZINC (BY SIMILARITY).
FT METAL 159 159 ZINC (BY SIMILARITY).
FT METAL 162 162 ZINC (BY SIMILARITY).
SQ SEQUENCE 668 AA; 77386 MW; FBC5734FF5FEF015 CRC64;

Query Match 39.7%; Score 48; DB 1; Length 668;
Best Local Similarity 53.3%; Pred. No. 24;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 6 LRPEDGGQAEDE 20
I::: :||: ||| :|
DB 547 LLPESGEGEGQDDE 561

RESULT 12
NKX1_BOVIN
ID NKX1_BOVIN STANDARD; PRT; 1216 AA.
AC Q28139; O46384;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-
DE exchange protein 1) (Retinal rod Na-Ca+K exchanger).
DE SLC24A1 OR NCKX1.
GN SLC24A1 OR NCKX1.

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| | | | | |
|-----------------------|--|---|------------------|--|
| FT | TRANSMEM | 580 | 600 | POTENTIAL. |
| FT | DOMAIN | 601 | 1024 | CYTOPLASMIC (POTENTIAL). |
| FT | TRANSMEM | 1025 | 1045 | POTENTIAL. |
| FT | DOMAIN | 1046 | 1052 | EXTRACELLULAR (POTENTIAL). |
| FT | TRANSMEM | 1053 | 1073 | POTENTIAL. |
| FT | DOMAIN | 1074 | 1088 | CYTOPLASMIC (POTENTIAL). |
| FT | TRANSMEM | 1089 | 1109 | POTENTIAL. |
| FT | DOMAIN | 1110 | 1127 | EXTRACELLULAR (POTENTIAL). |
| FT | TRANSMEM | 1128 | 1148 | POTENTIAL. |
| FT | DOMAIN | 1149 | 1157 | CYTOPLASMIC (POTENTIAL). |
| FT | TRANSMEM | 1158 | 1178 | POTENTIAL. |
| FT | DOMAIN | 1179 | 1185 | EXTRACELLULAR (POTENTIAL). |
| FT | TRANSMEM | 1186 | 1206 | POTENTIAL. |
| FT | DOMAIN | 1207 | 1216 | CYTOPLASMIC (POTENTIAL). |
| FT | DOMAIN | 796 | 928 | 8 X 17 AA TANDEM REPEATS OF D-E-D-E-G-E-I-Q-A-G-B-[GA]-G-E-V-[EK]-G. 1 (APPROXIMATE). 2. 3. 4. 5. 6. 7. 8 (APPROXIMATE). ALPHA-1. POLY-GLU. PHOSPHORYLATION (POTENTIAL). N-LINKED (GLCNAC..) (POTENTIAL). N-LINKED (GLCNAC..) (POTENTIAL). Missing (in isoform 2). /FTID=VSP_006159. MISSING (IN REF. 1; AA SEQUENCE). MISSING (IN REF. 1; AA SEQUENCE). MISSING (IN REF. 1; AA SEQUENCE). |
| Query Match | | | 39.7%; Score 48; | DB 1; Length 1216; |
| Best Local Similarity | | | 45.0%; | Pred. No. 44; |
| Matches | 9; | Conservative | 5; | Mismatches 6; Indels 0; Gaps |
| Oy | 4 | GWLRPDGGQAGAEDELEV 23 :: : : : | | |
| Dd | 816 | GEIQAGEGVEGEDGEI 835 | | |
| RESULT 13 | | | | |
| OPRK_CAVPO | | | | |
| ID | OPRK_CAVPO | STANDARD; | PRT; | 380 AA. |
| AD | P41144; | | | |
| DT | 01-FEB-1995 (Rel. 31, Created) | | | |
| DT | 01-FEB-1995 (Rel. 31, Last sequence update) | | | |
| DT | 01-NOV-1997 (Rel. 35, Last annotation update) | | | |
| DN | Kappa-type opioid receptor (KOR-1). | | | |
| GE | OPRk1. | | | |
| OS | Cavia porcellus (Guinea pig). | | | |
| OC | Eukaryota; Metazoa; Chordata; | | | |
| CC | Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia. | | | |
| RN | [NCBI_TaxID=10141; | | | |
| OX | [1] | | | |
| RC | SEQUENCE FROM N.AA. | | | |
| RP | STRAIN=Hartley; TISSUE=Brain; | | | |
| RX | MEDLINE=94224825; PubMed=8170987; | | | |
| RA | Xie G.X., Meng F., Mansour A., Thompson R.C., Hoversten M.T., | | | |
| RA | Goldstein A., Watson S.J., Akil H.; | | | |
| RT | "Primary structure and functional expression of a guinea pig kappa | | | |
| RT | opioid (dynorphin) receptor"; | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 91:3779-3783(1994). | | | |
| -/- | FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM | | | |
| CC | ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR | | | |
| CC | FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF | | | |
| CC | AUTONOMIC AND NEUROENDOCRINE FUNCTIONS. | | | |

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CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: U04092; AAA67171.1; -.
DR PIR: A55259; A55259.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECP_FL2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL).
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 380 AA; 42736 MW; 4FF053834DBBA623 CRC64;

Query Match 38.8%; Score 47; DB 1; Length 380;
Best Local Similarity 38.1%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAEDELE 22
DQ 30 LPGAEPDGNAGSPQDELE 50
DI DDX8_ARATH STANDARD; PRT; 1168 AA.
AC Q38953; Q9LRV0;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Putative pre-mRNA splicing factor ATP-dependent RNA helicase.
GN AT3G26560 OR MFE16.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=37086699; PubMed=8932388;
RA Quigley F., Dao P., Cottet A., Mache R.;
RT "Sequence analysis of an 81 kb contig from Arabidopsis thaliana
RL chromosome III.";
RL Nucleic Acids Res. 24:4313-4318(1996).
RN [2]
```

```
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
CC -1- FUNCTION: COULD ACT LATE IN THE SPLICING OF PRE-MRNA AND MEDIATE
CC THE RELEASE OF THE SPLICED MRNA FROM SPLICEOSOMES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. DEAH
CC SUBFAMILY. DDX8/PRP22 ORTHOLOG.
CC -1- SIMILARITY: Contains 1 S1 motif domain.
CC -1- CAUTION: Ref.1 sequences differ from that shown due to a
CC frameshift in position 57.
CC -----
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CC -----
DR EMBL: X98130; CAA66825.1; ALT_FRAME.
DR EMBL: X97970; CAA66613.1; ALT_FRAME.
DR EMBL: AB028611; BAB01838.1; -.
DR HSP: P05055; ISRO.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR002464; DEAH_box.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR003029; S1.
DR Pfam: PF00271; helicase_C; 1.
DR Pfam: PF00575; S1; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
DR SMART: SM00316; S1; 1.
DR PROSITE: PS00690; DEAH_ATP_HELICASE; 1.
DR PROSITE: PS00126; S1; 1.
KW Hypothetical protein; mRNA processing; mRNA splicing; Helicase;
KW ATP-binding; Nuclear protein.
FT DOMAIN 214 283 S1 MOTIF.
FT NP_BIND 518 545 ATP (POTENTIAL).
FT SITE 635 638 DEAH_BOX.
FT DOMAIN 777 780 POLY-PRO.
SQ SEQUENCE 1168 AA; 134156 MW; B3632DE47A7690C CRC64;

Query Match 38.8%; Score 47; DB 1; Length 1168;
Best Local Similarity 57.9%; Pred. No. 59;
Matches 11; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

QY 9 EDGG----QAEGAEDELEV 23
DQ 372 EDGGMLYQEGAEDELEI 390
DI MM14_PIG STANDARD; PRT; 580 AA.
AC Q3XT90;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update).
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Matrix metalloproteinase-14 precursor (EC 3.4.24.-) (MMP-14)
DE (Membrane-type matrix metalloproteinase 1) (MT-MMP 1) (MTMMP1)
DE (Membrane-type-1 matrix metalloproteinase) (MT1-MMP) (MT1MMP).
GN MMP14.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
```


Search completed: September 11, 2003, 17:21:44
Job time : 3.32086 secs

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 21.893 Seconds
(without alignments)
271.100 Million cell updates/sec

Title: US-09-853-253-5

Perfect score: 121

Sequence: 1 ALAGWLRPDGGQAGAEDELEV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertibrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % Match | Length | ID | Description |
|------------|-------|---------------|--------|-----------|--------------------|
| 1 | 119 | 98.3 | 117 | 4 Q8TAT9 | Q8tat9 homo sapien |
| 2 | 92 | 76.0 | 117 | 11 Q8CH53 | Q8ch53 meriones un |
| 3 | 59 | 48.8 | 1208 | 5 Q815T3 | Q815t3 plasmodium |
| 4 | 59 | 48.8 | 1264 | 5 Q9U445 | Q9u445 plasmodium |
| 5 | 55 | 45.5 | 183 | 10 Q8LNL6 | Q8lnl6 oryza sativ |
| 6 | 53 | 43.8 | 202 | 15 Q90P58 | Q90p58 human immun |
| 7 | 53 | 43.8 | 1228 | 5 Q27724 | Q27724 plasmodium |
| 8 | 52 | 43.0 | 201 | 15 Q90P50 | Q90p50 human immun |
| 9 | 52 | 43.0 | 232 | 16 Q916L1 | Q916l1 pseudomonas |
| 10 | 52 | 43.0 | 249 | 12 Q82036 | Q82036 hirame rhab |
| 11 | 52 | 43.0 | 392 | 12 Q9QL89 | Q9ql89 hirame rhab |
| 12 | 52 | 43.0 | 977 | 6 Q95169 | Q95169 capra hircu |
| 13 | 51.5 | 42.6 | 436 | 5 Q9N638 | Q9n638 caenorhabdi |
| 14 | 51 | 42.1 | 158 | 16 Q8XW90 | Q8xw90 raistonia s |
| 15 | 51 | 42.1 | 201 | 15 Q90NL5 | Q90nl5 human immun |
| 16 | 51 | 42.1 | 604 | 16 Q8UFA5 | Q8ufa5 agrobacteri |

| | | | | | |
|----|------|------|-----|-----------|--------------------|
| 17 | 51 | 42.1 | 609 | 2 Q9RH77 | Q9rh77 bradyrhizob |
| 18 | 50 | 41.3 | 131 | 16 Q9RV90 | Q9rv90 deinococcus |
| 19 | 50 | 41.3 | 202 | 15 Q90P76 | Q90p76 human immun |
| 20 | 50 | 41.3 | 202 | 15 Q90P77 | Q90p77 human immun |
| 21 | 50 | 41.3 | 472 | 10 Q8LRD5 | Q8lrd5 oryza sativ |
| 22 | 50 | 41.3 | 582 | 6 Q9XSP0 | Q9xsp0 capra hircu |
| 23 | 50 | 41.3 | 582 | 6 Q9GLE4 | Q9gle4 bos taurus |
| 24 | 49.5 | 40.9 | 484 | 16 Q9RZ17 | Q9rz17 deinococcus |
| 25 | 49 | 40.5 | 201 | 15 Q90P55 | Q90p55 human immun |
| 26 | 49 | 40.5 | 201 | 15 Q90NK8 | Q90nk8 human immun |
| 27 | 49 | 40.5 | 286 | 12 Q8QRU5 | Q8qrus chimpanzee |
| 28 | 48.5 | 40.1 | 110 | 10 Q93VB3 | Q93vb3 oryza sativ |
| 29 | 48.5 | 40.1 | 172 | 2 Q9RBY2 | Q9rby2 pseudomonas |
| 30 | 48.5 | 40.1 | 172 | 2 Q9R2S2 | Q9r2s2 pseudomonas |
| 31 | 48.5 | 40.1 | 269 | 2 Q9ETM8 | Q9etm8 pseudomonas |
| 32 | 48 | 39.7 | 106 | 16 Q8ELH4 | Q8elh4 oceanobacil |
| 33 | 48 | 39.7 | 115 | 10 Q8LI79 | Q8li79 oryza sativ |
| 34 | 48 | 39.7 | 120 | 15 Q78494 | Q78494 human immun |
| 35 | 48 | 39.7 | 201 | 15 Q90P53 | Q90p53 human immun |
| 36 | 48 | 39.7 | 201 | 15 Q90NL3 | Q90nl3 human immun |
| 37 | 48 | 39.7 | 201 | 15 Q90NL6 | Q90nl6 human immun |
| 38 | 48 | 39.7 | 201 | 15 Q90NL0 | Q90nl0 human immun |
| 39 | 48 | 39.7 | 201 | 15 Q90NLI | Q90nl1 human immun |
| 40 | 48 | 39.7 | 201 | 15 Q90NMI | Q90nm1 human immun |
| 41 | 48 | 39.7 | 201 | 15 Q90NM2 | Q90nm2 human immun |
| 42 | 48 | 39.7 | 201 | 15 Q90NL9 | Q90nl9 human immun |
| 43 | 48 | 39.7 | 202 | 15 Q90P31 | Q90p31 human immun |
| 44 | 48 | 39.7 | 202 | 15 Q90P37 | Q90p37 human immun |
| 45 | 48 | 39.7 | 211 | 10 Q943L4 | Q943l4 oryza sativ |

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY; PRT; 117 AA.
AC Q8TAT9;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Ghrelin.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC025791; AAH25791.1; -.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04543; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
SQ SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;

Query Match 98.3%; Score 119; DB 4; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.6e-09;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAGAEDELEV 23

|||||

Db 52 ALAGWLRPDGGQAGAEDELEV 74

RESULT 2

Q8CH53 PRELIMINARY; PRT; 117 AA.
ID Q8CH53;
AC Q8CH53;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Mariones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Mariones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA SUZUKI H., Ota T., Masaoaka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF42491; AAC06965.1; -.
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 76.0%; Score 92; DB 11; Length 117;
Best Local Similarity 73.9%; Pred. No. 1.3e-05;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQGAEGAEDELE 23
DB 52 ALEGWLRPDGGQGAEGAEDELEI 74

RESULT 3
Q815T3
ID Q815T3 PRELIMINARY; PRT; 1208 AA.
AC Q815T3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE P-type ATPase, putative.
GN PTL0590C
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Partha M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McRadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014846; AAN36207.1; -.
SQ SEQUENCE 1208 AA; 133873 MW; 25AA7752E707E621 CRC64;

Query Match 48.8%; Score 59; DB 5; Length 1208;
Best Local Similarity 52.6%; Pred. No. 8.2;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 GWRPDPGGQGAEGAEDELE 22
DB 1072 GWCRPKDKTSDGYNDELE 1090

RESULT 4
Q9U445
ID Q9U445 PRELIMINARY; PRT; 1264 AA.
AC Q9U445;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P-type ATPase4.

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GN ATPASE4.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21179120; PubMed=11145964;
RA Krishna S., Woodrow C., Webb R., Penny J., Takeyasu K., Kimura M.,
RA East J.M.;
RT "Expression and Functional Characterization of a Plasmodium falciparum
RT Ca2+-ATPase (P1ATP4) Belonging to a Subclass Unique to Apicomplexan
RT Organisms.";
RL J. Biol. Chem. 276:10782-10787(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
CC ATPASES).
DR EMBL; AF203980; AAF17245.1; -.
DR HSP; P04191; IEUL.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 5.
DR PROSITE; PS00154; ATPASE_E1-E2; 1.
KW ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SQ SEQUENCE 1264 AA; 140261 MW; 638142BB1B433640 CRC64;

Query Match 48.8%; Score 59; DB 5; Length 1264;
Best Local Similarity 52.6%; Pred. No. 8.6;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 GWRPDPGGQGAEGAEDELE 22
DB 1128 GWCRPKDKTSDGYNDELE 1146

RESULT 5
Q8LNL6
ID Q8LNL6 PRELIMINARY; PRT; 183 AA.
AC Q8LNL6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OSJNBA0071120.2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartodiaceae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA McCombie W.R., Spiegel L., de la Bastide M., Preston R., Ferraro K.,
RA Kuit K., Nascimento L., Zutavern T., Ballifa V., Bell M., Baker J.,
RA Miller B., Katzenberger F., Muller S., King L., Sullivan P., Yang C.,
RA Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone
RT OSJNBA0071120, from chromosome 10, complete sequence.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC074355; AAM74240.1; -.
DR Gramene; Q8LNL6; -.
KW Hypothetical protein.
SQ SEQUENCE 183 AA; 20492 MW; DE73BD8607292D7B CRC64;

Query Match 45.5%; Score 55; DB 10; Length 183;
Best Local Similarity 47.6%; Pred. No. 4.2;
Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

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QY 3 AGWLRPEDGGQAGAEDELEV 23
 |||: ||| | | : ||
 Db 53 AGWIETEDGSDSESDSEV 73

RESULT 6

Q90P58
 ID Q90P58 PRELIMINARY; PRT; 202 AA.
 AC Q90P58;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nickle D.C.;
 RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF370911; AAK66310.1; -;
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 202
 SQ SEQUENCE 202 AA; 22572 MW; 4CB9ACAFBFB14314 CRC64;

Query Match 43.8%; Score 53; DB 15; Length 202;
 Best Local Similarity 45.5%; Pred. No. 9.1;
 Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGAEDELEV 23
 : | | | | | : | | | |
 Db 180 ITGLLTRDGGGGGTDETEV 201

RESULT 7

Q27724
 ID Q27724 PRELIMINARY; PRT; 1228 AA.
 AC Q27724;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE P-type ATPase.
 GN PFATPASE4.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=K1;
 RC MEDLINE=96408665; PubMed=8813672;
 RX Dyer M., Jackson M., McWhinney C., Zhao G., Mikkelsen R.;
 RT "Analysis of a cation-transporting ATPase of Plasmodium falciparum.";
 RL Mol. Biochem. Parasitol. 78:1-12(1996).
 CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES).
 CC EMBL; U39298; AAC47167.1; -;
 DR HSSP; P04191; 1EUL.
 DR InterPro; IPR001757; ATPase_E1-E2.
 DR InterPro; IPR006068; Cation_ATPase_C.
 DR InterPro; IPR004014; Cation_ATPase_N.
 DR InterPro; IPR005834; Hydrolase.
 DR InterPro; IPR000695; H_ATPase.
 DR Pfam; PF00689; Cation_ATPase_C; 1.
 DR Pfam; PF00690; Cation_ATPase_N; 1.
 DR Pfam; PF00122; E1-E2_ATPase; 1.
 DR Pfam; PF00702; Hydrolase; 1.

DR PRINTS; PRO0119; CATAPASE.
 DR PRINTS; PRO0120; HATPASE.
 DR TIGRFAMS; TIGR01494; ATPase_p-type; 5.
 DR PROSITE; PS00154; ATPASE_E1-E2; 1
 KW ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
 SQ SEQUENCE 1228 AA; 135989 MW; 32C3CFD324964CBE CRC64;

Query Match 43.8%; Score 53; DB 5; Length 1228;
 Best Local Similarity 50.0%; Pred. No. 61;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 WLRPEDGGQAGAEDELE 22
 | | | | : | | | | |
 Db 1131 WCRPKDNKTSGDYNDLE 1148

RESULT 8

Q90P50
 ID Q90P50 PRELIMINARY; PRT; 201 AA.
 AC Q90P50;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nickle D.C.;
 RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF370919; AAK66318.1; -;
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 201
 SQ SEQUENCE 201 AA; 22550 MW; 6CAF6C4609BA517 CRC64;

Query Match 43.0%; Score 52; DB 15; Length 201;
 Best Local Similarity 45.5%; Pred. No. 13;
 Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGAEDELEV 23
 : | | | | | : | | | |
 Db 179 ITGLLTRDGGGGGTDETEV 200

RESULT 9

Q916L1
 ID Q916L1 PRELIMINARY; PRT; 232 AA.
 AC Q916L1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Probable transcriptional regulator.
 GN PA0279.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.W.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 405:959-964(2000).
CC 1- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AE004486; AAC03668.1; -.
DR InterPro; IPR001845; HTH_ArsR.
DR Pfam; PF01022; HTH_5; 1.
DR PRINTS; PR00778; HTHARSR.
DR SMART; SM00418; HTH_ArsR; 1.
KW DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 232 AA; 24440 MW; E3C29187694CF936 CRC64;

Query Match 43.0%; Score 52; DB 16; Length 232;
Best Local Similarity 72.7%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GWRPQDGSRA 212
Db 202 GWRPQDGSRA 212
||||:|||||

RESULT 10

Q82036 PRELIMINARY; PRT; 249 AA.
AC Q82036;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Hirame rhabdovirus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=38142;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8401-H;
RA Nishizawa T.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; D45422; BAA08261.1; -.
DR InterPro; IPR004902; Rhabdo_ncap_2.
DR Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ SEQUENCE 249 AA; 26936 MW; 62FF2BFA5D47DB89 CRC64;

Query Match 43.0%; Score 52; DB 12; Length 249;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 EDGGQAEAGDE 20
Db 235 EDGGEDEGEDE 246
||||:|||||

RESULT 11

Q9QL89 PRELIMINARY; PRT; 392 AA.
AC Q9QL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Hirame rhabdovirus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=38142;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA 9703;
RA Oh H.K., Choi T.J.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104985; AAF14116.1; -.
SQ SEQUENCE 392 AA; 42465 MW; CSA282238FC7A638 CRC64;

DR InterPro; IPR004902; Rhabdo_ncap_2.
DR Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ SEQUENCE 392 AA; 42465 MW; CSA282238FC7A638 CRC64;

Query Match 43.0%; Score 52; DB 12; Length 392;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 EDGGQAEAGDE 20
Db 378 EDGGEDEGEDE 389
||||:|||||

RESULT 12

Q95169 PRELIMINARY; PRT; 977 AA.
AC Q95169;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Skeletal muscle voltage-gated chloride channel gClc-1 (Fragment).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97008165; PubMed=8855341;
RA Beck C.L., Fahlke C., George A.L.;
RT "Molecular basis for decreased muscle chloride conductance in the
RT myotonic goat.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:11248-11252(1996).
DR EMBL; U60275; AAC48666.1; -.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR001807; Cl-channel_volt.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
FT NON_TER 1
SQ SEQUENCE 977 AA; 107894 MW; 1E462B3CB307A148 CRC64;

Query Match 43.0%; Score 52; DB 6; Length 977;
Best Local Similarity 62.5%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWRPQDGSRA 19
Db 895 GWSLPEDGAGATGAGD 910
||||:|||||

RESULT 13

Q9N638 PRELIMINARY; PRT; 436 AA.
AC Q9N638;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F37D6.6 protein.
GN F37D6.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC WILKINSON J.;
RA Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;

| | |
|----|--|
| RA | none; |
| RT | *genome sequence of the nematode <i>C.elegans</i> : A platform for |
| RT | investigating biology.*; |
| RL | Science 282:2012-2018(1998). |
| RN | [3] |
| RP | SEQUENCE FROM N.A. |
| RA | McMurray A.A.; |
| RL | Submitted (JUN-1996) to the EMBL/GenBank/DBDJ databases. |
| DR | EMBL; Z79600; CAB70221.1; -. |
| DR | EMBL; Z79540; CAB70221.1; JOINED. |
| DR | EMBL; Z79540; CAB70215.1; -. |
| DR | EMBL; Z79600; CAB70215.1; JOINED. |
| DR | WormPep; F37D6.6; CE24960. |
| DR | InterPro: IPR001132; Dwarfin. |
| DR | InterPro: IPR003619; Dwarfin_A. |
| DR | Pfam; PF03166; MH2; 1. |
| DR | SMART; SM00523; DWA; 1. |
| DR | SMART; SM00524; DWB; 1. |
| SQ | SEQUENCE 436 AA; 49496 MW; E0C71263BC580EE CRC64; |

Query Match 42.6%; Score 51.5; DB 5; Length 436;
Best Local Similarity 52.9%; Pred. No. 34;
Matches 9; Conservative 5; Mismatches 2; Indels

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QY      5 WLRPE-DGGQAEGAEDE 20
        |:| | | :| | :| | | :
Db     169 WIRPETNGGDDDGSEDK 189

```

RESULT 14

| | | | |
|--------|--|------|---------|
| Q8XW90 | PRELIMINARY; | PRT; | 158 AA. |
| ID | Q8XW90 | | |
| DC | Q8XW90; | | |
| DT | 01-MAR-2002 (TREMBLrel. 20, Created) | | |
| DT | 01-MAR-2002 (TREMBLrel. 20, Last sequence update) | | |
| DT | 01-MAR-2003 (TREMBLrel. 23, Last annotation update) | | |
| DE | Hypothetical protein RSC2585. | | |
| DE | RSC2585 OR RS00797. | | |
| GN | Ralstonia solanacearum (Pseudomonas solanaceum). | | |
| OS | Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; | | |
| OC | Ralstoniaceae; Ralstonia. | | |
| OC | NCBI_TaxID=305; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=GM11000; | | |
| RC | MEDLINE=21681879; PubMed=11823852; | | |
| RA | Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., | | |
| RA | Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., | | |
| RA | Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N., | | |
| RA | Caspin C., Lavie W., Moisan A., Robert C., Saurin W., Schiex T., | | |
| RA | Sigauter P., Thebault P., Whalen M., Wincker P., Levy M., | | |
| RA | Weissenbach J., Boucher C.A.; | | |
| RL | "Genome sequence of the plant pathogen Ralstonia solanacearum."; | | |
| RT | Nature 415:497-502(2002). | | |
| DR | EMBL; AL646070; CAD16292.1; -; | | |
| DR | InterPro; IPR002145; WTH_CopG. | | |
| DR | Pfam; PF01402; WTH_4; 1. | | |
| KW | Hypothetical protein; Complete proteome. | | |
| SQL | SEQUENCE 158 AA; 17814 MW; C9BA42BF9C10E1BC CRC64; | | |

Query Match 42.1%; Score 51; DB 16; Length 158;
Best Local Similarity 58.8%; Pred. No. 14;
Matches 10; Conservative 1; Mismatches 6; Indels

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QY      1  ALAGWLRPEDGGQAEGA 17
        ||| ||| : ||| |||
Db     36  ALASWLSPDAGDQREAA 52

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RESULT 15

Q90NL5
ID Q90NL5
AC Q90NL5; PRT; 201 AA.

| | | |
|----|--|---|
| DT | 01-DEC-2001 | (TREMblrel. 19, Created) |
| DT | 01-DEC-2001 | (TREMblrel. 19, Last sequence update) |
| DT | 01-OCT-2002 | (TREMblrel. 22, Last annotation update) |
| DE | Envelope glycoprotein (Fragment). | |
| DE | ENV. | |
| OS | Human immunodeficiency virus 1. | |
| OS | Viruses; Retroid viruses; Retroviridae; Lentivirus. | |
| OX | NCBI_TaxID=11676; | |
| OX | 11; | |
| RP | SEQUENCE FROM N.A. | |
| RA | Nickie D.C.; | |
| RT | "A Persistent Reservoir for HIV-1 in Alveolar Macrophages."; | |
| RL | Submitted (APR-2001) to the EMBL/GenBank/DBJ databases. | |
| DR | EMBL; AF371104; AK66503.1; | |
| DR | InterPro: IPR000777; GP120. | |
| DR | Pfam: PF00516; GP120; 1. | |
| KW | AIDS; Coat protein; Glycoprotein. | |
| FT | NON_TER | 1 |
| FT | FT | 201 |
| FT | NON_TER | 201 |
| SO | SEQUENCE | 201 AA: 22470 MW: E1993A2A412EC118 CRC64: |

Query Match 42.1%; Score 51; DB 15; Length 201;
Best Local Similarity 40.9%; Pred. NO. 18;
Matches 9; Conservative 4; Mismatches 9; Indels

| | | | |
|----------------|-----|--------------------------|-----|
| Qy | 2 | LAGWLRPEDGGQAEGADELEV | 23 |
| | | : : | |
| D _b | 179 | ITGLLLT RDGGCGNGT DNETEI | 200 |

Search completed: September 11, 2003, 17:30:28
Job time : 22.893 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 17:27:22 : Search time 24.2299 Seconds
(without alignments)
150.669 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 23

Sequence: 1 ALAGWLRPEDGGQAEGBEDEV 23

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 23 | 100.0 | 23 | AAE23840 | Human zsig33-linker |
| 2 | 23 | 100.0 | 23 | AAE23841 | Human zsig33-linker |
| 3 | 23 | 100.0 | 23 | AAE15885 | Human zsig33-linker |
| 4 | 23 | 100.0 | 23 | AAE15886 | Human zsig33-linker |
| 5 | 23 | 100.0 | 24 | AAE23839 | Human zsig33-linker |
| 6 | 23 | 100.0 | 24 | AAE15884 | Human zsig33-linker |
| 7 | 23 | 100.0 | 91 | AAE33410 | Human exon 3-delet |
| 8 | 23 | 100.0 | 116 | AAE60517 | Human des-Gln14-gh |
| 9 | 23 | 100.0 | 117 | AAW87991 | Protein designated |

| | | | | | | |
|----|----|-------|------|----|-----------|--------------------|
| 10 | 23 | 100.0 | 117 | 21 | AAW87236 | Human signal pepti |
| 11 | 23 | 100.0 | 117 | 22 | AAW38890 | Human polypeptide |
| 12 | 23 | 100.0 | 117 | 22 | AAW38890 | Human zsig33 polyp |
| 13 | 23 | 100.0 | 117 | 22 | AAW62649 | zsig33 protein. H |
| 14 | 23 | 100.0 | 117 | 22 | AAW60511 | Human ghrelin prep |
| 15 | 23 | 100.0 | 117 | 23 | ABW78319 | Amino acid sequenc |
| 16 | 23 | 100.0 | 117 | 23 | AAE23838 | Human zsig33 prote |
| 17 | 23 | 100.0 | 117 | 23 | AAE15883 | Human zsig33 prote |
| 18 | 23 | 100.0 | 117 | 24 | ABU65790 | Human PRO polypept |
| 19 | 23 | 100.0 | 117 | 24 | ABU67066 | Human secreted/tra |
| 20 | 23 | 100.0 | 117 | 24 | ABU59871 | Novel secreted and |
| 21 | 23 | 100.0 | 117 | 24 | ABU59124 | Novel human secret |
| 22 | 23 | 100.0 | 117 | 24 | ABU59271 | Human secreted/tra |
| 23 | 23 | 100.0 | 117 | 24 | ABU59420 | Novel human secret |
| 24 | 23 | 100.0 | 117 | 24 | ABU60555 | Human secreted/tra |
| 25 | 23 | 100.0 | 117 | 24 | ABU58046 | Human PRO polypept |
| 26 | 23 | 100.0 | 117 | 24 | ABU58977 | Human secreted/tra |
| 27 | 23 | 100.0 | 117 | 24 | AAE33409 | Human preproghreli |
| 28 | 23 | 100.0 | 117 | 24 | ABU13937 | Human PRO1066 poly |
| 29 | 23 | 100.0 | 117 | 24 | ABU10892 | Human PRO polypept |
| 30 | 23 | 100.0 | 118 | 21 | AAW66708 | Membrane-bound pro |
| 31 | 23 | 100.0 | 118 | 22 | AAU12392 | Human PRO1066 poly |
| 32 | 23 | 100.0 | 118 | 22 | AAW65231 | Human PRO1066 (UNQ |
| 33 | 23 | 100.0 | 126 | 22 | AAW40676 | Human polypeptide |
| 34 | 10 | 43.5 | 89 | 22 | AAW60523 | Bovine ghrelin pre |
| 35 | 8 | 34.8 | 334 | 21 | AAW629677 | Arabidopsis thalia |
| 36 | 8 | 34.8 | 428 | 21 | AAW629676 | Arabidopsis thalia |
| 37 | 8 | 34.8 | 483 | 21 | AAW629675 | Arabidopsis thalia |
| 38 | 7 | 30.4 | 311 | 19 | AAW36129 | Snpr activator pro |
| 39 | 7 | 30.4 | 311 | 21 | AAW30494 | Amino acid sequenc |
| 40 | 7 | 30.4 | 442 | 23 | ABP38188 | Staphylococcus epi |
| 41 | 7 | 30.4 | 1931 | 22 | ABB66948 | Drosophila melanog |
| 42 | 6 | 26.1 | 14 | 22 | AAW66893 | Human peptide #168 |
| 43 | 6 | 26.1 | 26 | 24 | AAE33406 | PD-1_Ctad12 peptid |
| 44 | 6 | 26.1 | 26 | 24 | ABU18534 | PD-1-related pepti |
| 45 | 6 | 26.1 | 39 | 20 | AAW50239 | Neutrophil-activat |

ALIGNMENTS

RESULT 1
AAE23840
ID AAE23840 standard; peptide; 23 AA.
XX
AC AAE23840;
XX

DT 10-SEP-2002 (first entry)
XX
DE Human zsig33-linker peptide #2.
XX

KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.

OS Homo sapiens.

XX US2002055156-A1.

XX 09-MAY-2002.

XX 10-MAY-2001; 2001US-0853253.

XX 11-MAY-2000; 2000US-203300P.

XX (JASP/) JASPERS S R.

XX (SHEP/) SHEPPARD P O.

XX (DEIS/) DEISHER T A.

XX (BISH/) BISHOP P D.

XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI; 2002-443750/47.

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones -
PT
PT
PS Claim 1; Page 28; 34pp; English.
XX
CC The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 23; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
DB 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 2
AAE23841
ID AAE23841 standard; peptide; 23 AA.
XX
AC AAE23841;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human zsig33-linker peptide #3.
XX
KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.
XX
OS Homo sapiens.
XX
PN US2002055156-A1.
XX
PD 09-MAY-2002.
XX
PF 10-MAY-2001; 2001US-0853253.
XX
PR 11-MAY-2000; 2000US-203300P.
XX
PA (JASP/) JASPERS S R.
PA (SHEP/) SHEPPARD P O.
PA (DEIS/) DEISHER T A.
PA (BISH/) BISHOP P D.
XX
PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX
DR WPI; 2002-443750/47.
XX
PT ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones -
PS Claim 1; Page 28; 34pp; English.
XX
CC The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 23; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
DB 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 3
AAE15885
ID AAE15885 standard; peptide; 23 AA.
XX
AC AAE15885;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human zsig33-linker peptide #2.
XX
KW Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
KW adsorption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33-linker peptide.
XX
OS Homo sapiens.
XX
PN WO200187933-A2.
XX
PD 22-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-US15091.
XX
PR 11-MAY-2000; 2000US-0569271.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX
DR WPI; 2002-082982/11.
DR N-PSDB; AAD25760.
XX
PT New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and
PT treating gastrointestinal and growth related diseases, comprises

FT XX /note= "Hydrophilic region"
 PN XX US2002055156-A1.
 XX XX
 PD XX 09-MAY-2002.
 XX XX
 PF XX 10-MAY-2001; 2001US-0853253.
 XX XX
 PR XX 11-MAY-2000; 2000US-203300P.
 XX XX
 PA (JASP/) JASPERS S R.
 PA (SHEP/) SHEPPARD P O.
 PA (DEIS/) DEISHER T A.
 PA (BISH/) BISHOP P D.
 XX XX
 PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 XX XX
 DR WPI: 2002-443750/47.
 DR N-PSDB: AAD38239.
 XX XX
 PT ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
 PT contractility, nutrient uptake, growth hormones and/or secretion of
 PT digestive/pancreatic enzymes and hormones
 XX XX
 PS Claim 1; Page 28; 34pp; English.
 XX XX
 CC The invention relates to zsig33-like peptides and their corresponding
 CC nucleic acids and methods for modulating gastric contractility, nutrient
 CC uptake, growth hormones, secretion of digestive enzymes and hormones.
 CC The sequences of the invention are used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate ZSIG33 expression.
 CC The nucleic acids of the invention and their complements are used as
 CC DNA probes in diagnostic assays to detect and quantitate the presence
 CC of similar nucleic acids in samples, and therefore which patients may be
 CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
 CC in the production of antibodies against ZSIG33 and in assays to identify
 CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
 CC and antagonists are used to down regulate expression and activity. The
 CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
 CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
 CC assay (ELISA)). The peptides and nucleic acids of the invention are used
 CC to modulate gastric contractility, nutrient uptake, growth hormones, the
 CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
 CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
 CC and zsig33-like peptide is used in protein therapy. The present sequence
 CC is human zsig33-like peptide, zsig33-linker peptide.
 XX XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 23; DB 23; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.1e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGGAEGAEDELEV 23
 DB 1 ALAGWLRPEDGGGAEGAEDELEV 23
 RESULT 6
 AAE15884
 ID AAE15884 standard; peptide; 24 AA.
 AC AAE15884;
 XX XX
 DT 26-MAR-2002 (first entry)
 DE Human zsig33-linker peptide #1.
 XX XX
 KW Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
 KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
 KW adsorption enhancer; gastrointestinal disease; growth related disease;
 KW inflammation; gene therapy; growth regulation; blood vessel formation;
 KW HIV; zsig33-linker peptide.

XX Homo sapiens.
 OS XX
 FH XX Location/Qualifiers
 FT Key 6..22
 FT Region /note= "Hydrophilic antigenic site"
 FT Region 7..18
 FT Region /note= "Hydrophilic region"
 XX XX
 PN W0200187933-A2.
 XX XX
 PD 22-NOV-2001.
 XX XX
 PF 10-MAY-2001; 2001WO-US15091.
 XX XX
 PR 11-MAY-2000; 2000US-0569271.
 XX XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX XX
 PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 XX XX
 DR WPI: 2002-082982/11.
 DR N-PSDB: AAD25760.
 XX XX
 PT New polypeptides, useful for modulating gastric contractility, nutrient
 PT uptake, pancreatic secretion of hormones, digestive enzymes and
 PT treating gastrointestinal and growth related diseases, comprises
 PT zsig33-like peptides -
 XX XX
 PS Claim 1a; Page 81; 89pp; English.
 XX XX
 CC The invention relates to zsig33-like peptides (ZS33LP) including
 CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and
 CC zsig33-epsilon peptides and nucleic acid molecules encoding such
 CC zsig33-like peptides. ZS33LP peptides activate the immune system
 CC in boosting immunity to infectious diseases, treating immunocompromised
 CC patients such as human immunodeficiency virus (HIV) patients, in
 CC improving vaccines and in treatment of bacterial, viral, protozoal and
 CC fungal infections. Peptides of the invention are used to identify and
 CC isolate receptors involved in growth regulation in the liver, blood
 CC vessel formation and other developmental processes. They are useful for
 CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
 CC growth and/or differentiation of tumour cells, as additives to anti-
 CC hypoglycaemic preparations containing glucose and as adsorption
 CC enhancers for oral drugs which require fast nutrient action and to
 CC stimulate glucose-induced insulin release. They are also useful as
 CC research reagents for the expansion, differentiation, growth factor and
 CC hormone secretion and/or cell-cell interactions of tissues associated
 CC with gastrointestinal system, brain and central nervous system. These
 CC molecules are useful for treating dysfunction associated with contractile
 CC tissues or to suppress or enhance contractility in vivo and to treat
 CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
 CC acids and/or antibodies are useful for treating disorders associated
 CC with gastrointestinal contractility, secretion of digestive enzymes,
 CC hormone and acids, secretion of hormones in the pancreas and/or brain,
 CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
 CC and regulation of nutrient absorption. Sequences of the invention are
 CC useful in gene therapy. The present sequence is human zsig33-linker
 CC peptide.
 XX XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 23; DB 23; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.1e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGGAEGAEDELEV 23
 DB 1 ALAGWLRPEDGGGAEGAEDELEV 23
 RESULT 7
 AAE33410

ID AAE33410 standard; Protein; 91 AA.
 AC AAE33410;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human exon 3-deleted ghrelin protein.
 XX
 KW Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
 KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
 KW cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN W0200290387-A1.
 XX
 PD 14-NOV-2002.
 XX
 XX 10-MAY-2002; 2002WO-AU00582.
 XX
 PF 10-MAY-2001; 2001AU-0004919.
 PR 17-DEC-2001; 2001AU-0009567.
 XX
 PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 PI Chopin LK, Jeffery PL, Herington AC;
 XX
 DR WPI; 2003-111957/10.
 DR N-PSDB; AAD50726.
 XX
 XX Identifying a cancer cell or tissue for treating prostate, ovarian,
 PT breast cancer, or benign prostatic hyperplasia, by detecting the
 PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
 PT 1b proteins or nucleic acids -
 XX
 PS Claim 14; Page 34; 50pp; English.
 XX
 CC The invention relates to a method for identifying a cancer cell or
 CC tissue of the reproductive system by detecting expression of a ghrelin,
 CC an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic
 CC acids. The antibodies, exon 3-deleted form of preproghrelin and
 CC antagonists are useful for treating cancer of the reproductive system
 CC such as prostate, ovarian, breast, cervical or uterine cancer,
 CC choriocarcinoma or benign prostatic hyperplasia. The present sequence
 CC is human exon 3-deleted ghrelin protein.
 XX
 SQ Sequence 91 AA;
 Query Match 100.0%; Score 23; DB 24; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 8
 AAB60517
 ID AAB60517 standard; Protein; 116 AA.
 XX
 AC AAB60517;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
 XX
 KW Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX

PN W0200107475-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-JP04907.
 XX
 PR 23-JUL-1999; 99JP-0210002.
 PR 29-NOV-1999; 99JP-0338841.
 PR 26-APR-2000; 2000JP-0126623.
 XX
 PA (KANG/) KANGAWA K.
 XX
 PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 XX
 DR WPI; 2001-159704/16.
 DR N-PSDB; AAF59647.
 XX
 XX New peptide compounds which induce growth hormone secretion and
 PT elevate cell calcium concentrations, useful in treatment and diagnosis
 PT of infant growth disorders -
 XX
 PS Claim 3; Page 186-187; 210pp; Japanese.
 XX
 CC The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX
 SQ Sequence 116 AA;
 Query Match 100.0%; Score 23; DB 22; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 51 ALAGWLRPEDGGQAGAEDELEV 73
 RESULT 9
 AAW87991
 ID AAW87991 standard; Protein; 117 AA.
 XX
 AC AAW87991;
 XX
 DT 07-APR-1999 (first entry)
 XX
 DE Protein designated zsig33.
 XX
 KW Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
 KW nutrient absorption regulation; obesity; metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 PI Key Location/Qualifiers
 FT Peptide 1..23 /note= "signal peptide"
 FT Protein 24..117 /note= "mature protein"
 FT
 XX

PN WO9842840-A1.
 XX 01-OCT-1998.
 XX 23-MAR-1998; 98WO-US05620.
 XX 24-MAR-1997; 97US-0822897.
 PR 24-MAR-1997; 97US-0041102.
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Delsher TA, Sheppard PO;
 XX WPI; 1999-070071/06.
 DR N-PSDB; AAX04550.
 XX
 XX Human polypeptide having homology to motilin, zsig33 - useful e.g.
 PT to treat gastrointestinal motility disorders, obesity etc. and to
 PT identify antagonists to treat gastrointestinal hypermotility
 XX
 PS Claim 13; Page 55-56; 69pp; English.
 XX
 CC The present sequence represents a protein designated zsig33. The nucleic
 CC acids are strongly expressed in stomach tissue. The polypeptide (or
 CC allelic variants/orologs) can be used to stimulate gastric motility,
 CC measured as increased transit time or gastric emptying of an ingested
 CC substance in mammals. The products are used to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes/acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
 CC absorption regulation. zsig33 polypeptides may also be important
 CC neurologically, since the family of gut-brain peptides to which the
 CC homologous protein motilin belongs has been associated with neurological
 CC and CNS functions. They may therefore be used e.g. to regulate satiety
 CC or treat obesity and other metabolic disorders where neurological
 CC feedback modulates nutritional absorption. They are useful to identify
 CC zsig33 agonists, antagonists and ligands and to produce antibodies.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 23; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
 Db 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 10
 ID AAY87236 standard; Protein: 117 AA.
 XX
 AC AAY87236;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE Human signal peptide containing protein HSpp-13 SEQ ID NO:13.
 XX
 KW Human; signal peptide-containing protein; HSpp; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 PN WO200000610-A2.
 XX

PD 06-JAN-2000.
 XX 25-JUN-1999; 99WO-US14484.
 XX 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX (INCY-) INCYTE PHARM INC.
 XX
 XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX WPI: 2000-160673/14.
 DR N-PSDB; AAZ98121.
 XX
 XX New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease -
 XX
 PS Claim 1; Page 168-169; 327pp; English.
 XX
 CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSpp-1 to HSpp-134. HSpps have
 CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can
 CC be used in gene therapy. HSpps can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSpp. Antagonists of
 CC HSpp are used to treat or prevent disorders associated with increased
 CC activity or function of HSpp. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC aschma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSpp
 CC nucleic acids can be used for the recombinant production of HSpp, for
 CC detecting HSpp in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSpp are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSpp-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSpp
 CC from natural sources.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 23; DB 21; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
 Db 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 11
 ID AAM38890 standard; Protein: 117 AA.
 XX
 AC AAM38890;
 XX
 XX 22-OCT-2001 (first entry)
 DT
 XX Human polypeptide SEQ ID NO 2035.
 DE
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW Leukaemia.
XX Homo sapiens.
XX WO200153312-A1.
XX 26-JUL-2001.
XX 26-DEC-2000; 2000WO-US34263.
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0522317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX WPI: 2001-442253/47.
XX N-PSDB; AA158046.
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX Example 3; SEQ ID NO 2035; 10078pp; English.
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AA138642-AA142213) with nootropic,
XX immunosuppressant and cytoskeletal activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.
XX Sequence 117 AA;
XX Query Match 100.0%; Score 23; DB 22; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-14;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 ALAGWLRLPEDGGGAEGAEDELEV 23
XX Db 52 ALAGWLRLPEDGGGAEGAEDELEV 74
XX RESULT 12
XX AAB62649
XX ID AAB62649 standard; Protein; 117 AA.
XX AC AAB62649;
XX 23-JUL-2001 (first entry)
XX DT Human zslg33 polypeptide.
XX DE
XX XX

KW zslg33; signal transduction; hormone; enzyme; neural development;
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
KW glucose; osteopathic; anorectic; vulnerable; immunomodulator; GHS-R;
KW G-protein coupled receptor.
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX Peptide 24..37
XX /note= "specifically claimed fragment that binds to
XX the GHS-R"
XX WO200138355-A2.
XX 31-MAY-2001.
XX 22-NOV-2000; 2000WO-US32074.
XX 22-NOV-1999; 99US-0166765.
XX (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO, Jaspers SR, Delisher TA, Bishop PD;
XX WPI: 2001-355879/37.
XX N-PSDB; AA83678.
XX Forming reversible peptide receptor complex for purifying cell and
XX peptides, stimulating signal transduction and modulating hormone
XX secretion, involves contacting a receptor with zslg33 polypeptide -
XX Claim 1; Page 93-94; 111pp; English.
XX The invention relates to a method of forming a reversible peptide-
XX receptor complex that involves providing an immobilized receptor, and
XX contacting the receptor with a zslg33 peptide (comprising residues 24-37
XX of AAB62649), where the receptor binds to the zslg33 peptide. The method
XX is useful for purifying cells, purifying a peptide, stimulating signal
XX transduction in a cell expressing a receptor. It is also useful for
XX modulating secretion of hormones, neural development and/or utilization,
XX gastric contractility, nutrient uptake, secretion of digestive and
XX pancreatic enzymes and hormones, secretion of insulin-like growth factor
XX -I, secretion of non-zslg33 proteins. It is useful for modulating growth
XX hormone secretion in a mammal having a disease associated with abnormal
XX levels of growth hormone, such as osteoporosis, bone repair, bone
XX remodeling, low osteoblast levels, cartilage repair and remodeling,
XX skeletal dysplasia, immune suppression, obesity, growth retardation,
XX protein catabolic responses after surgery, cachexia, protein loss,
XX dwarfism, wound healing and ovulation induction, treating a mammal having
XX a metabolic disorder requiring neurological feedback, such as satiety
XX regulation, glucose absorption and metabolism and neuropathy-associated
XX gastrointestinal disorders, and stimulating glucose-induced insulin
XX release in a mammal. The present sequence represents the human zslg33
XX polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
XX Sequence 117 AA;
XX Query Match 100.0%; Score 23; DB 22; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-14;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 ALAGWLRLPEDGGGAEGAEDELEV 23
XX Db 52 ALAGWLRLPEDGGGAEGAEDELEV 74
XX RESULT 13
XX AAB20101
XX ID AAB20101 standard; Protein; 117 AA.
XX AC AAB20101;
XX XX

DT 23-APR-2001 (first entry)
XX zsig33 protein.
DE
XX SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
KW nutritional absorption modulator; growth hormone secretagogue;
KW therapy; human.
XX
OS Homo sapiens.
XX
PH Location/Qualifiers
FT Peptide
FT 1..23
FT /label= Signal_peptide
FT Protein
FT 24..117
FT /label= Mature_protein
FT Peptide
FT 24..34
FT /label= SGIP_peptide
FT /note= "this peptide is claimed in Claim 1"
XX
PN WO200100830-A1.
XX
XX
XX 04-JAN-2001.
XX
XX 30-JUN-2000; 2000WO-US18306.
XX
XX 30-JUN-1999; 99US-0345157.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
XX WPI; 2001-123010/13.
XX
XX N-PSDB; AAF30033.
XX
XX Novel variants of SGIP peptides for modulating contractility in
XX duodenum or jejunum tissue, pancreatic secretion of hormones and
XX digestive enzymes, inducing growth hormone secretion or modulating
XX gastric emptying -
XX
XX Disclosure; 54; 61pp; English.
XX
XX The present sequence is that of zsig33, a secreted protein with
XX homology to motilin (see AAB20102). zsig33 is expressed at high
XX levels in the stomach, and at lower levels in the small intestine
XX and pancreas. A novel peptide fragment of zsig33, termed SGIP (see
XX AAB20100), is claimed. SGIP is a ligand for growth hormone
XX secretagogue receptor, and is therefore useful for modulating
XX secretion of growth hormone and insulin like growth factor 1.
XX SGIP, and variant SGIP peptides, are used in claimed methods for
XX stimulating contractility in duodenum or jejunum tissue,
XX modulating pancreatic secretion of hormones and digestive enzymes,
XX inducing growth hormone secretion, and modulating gastric emptying.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 23; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQGAEGAEDELEV 23
Db 52 ALAGWLRPEDGGQGAEGAEDELEV 74

RESULT 14
AAB60511
ID AAB60511 standard; Protein; 117 AA.
XX
AC AAB60511;
XX
XX 24-APR-2001 (first entry)
XX
DE Human ghrelin preproprotein, SEQ ID NO:5.

XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
KW calcium concentration elevation; infant growth disorder;
KW growth hormone deficiency.
XX
OS Homo sapiens.
XX
PN WO200107475-A1.
XX
XX 01-FEB-2001.
XX
XX 24-JUL-2000; 2000WO-JP04907.
XX
XX 23-JUL-1999; 99JP-0210002.
XX 29-NOV-1999; 99JP-0338841.
XX 26-APR-2000; 2000JP-0126623.
XX
XX (KANG/) KANGAWA K.
XX
XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
XX
XX WPI; 2001-159704/16.
XX
XX N-PSDB; AAF59645.
XX
XX New peptide compounds which induce growth hormone secretion and
XX elevate cell calcium concentrations, useful in treatment and diagnosis
XX of infant growth disorders -
XX
XX Claim 3; Page 182; 210pp; Japanese.
XX
XX The invention relates to a novel peptide compound or its salt which
XX induces the secretion of growth hormone and/or elevates calcium ion
XX concentration in cells. The peptides are ghrelin homologues and are
XX characterised in that at least one amino acid has been substituted by
XX a modified amino acid and/or a non-amino acid compound. The invention
XX also encompasses the unmodified peptides; the DNA encoding the peptides;
XX vectors and host cells comprising such DNA; a method of producing the
XX peptides comprising recombinant production, optionally followed by
XX chemical modification; an antibody specific for a peptide of the
XX invention; and an assay and kit for detecting the peptides. The peptides
XX of the invention are useful for treating and/or diagnosing diseases
XX caused by a deficiency in growth hormone expression or activity. In
XX particular, they are useful for promoting infant growth due to growth
XX hormone deficiency. The compounds of the invention are safe with
XX no accompanying side effects. The present sequence represents a
XX ghrelin-type growth hormone secretagogue (GHS) precursor protein
XX of the invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 23; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQGAEGAEDELEV 23
Db 52 ALAGWLRPEDGGQGAEGAEDELEV 74

RESULT 15
ABB78319
ID ABB78319 standard; Protein; 117 AA.
XX
XX ABB78319;
XX
XX 05-DEC-2002 (first entry)
XX
XX Amino acid sequence of a human zsig33.
XX
XX Short gastrointestinal peptide; SGIP; zsig33; motilin.
XX
XX Homo sapiens.
XX

FH Key Location/Qualifiers
FT Peptide 1..23
FT Protein /note= "signal peptide"
FT 24..119
FT /note= "mature protein"
XX US6420521-B1.
PN 16-JUL-2002.
XX
PD 30-JUN-2000; 2000US-0608810.
XX
PF 30-JUN-1999; 99US-141592P.
XX
PR (ZYMO) ZYMOGENETICS INC.
XX
PA Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
PI WPI; 2002-634794/68.
XX N-PSDB; ABV72214.
DR
XX
PT New Short Gastrointestinal Peptide, which has homology to motilin,
PT useful for preventing, diagnosing and treating gastrointestinal
PT disorders -
XX
PS Disclosure; Columns 39-40; 23pp; English.
XX
SS
CC The present sequence represents human zsig33. The specification describes
CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.
CC SGIP has homology to motilin. The SGIP peptide may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate SGIP expression. For example, SGIP may be used to treat
CC disorders associated with decreased expression by rectifying mutations
CC or deletions in a patient's genome that affect the activity of SGIP by
CC expressing inactive proteins or to supplement the patients own production
CC of SGIP. SGIP may also be used as an antigen in the production of
CC antibodies against SGIP and in assays to identify modulators of SGIP
CC expression and activity. The anti-SGIP antibodies, agonists and
CC antagonists may also be used to regulate expression and activity. The
CC anti-SGIP antibodies may also be used as diagnostic agents for detecting
XX the presence of SGIP in samples.
SQ Sequence 117 AA;
Query Match 100.0%; Score 23; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRLRPEDGGQAGAEDELEV 23
Db 52 ALAGWLRLRPEDGGQAGAEDELEV 74
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Job time : 25.2299 secs

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:48:42 ; Search time 7.87166 Seconds
(without alignments)
123.627 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 23
Sequence: 1 ALAGWLRPEDGGQAEDELEV 23

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 23 | 100.0 | 117 | 3 | US-09-046-479-2 |
| 2 | 23 | 100.0 | 117 | 4 | US-08-822-897C-2 |
| 3 | 23 | 100.0 | 117 | 4 | US-09-608-810A-4 |
| 4 | 23 | 100.0 | 117 | 4 | US-09-996-243-268 |
| 5 | 7 | 30.4 | 442 | 4 | US-09-134-001C-3033 |
| 6 | 7 | 30.4 | 552 | 4 | US-09-252-991A-27032 |
| 7 | 7 | 30.4 | 599 | 4 | US-09-252-991A-20368 |
| 8 | 7 | 30.4 | 981 | 4 | US-09-252-991A-16798 |
| 9 | 6 | 26.1 | 39 | 1 | US-08-428-488-13 |
| 10 | 6 | 26.1 | 97 | 2 | US-08-403-852D-31 |
| 11 | 6 | 26.1 | 97 | 3 | US-08-510-646B-32 |
| 12 | 6 | 26.1 | 97 | 3 | US-09-231-818-31 |
| 13 | 6 | 26.1 | 129 | 3 | US-09-135-994-12 |
| 14 | 6 | 26.1 | 129 | 4 | US-09-684-843A-12 |
| 15 | 6 | 26.1 | 183 | 4 | US-09-198-452A-612 |
| 16 | 6 | 26.1 | 199 | 4 | US-09-252-991A-32089 |
| 17 | 6 | 26.1 | 202 | 4 | US-09-252-991A-26333 |
| 18 | 6 | 26.1 | 259 | 4 | US-09-252-991A-17300 |
| 19 | 6 | 26.1 | 288 | 1 | US-08-396-650-1 |
| 20 | 6 | 26.1 | 288 | 1 | US-08-768-626-1 |
| 21 | 6 | 26.1 | 292 | 4 | US-09-252-991A-18951 |
| 22 | 6 | 26.1 | 292 | 4 | US-09-252-991A-30162 |
| 23 | 6 | 26.1 | 305 | 4 | US-09-328-352-6794 |
| 24 | 6 | 26.1 | 326 | 4 | US-09-252-991A-33000 |
| 25 | 6 | 26.1 | 329 | 4 | US-09-843-297-2 |
| 26 | 6 | 26.1 | 359 | 4 | US-09-266-965-120 |
| 27 | 6 | 26.1 | 366 | 4 | US-09-252-991A-29569 |

| | | | | | | |
|----|---|------|-----|---|----------------------|-------------------|
| 28 | 6 | 26.1 | 378 | 4 | US-09-325-932A-158 | Sequence 158, App |
| 29 | 6 | 26.1 | 399 | 4 | US-09-252-991A-25687 | Sequence 25687, A |
| 30 | 6 | 26.1 | 402 | 3 | US-09-464-483-4 | Sequence 4, Appl1 |
| 31 | 6 | 26.1 | 402 | 3 | US-09-414-664-4 | Sequence 4, Appl1 |
| 32 | 6 | 26.1 | 489 | 4 | US-09-252-991A-22896 | Sequence 22896, A |
| 33 | 6 | 26.1 | 502 | 4 | US-09-207-388-19 | Sequence 19, Appl |
| 34 | 6 | 26.1 | 510 | 4 | US-09-252-991A-17695 | Sequence 2, Appl1 |
| 35 | 6 | 26.1 | 529 | 3 | US-09-464-483-2 | Sequence 2, Appl1 |
| 36 | 6 | 26.1 | 529 | 3 | US-09-414-664-2 | Sequence 2, Appl1 |
| 37 | 6 | 26.1 | 531 | 1 | US-08-531-601-1 | Sequence 1, Appl1 |
| 38 | 6 | 26.1 | 531 | 2 | US-08-859-032-1 | Sequence 1, Appl1 |
| 39 | 6 | 26.1 | 535 | 1 | US-08-737-597-10 | Sequence 10, Appl |
| 40 | 6 | 26.1 | 548 | 4 | US-09-207-388-23 | Sequence 23, Appl |
| 41 | 6 | 26.1 | 550 | 4 | US-09-207-388-20 | Sequence 20, Appl |
| 42 | 6 | 26.1 | 568 | 4 | US-09-207-388-22 | Sequence 22, Appl |
| 43 | 6 | 26.1 | 568 | 4 | US-09-207-388-24 | Sequence 24, Appl |
| 44 | 6 | 26.1 | 570 | 4 | US-09-207-388-21 | Sequence 21, Appl |
| 45 | 6 | 26.1 | 588 | 4 | US-09-252-991A-31356 | Sequence 31356, A |

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-09-046-479-2

Query Match 100.0%; Score 23; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | |
|--|---------------------------|------------|
| | PRIOR APPLICATION NUMBER: | 60/0899655 |
| | PRIOR FILING DATE: | 1998-06-17 |
| | PRIOR APPLICATION NUMBER: | 60/089801 |
| | PRIOR FILING DATE: | 1998-06-18 |
| | PRIOR APPLICATION NUMBER: | 60/089907 |
| | PRIOR FILING DATE: | 1998-06-18 |
| | PRIOR APPLICATION NUMBER: | 60/089908 |
| | PRIOR FILING DATE: | 1998-06-18 |
| | PRIOR APPLICATION NUMBER: | 60/089947 |
| | PRIOR FILING DATE: | 1998-06-19 |
| | PRIOR APPLICATION NUMBER: | 60/089948 |
| | PRIOR FILING DATE: | 1998-06-19 |
| | PRIOR APPLICATION NUMBER: | 60/089952 |
| | PRIOR FILING DATE: | 1998-06-19 |
| | PRIOR APPLICATION NUMBER: | 60/090246 |
| | PRIOR FILING DATE: | 1998-06-22 |
| | PRIOR APPLICATION NUMBER: | 60/090252 |
| | PRIOR FILING DATE: | 1998-06-22 |
| | PRIOR APPLICATION NUMBER: | 60/090254 |
| | PRIOR FILING DATE: | 1998-06-22 |
| | PRIOR APPLICATION NUMBER: | 60/090349 |
| | PRIOR FILING DATE: | 1998-06-23 |
| | PRIOR APPLICATION NUMBER: | 60/090355 |
| | PRIOR FILING DATE: | 1998-08-23 |
| | PRIOR APPLICATION NUMBER: | 60/090429 |
| | PRIOR FILING DATE: | 1998-08-24 |
| | PRIOR APPLICATION NUMBER: | 60/090431 |
| | PRIOR FILING DATE: | 1998-06-24 |
| | PRIOR APPLICATION NUMBER: | 60/090435 |
| | PRIOR FILING DATE: | 1998-08-24 |
| | PRIOR APPLICATION NUMBER: | 60/090444 |
| | PRIOR FILING DATE: | 1998-06-24 |
| | PRIOR APPLICATION NUMBER: | 60/090445 |
| | PRIOR FILING DATE: | 1998-06-24 |
| | PRIOR APPLICATION NUMBER: | 60/090472 |
| | PRIOR FILING DATE: | 1998-08-24 |
| | PRIOR APPLICATION NUMBER: | 60/090535 |
| | PRIOR FILING DATE: | 1998-06-24 |
| | PRIOR APPLICATION NUMBER: | 60/090540 |
| | PRIOR FILING DATE: | 1998-06-24 |
| | PRIOR APPLICATION NUMBER: | 60/090542 |
| | PRIOR FILING DATE: | 1998-08-24 |
| | PRIOR APPLICATION NUMBER: | 60/090557 |
| | PRIOR FILING DATE: | 1998-06-24 |
| | PRIOR APPLICATION NUMBER: | 60/090676 |
| | PRIOR FILING DATE: | 1998-06-25 |
| | PRIOR APPLICATION NUMBER: | 60/090678 |
| | PRIOR FILING DATE: | 1998-06-25 |
| | PRIOR APPLICATION NUMBER: | 60/090690 |
| | PRIOR FILING DATE: | 1998-06-25 |
| | PRIOR APPLICATION NUMBER: | 60/090694 |
| | PRIOR FILING DATE: | 1998-06-25 |
| | PRIOR APPLICATION NUMBER: | 60/090695 |
| | PRIOR FILING DATE: | 1998-06-25 |
| | PRIOR APPLICATION NUMBER: | 60/090696 |
| | PRIOR FILING DATE: | 1998-06-25 |
| | PRIOR APPLICATION NUMBER: | 60/090662 |
| | PRIOR FILING DATE: | 1998-06-26 |
| | PRIOR APPLICATION NUMBER: | 60/090863 |
| | PRIOR FILING DATE: | 1998-06-26 |
| | PRIOR APPLICATION NUMBER: | 60/091360 |
| | PRIOR FILING DATE: | 1998-07-01 |
| | PRIOR APPLICATION NUMBER: | 60/091478 |
| | PRIOR FILING DATE: | 1998-07-02 |
| | PRIOR APPLICATION NUMBER: | 60/091544 |
| | PRIOR FILING DATE: | 1998-07-01 |
| | PRIOR APPLICATION NUMBER: | 60/091519 |
| | PRIOR FILING DATE: | 1998-07-02 |
| | PRIOR APPLICATION NUMBER: | 60/091626 |
| | PRIOR FILING DATE: | 1998-07-02 |
| | PRIOR APPLICATION NUMBER: | 60/091633 |
| | PRIOR FILING DATE: | 1998-07-02 |
| | PRIOR APPLICATION NUMBER: | 60/091978 |

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPDGGQAGAEDELEV 23
Db 52 ALAGWLRPDGGQAGAEDELEV 74
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RESULT 5

US-09-134-001C-3033
; Sequence 3033, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3033
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3033

Query Match 30.4%; Score 7; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DGGQAG 16
Db 189 DGGQAG 195
|||||

RESULT 6

US-09-252-991A-27032
; Sequence 27032, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27032
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27032

Query Match 30.4%; Score 7; DB 4; Length 552;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DGGQAG 16

Db 22 DGGQAG 28
|||||

RESULT 7

US-09-252-991A-20368
; Sequence 20368, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20368
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20368

Query Match 30.4%; Score 7; DB 4; Length 599;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGQAEGA 17
Db 383 GGQAEGA 389
|||||

RESULT 8

US-09-252-991A-16798
; Sequence 16798, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16798
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16798

Query Match 30.4%; Score 7; DB 4; Length 981;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7
Db 136 ALAGWLR 142
|||||

RESULT 9

US-08-428-488-13
; Sequence 13, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE

;; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
;; NUMBER OF SEQUENCES: 107
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/428,488
;; FILING DATE: 27-APR-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Baumeister, Mary Katherine
;; REGISTRATION NUMBER: 26,254
;; REFERENCE/DOCKET NUMBER: 028724-087
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 39 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1
;; OTHER INFORMATION: /note= "Position 1 - H-Ser."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 39
;; OTHER INFORMATION: /note= "Position 39.- Phe-OH."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 30
;; OTHER INFORMATION: /note= "Position 30 - Glu-NH2."
;; US-08-428-488-13

Query Match 26.1%; Score 6; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GADEL 21
Db 26 GADEL 31

RESULT 10
US-08-403-852D-31
; Sequence 31, Application US/08403852D
; Patent No. 5891695
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; BIOSYNTHESIS OF STREPTOGRAMINS, NUCLEOTIDE SEQUENCES
; CODING FOR THESE POLYPEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 43

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/403,852D
;; FILING DATE: 10-MAY-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR 93/00923
;; FILING DATE: 25-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 92/11441
;; FILING DATE: 25-SEP-1992
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03806.0054-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 97 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-403-852D-31

Query Match 26.1%; Score 6; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAE 18
Db 2 QAEGAE 7

RESULT 11
US-08-510-646B-32
; Sequence 32, Application US/08510646B
; Patent No. 6077699
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; BIOSYNTHESIS OF STREPTOGRAMINS, NUCLEOTIDE SEQUENCES
; CODING FOR THESE POLYPEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/510.646B
;; FILING DATE: 03-AUG-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/403.852
;; FILING DATE: 10-MAY-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR 93/00923
;; FILING DATE: 25-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 92/11441
;; FILING DATE: 25-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03806.0054-01000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 32:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 97 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-510-646B-32

Query Match 26.1%; Score 6; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAE 18
Db 111111
2 QAEGAE 7

RESULT 12

US-09-231-818-31
; Sequence 31, Application US/09231818
; Patent No. 6171846

GENERAL INFORMATION:

;; APPLICANT: Blanc, Veronique
;; APPLICANT: Blanche, Francis
;; APPLICANT: Crouzet, Joel
;; APPLICANT: Jacques, Nathalie
;; APPLICANT: Lacroix, Patricia
;; APPLICANT: Thibaut, Denis
;; APPLICANT: Zagorec, Monique
;; APPLICANT: Debussche, Laurent
;; APPLICANT: De Crecy-Lagard, Valerie
;; TITLE OF INVENTION: Polypeptides Involved In The
;; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
;; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/231,818
;; FILING DATE:
;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/08/403.852
;; FILING DATE: 10-MAY-1995
;; APPLICATION NUMBER: PCT/FR 93/00923
;; FILING DATE: 25-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 92/11441
;; FILING DATE: 25-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03806.0054-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 97 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-231-818-31

Query Match 26.1%; Score 6; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAE 18
Db 111111
2 QAEGAE 7

RESULT 13

US-09-135-994-12
; Sequence 12, Application US/09135994A
; Patent No. 6280938

GENERAL INFORMATION:

;; APPLICANT: Ranum et al.
;; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
;; FILE REFERENCE: University of Minnesota
;; CURRENT APPLICATION NUMBER: US/09/135,994A
;; CURRENT FILING DATE: 1998-08-18
;; EARLIER APPLICATION NUMBER: 60/056,170
;; EARLIER FILING DATE: 1997-08-19
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 12
;; LENGTH: 129
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-135-994-12

Query Match 26.1%; Score 6; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RPEDGG 12
Db 111111
57 RPEDGG 62

RESULT 14

US-09-684-843A-12
; Sequence 12, Application US/09684843A
; Patent No. 6514755

GENERAL INFORMATION:

;; APPLICANT: Ranum et al.
;; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
;; FILE REFERENCE: Regents of the University of Minnesota
;; CURRENT APPLICATION NUMBER: US/09/684,843A
;; CURRENT FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: 60/056,170
;; PRIOR FILING DATE: 1997-08-19
;; PRIOR APPLICATION NUMBER: 09/135,994

; PRIOR FILING DATE: 1998-08-18
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 129
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-684-843A-12

Query Match 26.1%; Score 6; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RPEDGG 12
 Db 57 RPEDGG 62

RESULT 15
 US-09-198-452A-612
 ; Sequence 612, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Grifpals, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 612
 ; LENGTH: 183
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 US-09-198-452A-612

Query Match 26.1%; Score 6; DB 4; Length 183;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AEGAEED 19
 Db 155 AEGAEED 160

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OM protein - protein search, using sw model

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237.266 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 23

Sequence: 1 ALAGWLRPEDGGGAEGAEDELEV 23

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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 23 | 100.0 | 23 | 9 | US-09-853-253-6 |
| 3 | 23 | 100.0 | 24 | 9 | US-09-853-253-4 |
| 4 | 23 | 100.0 | 117 | 9 | US-09-794-987-2 |
| 5 | 23 | 100.0 | 117 | 9 | US-09-853-253-2 |
| 6 | 23 | 100.0 | 117 | 9 | US-09-989-722-268 |
| 7 | 23 | 100.0 | 117 | 9 | US-09-989-723-268 |
| 8 | 23 | 100.0 | 117 | 9 | US-09-989-279-268 |
| 9 | 23 | 100.0 | 117 | 9 | US-09-989-727-268 |
| 10 | 23 | 100.0 | 117 | 10 | US-09-989-731-268 |
| 11 | 23 | 100.0 | 117 | 10 | US-09-989-732-268 |
| 12 | 23 | 100.0 | 117 | 10 | US-09-991-073-268 |
| 13 | 23 | 100.0 | 117 | 10 | US-09-990-442-268 |
| 14 | 23 | 100.0 | 117 | 10 | US-09-991-163-268 |
| 15 | 23 | 100.0 | 117 | 10 | US-09-993-604-268 |

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| 16 | 23 | 100.0 | 117 | 10 | US-09-990-456-268 | Sequence 268, App |
| 17 | 23 | 100.0 | 117 | 10 | US-09-989-721-268 | Sequence 268, App |
| 18 | 23 | 100.0 | 117 | 10 | US-09-992-598-268 | Sequence 268, App |
| 19 | 23 | 100.0 | 117 | 10 | US-09-989-293A-268 | Sequence 268, App |
| 20 | 23 | 100.0 | 117 | 10 | US-09-989-735-268 | Sequence 268, App |
| 21 | 23 | 100.0 | 117 | 10 | US-09-990-444-268 | Sequence 268, App |
| 22 | 23 | 100.0 | 117 | 10 | US-09-991-181-268 | Sequence 268, App |
| 23 | 23 | 100.0 | 117 | 10 | US-09-989-730-268 | Sequence 268, App |
| 24 | 23 | 100.0 | 117 | 10 | US-09-990-436-268 | Sequence 268, App |
| 25 | 23 | 100.0 | 117 | 10 | US-09-993-687-268 | Sequence 268, App |
| 26 | 23 | 100.0 | 117 | 11 | US-09-989-734-268 | Sequence 268, App |
| 27 | 23 | 100.0 | 117 | 11 | US-09-997-653-268 | Sequence 268, App |
| 28 | 23 | 100.0 | 117 | 11 | US-09-993-667-268 | Sequence 268, App |
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| 35 | 23 | 100.0 | 117 | 11 | US-09-989-156-268 | Sequence 268, App |
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| 42 | 23 | 100.0 | 117 | 11 | US-09-997-559-268 | Sequence 268, App |
| 43 | 23 | 100.0 | 117 | 11 | US-09-997-601-268 | Sequence 268, App |
| 44 | 23 | 100.0 | 117 | 11 | US-09-990-443-268 | Sequence 268, App |
| 45 | 23 | 100.0 | 117 | 11 | US-09-991-854-268 | Sequence 268, App |

ALIGNMENTS

RESULT 1
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; Sequence 5, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-5

Query Match 100.0%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 9e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ALAGWLRPEDGGGAEGAEDELEV 23

RESULT 2
US-09-853-253-6
; Sequence 6, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN

[illegible]

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RESULT 6

US-09-989-722-268

Sequence 268, Application US/09989722

Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC63

CURRENT APPLICATION NUMBER: US/09/989,722

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

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PRIOR FILING DATE: 1997-11-24

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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 268 Application US/09989723
; Patent No. US20020072092A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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Query Match 100.0%; Score 23; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 8
US-09-989-279-268
; Sequence 268, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C56
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Query Match 100.0%; Score 23; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; PRIOR FILING DATE: 2001-11-19
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| ; | APPLICANT: | Watanabe, Colin K. |
| ; | APPLICANT: | Williams, P. Mickey |
| ; | APPLICANT: | Wood, William I. |
| ; | APPLICANT: | Zhang, Zemin |
| ; | TITLE OF INVENTION: | Secreted and Transmembrane Polypeptides and Nucleic |
| ; | TITLE OF INVENTION: | Acids Encoding the Same |
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Query Match 100.0%; Score 23; DB 10; Length 117;

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 ; APPLICANT: Zhang, Zemin
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 ; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
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; PRIOR APPLICATION NUMBER: 60/090696
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
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; PRIOR APPLICATION NUMBER: 60/090863
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
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; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
;
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
;
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
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DB 52 ALAGWLRPEDGGQAGAEDELEV 74
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RESULT 12
US-09-991-073-268
; Sequence 268, Application US/09991073
; Patent No. US2002012756A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186

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; PRIOR FILING DATE: 1998-07-01
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 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.5e-15;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQGAEGAEDEV 23
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 Db 52 ALAGWLRPEDGGQGAEGAEDEV 74

RESULT 13

US-09-990-442-268

; Sequence 268, Application US/09990442

; Patent No. US20020132252A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC8
 ; CURRENT APPLICATION NUMBER: US/09/990,442
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/075945
 ; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910
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 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
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 ; PRIOR FILING DATE: 1998-05-07
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; PRIOR APPLICATION NUMBER: 60/091626
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
;
Query Match 100.0%; Score
Best Local Similarity 100.0%; Pred.
Matches 23; Conservative 0; MIs
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Qy 1 ALAGWLRLPDGGQAGBADELEV 23
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Db 52 ALAGWLRLPDGGQAGBADELEV 74
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RESULT 14
US-09-991-163-268
; Sequence 268, Application US/09991163
; Patent No. US2002013253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoi, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Trans
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
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; PRIOR APPLICATION NUMBER: 60/078910
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RESULT 14

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; PRIOR FILING DATE: 1998-07-07
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Query Match      100.08; Score 23; DB 10; Length 117;
Best Local Similarity 100.08; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ALAGWLRPEDGGQGAEGAEDELEV 23
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Db      52 ALAGWLRPEDGGQGAEGAEDELEV 74

RESULT 15
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; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
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; PRIOR APPLICATION NUMBER: 60/088858
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; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
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2 PRIOR APPLICATION NUMBER: 60/089948
3 PRIOR FILING DATE: 1998-06-19
4 PRIOR APPLICATION NUMBER: 60/089952
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6 PRIOR APPLICATION NUMBER: 60/090246
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13 PRIOR FILING DATE: 1998-06-23
14 PRIOR APPLICATION NUMBER: 60/090355
15 PRIOR FILING DATE: 1998-06-23
16 PRIOR APPLICATION NUMBER: 60/090429
17 PRIOR FILING DATE: 1998-06-24
18 PRIOR APPLICATION NUMBER: 60/090431
19 PRIOR FILING DATE: 1998-06-24
20 PRIOR APPLICATION NUMBER: 60/090435
21 PRIOR FILING DATE: 1998-06-24
22 PRIOR APPLICATION NUMBER: 60/090444
23 PRIOR FILING DATE: 1998-06-24
24 PRIOR APPLICATION NUMBER: 60/090445
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26 PRIOR APPLICATION NUMBER: 60/090472
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52 PRIOR APPLICATION NUMBER: 60/091360
53 PRIOR FILING DATE: 1998-07-01
54 PRIOR APPLICATION NUMBER: 60/091478
55 PRIOR FILING DATE: 1998-07-02
56 PRIOR APPLICATION NUMBER: 60/091544
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58 PRIOR APPLICATION NUMBER: 60/091519
59 PRIOR FILING DATE: 1998-07-02
60 PRIOR APPLICATION NUMBER: 60/091626
61 PRIOR FILING DATE: 1998-07-02
62 PRIOR APPLICATION NUMBER: 60/091633
63 PRIOR FILING DATE: 1998-07-02
64 PRIOR APPLICATION NUMBER: 60/091978
65 PRIOR FILING DATE: 1998-07-07
66 PRIOR APPLICATION NUMBER: 60/091982
67 PRIOR FILING DATE: 1998-07-07
68 PRIOR APPLICATION NUMBER: 60/092182
69 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDEV 23
Db 52 ALAGWLRPEDGGQAGAEDEV 74

Search completed: September 11, 2003, 18:16:19
Job time : 15.1444 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:37 ; Search time 8.73262 Seconds
(without alignments)
253.289 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 23

Sequence: 1 ALAGWLRPEDGGQAGAEDELEV 23

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 23 | 100.0 | 117 | 1 A59316 | ghrelin precursor |
| 2 | 8 | 34.8 | 483 | 2 T04453 | hypothetical prote |
| 3 | 7 | 30.4 | 302 | 2 JH0572 | hypothetical prote |
| 4 | 7 | 30.4 | 344 | 2 A48990 | transcription regu |
| 5 | 7 | 30.4 | 910 | 2 B83451 | aconitate hydratase |
| 6 | 7 | 30.4 | 1239 | 1 Q0BE10 | BOLFI protein - hu |
| 7 | 6 | 26.1 | 69 | 2 C87574 | COLD-shock domain |
| 8 | 6 | 26.1 | 142 | 2 AB0401 | probable membrane |
| 9 | 6 | 26.1 | 175 | 2 E82118 | conserved hypothet |
| 10 | 6 | 26.1 | 178 | 2 A30230 | quiescence-specifi |
| 11 | 6 | 26.1 | 180 | 2 T46695 | hypothetical prote |
| 12 | 6 | 26.1 | 189 | 2 A91082 | hypothetical prote |
| 13 | 6 | 26.1 | 189 | 2 B85927 | hypothetical prote |
| 14 | 6 | 26.1 | 198 | 2 D69070 | imidazoleglycerol- |
| 15 | 6 | 26.1 | 223 | 2 A40866 | HL-60-induced diff |
| 16 | 6 | 26.1 | 237 | 2 T30002 | hypothetical prote |
| 17 | 6 | 26.1 | 265 | 2 A95298 | hypothetical prote |
| 18 | 6 | 26.1 | 267 | 1 CTPGP | corticotropin / li |
| 19 | 6 | 26.1 | 284 | 2 B25624 | tropomyosin I, tho |
| 20 | 6 | 26.1 | 284 | 2 A25624 | tropomyosin I, emb |
| 21 | 6 | 26.1 | 288 | 2 A55737 | PB-1 protein - hum |
| 22 | 6 | 26.1 | 289 | 2 T48894 | lipoprotein mtsA, |
| 23 | 6 | 26.1 | 289 | 2 H83433 | hypothetical prote |
| 24 | 6 | 26.1 | 290 | 2 H71852 | hypothetical prote |
| 25 | 6 | 26.1 | 299 | 2 T35144 | glutamate transpor |
| 26 | 6 | 26.1 | 302 | 2 T48871 | catechol 1,2-dioxy |
| 27 | 6 | 26.1 | 308 | 2 F72508 | probable hydrogena |
| 28 | 6 | 26.1 | 313 | 2 E82762 | conserved phosphog |
| 29 | 6 | 26.1 | 315 | 2 F64129 | probable phosphogl |

30 26.1 326 1 E69690 transcription repr
31 26.1 343 2 AH1823 30S ribosomal prot
32 26.1 343 2 T35063 probable prolipopr
33 26.1 345 2 A83526 hypothetical prote
34 26.1 346 2 AE3323 sam-dependent meth
35 26.1 350 2 S71923 cysteine proteinase
36 26.1 360 2 S59598 cysteine proteinase
37 26.1 376 2 AD2697 hypothetical prote
38 26.1 377 2 G97314 alcohol dehydrogen
39 26.1 377 2 T47471 cysteine proteinase
40 26.1 379 1 DCBSPK phosphoribosylamin
41 26.1 379 2 D82801 molybdopterin bios
42 26.1 383 2 F83321 hypothetical prote
43 26.1 384 2 H64505 hypothetical prote
44 26.1 385 2 T26404 hypothetical prote
45 26.1 391 2 AF3633 hypothetical membr

ALIGNMENTS

RESULT 1

A59316
ghrelin precursor - human
N: Alternate names: preproghrelin
C: Species: Homo sapiens (man)
C: Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C: Accession: A59316
R: Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A: Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A: Reference number: A59316; MUID:20067959; PMID:10604470
A: Accession: A59316
A: Status: not compared with conceptual translation
A: Molecule type: mRNA
A: Residues: 1-117 <KOJ>
A: Cross-references: GB:AB029434; NID:g6691571; PIDN:BA089371.1; PID:g6691572
A: Experimental source: tissue stomach endocrine cells
A: Note: submitted to GenBank, June 1999
C: Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (g.
C: Superfamily: motilin
C: Keywords: hormone; lipoprotein; stomach
F: 1-23/Domain: signal sequence #status predicted <SIG>
F: 24-51/Product: ghrelin #status predicted <MAT>
F: 52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F: 26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 23; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 4, 1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
DB 52 ALAGWLRPEDGGQAGAEDELEV 74
|||||

RESULT 2

T04453
hypothetical protein F4D11.80 - Arabidopsis thaliana
C: Species: Arabidopsis thaliana (mouse-ear cross)
C: Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C: Accession: T04453
R: Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Hoheisel, J.; Mewes,
submitted to the Protein Sequence Database, April 1998
A: Reference number: Z15360
A: Accession: T04453
A: Molecule type: DNA
A: Residues: 1-483 <BEV>
A: Cross-references: EMBL:AL022537
A: Experimental source: cultivar Columbia; BAC clone F4D11
C: GenBank: 4
A: Map position: 4
A: Introns: 17/3; 44/1; 94/1; 141/3; 206/2; 247/2; 345/3; 395/1; 434/2

A>Note: F4D11.80

Query Match 34.8%; Score 8; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAED 20
| | | | | | | |
Db 302 QAEGAED 309

RESULT 3

JH0572

hypotheical protein - Streptomyces lividans (fragment)

C:Species: Streptomyces lividans
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-1999

C:Accession: JH0572

R:Lichenstein, H.S.; Busse, L.A.; Smith, G.A.; Narhi, L.O.; McGinley, M.O.; Rohde, M.F.;

Gene 111, 125-130, 1992

A:Title: Cloning and Characterization of a gene encoding extracellular metalloprotease

A:Reference number: JH0571; MUID:92192468; PMID:1547948

A:Accession: JH0572

A:Molecule type: DNA

A:Residues: 1-302 <LIC>

A:Cross-references: GB:M09476; NID:g153411; PIDN:AAA26804.1; PID:g153412

A:Experimental source: strain TK24

A>Note: the authors translated the codon GTA for residue 260 as Asp

A>Note: this protein has a strong similarity to LysR family of transcriptional regulator

C:Superfamily: Pseudomonas putida regulatory protein catR

Query Match 30.4%; Score 7; DB 2; Length 302;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7

| | | | | | | |

Db 100 ALAGWLR 106

RESULT 4

A48990

transcription regulator LysR family homolog SnPr - Streptomyces lividans

C:Species: Streptomyces lividans

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000

C:Accession: A48990

R:Butler, M.J.; Davey, C.C.; Krygsman, P.; Walczyk, E.; Malek, L.T.

Can. J. Microbiol. 38, 912-920, 1992

A:Title: Cloning of genetic loci involved in endoprotease activity in Streptomyces livid

A:Reference number: A48990; MUID:93099553; PMID:11464066

A:Contents: 66

A:Accession: A48990

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-344 <BUT>

A>Note: sequence extracted from NCBI backbone (NCBIN:121210, NCBIPI:121213)

C:Superfamily: Pseudomonas putida regulatory protein catR

Query Match 30.4%; Score 7; DB 2; Length 344;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7

| | | | | | | |

Db 104 ALAGWLR 110

RESULT 5

B83451

aconitate hydratase 1 PA1562 [Imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: B83451

R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
A:Reference number: AB2950; MUID:20437337; PMID:10964043
A:Accession: B83451
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-910 <STO>
A:Cross-references: GB:AE004584; GB:AE004091; NID:g9947516; PIDN:AA04951.1; GSPDB:GN
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: acnA; PA1562
C:Superfamily: iron-responsive element-binding protein

Query Match 30.4%; Score 7; DB 2; Length 910;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7
| | | | | | | |
Db 65 ALAGWLR 71

RESULT 6

QB0E10

BOLFI protein - human herpesvirus 4 (strain B95-8)

C:Species: human herpesvirus 4, Epstein-Barr virus

C>Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999

C:Accession: A43041; A03752; S32995

R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.

Mol. Biol. Med. 1, 21-45, 1983

A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi

A:Reference number: A93065; MUID:85035713; PMID:6092825

A:Accession: A43041

A:Molecule type: DNA

A:Residues: 1-1239 <BAN>

A:Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24841.1; PID:g1334855

R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.

Nature 310, 207-211, 1984

A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.

A:Reference number: A03794; MUID:84270667; PMID:6087149

A:Contents: annotation; protein coding region

C:Superfamily: human herpesvirus 4 BOLFI protein

Query Match 30.4%; Score 7; DB 1; Length 1239;

Best Local Similarity 100.0%; Pred. No. 33;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AEGAED 20

| | | | | | | |

Db 696 AEGAED 702

RESULT 7

C87574

cold-shock domain family protein [Imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002

C:Accession: C87574

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: C87574

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-69 <STO>

A:Cross-references: GB:AE005673; NID:g13424199; PIDN:AAK24591.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2623

C:Superfamily: major cold shock protein; cold shock domain homology

Query Match 26.1%; Score 6; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PEDGGQ 13
|||||
DB 20 PEDGGQ 25

RESULT 8

AB0401

Probable membrane protein YPO3302 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001

C:Accession: AB0401

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AB0401

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-142 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC92534.1; PID:gl5981232; GSPDB:GN00175

C:Genetics:

A:Gene: YPO3302

C:Superfamily: hypothetical protein HI0489

Query Match 26.1%; Score 6; DB 2; Length 142;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAGWLR 7

|||||

DB 104 LAGWLR 109

RESULT 9

E82118

conserved hypothetical protein VC2111 [imported] - Vibrio cholerae (strain N16961 serog

C:Species: Vibrio cholerae

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: E82118

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: AB2035; MUID:20406833; PMID:10952301

A:Accession: E82118

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-175 <HE>

A:Cross-references: GB:AE004284; GB:AE003852; NID:g9656649; PIDN:AAF95256.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC2111

A:Map position: 1

Query Match 26.1%; Score 6; DB 2; Length 175;

Best Local Similarity 100.0%; Pred. No. 67;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GOAEGA 17

|||||

DB 54 GOAEGA 59

RESULT 10

A30230

quiescence-specific protein precursor - chicken

N:Alternate names: Ch21 protein

C:Species: Gallus gallus (chicken)

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 15-Nov-1996

C:Accession: A30230; A42581; A36595; A35491

R:Bedard, P.A.; Yannoni, Y.; Simmons, D.L.; Erikson, R.L.

Mol. Cell. Biol. 9, 1371-1375, 1989

A:Title: Rapid repression of quiescence-specific gene expression by epidermal growth

A:Reference number: A30230; MUID:89261749; PMID:2498647

A:Accession: A30230

A:Molecule type: mRNA

A:Residues: 1-178 <BED>

R:Dozin, B.; Descalzi, F.; Briata, L.; Hayashi, M.; Gentili, C.; Hayashi, K.; Quarto

J. Biol. Chem. 267, 2979-2985, 1992

A:Title: Expression, regulation, and tissue distribution of the Ch21 protein during c

A:Reference number: A42581; MUID:92147639; PMID:1737754

A:Accession: A42581

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-95, 'L', '97-178 <DO>

A:Experimental source: tibia hypertrophic cartilage

A>Note: sequence extracted from NCBI backbone (NCBI:80796, NCBIP:80797)

R:Cancedda, F.D.; Dozin, B.; Rossi, F.; Molina, F.; Cancedda, R.; Negri, A.; Ronchi,

J. Biol. Chem. 265, 19060-19064, 1990

A:Title: The Ch21 protein, developmentally regulated in chick embryo, belongs to the

A:Reference number: A36595; MUID:91035433; PMID:2229062

A:Accession: A36595

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 21-95, 'L', '97-178 <CAN>

A:Cross-references: GB:M37611

R:Cancedda, F.D.; Asaro, D.; Molina, F.; Cancedda, R.; Caruso, C.; Camardella, L.; Ne

Biochem. Biophys. Res. Commun. 168, 933-938, 1990

A:Title: The amino terminal sequence of the developmentally regulated CH21 protein sh

A:Reference number: A35491; MUID:90267487; PMID:2346493

A:Accession: A35491

A>Status: preliminary

A:Molecule type: protein

A:Residues: 21-48 <CA2>

C:Superfamily: lipocalin; lipocalin homology

F:1-21/Domain: signal sequence #status predicted <STG>

F:22-178/Product: quiescence-specific protein #status predicted <MAT>

F:25-173/Domain: lipocalin homology <LIP>

Query Match 26.1%; Score 6; DB 2; Length 178;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EDELEV 23

|||||

DB 65 EDELEV 70

RESULT 11

T46695

hypothetical protein ORF-180 [imported] - Lactobacillus helveticus plasmid pLH1

C:Species: Lactobacillus helveticus

C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 04-Mar-2000

C:Accession: T46695

R:Thompson, K.; McConville, K.J.; McReynolds, C.; Foley, S.

submitted to the EMBL Data Library, December 1997

A:Title: Complete sequence of plasmid pLH1 from Lactobacillus helveticus ATCC15

A:Reference number: 223135

A:Accession: T46695

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-180 <THO>

A:Cross-references: EMBL:AJ222725; PIDN:CAAL0962.1

A:Experimental source: ATCC 15009

C:Genetics:

A:Genome: plasmid pLH1

C:Superfamily: Lactobacillus helveticus plasmid pLH1 hypothetical protein ORF-180

Query Match 26.1%; Score 6; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
|||||
DB 31 ALAGWL 36

RESULT 12
A91082
hypothetical protein Ecs3625 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A91082
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA037048.1; PID:g13363096; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: Ecs3625

Query Match 26.1%; Score 6; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
|||||
DB 14 ALAGWL 19

RESULT 13
B85927
hypothetical protein Z4080 [imported] - Escherichia coli (strain O157:H7, substrain EDL5
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: B85927
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85927
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <STO>
A;Cross-references: GB:AE005174; NID:g13517231; PIDN:AAG57878.1; GSPDB:GN00145; UWGP:Z40
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4080

Query Match 26.1%; Score 6; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
|||||
DB 14 ALAGWL 19

RESULT 14
D69070
imidazoleglycerol-phosphate synthase - Methanobacterium thermoautotrophicum (strain Delt
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C;Accession: D69070
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: D69070
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-198 <MTH>
A;Cross-references: GB:AE000912; GB:AE000666; NID:g2622632; PIDN:AAB85999.1; PID:g262
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1524
A;Start codon: TTG
C;Superfamily: amidotransferase hisH; trpG homology

Query Match 26.1%; Score 6; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EGAEDE 20
|||||
DB 130 EGAEDE 135

RESULT 15
A40866
HL-60-induced differentiation immediate-early protein ETR101 - human
C;Species: Homo sapiens (man)
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 05-Nov-1999
C;Accession: A40866
R;Shimizu, N.; Ohta, M.; Fujiwara, C.; Sagara, J.; Mochizuki, N.; Oda, T.; Utiyama, H
J. Biol. Chem. 266, 12157-12161, 1991
A;Title: Expression of a novel immediate early gene during 12-O-tetradecanoylphorbol-
A;Reference number: A40866; MUID:91286224; PMID:2061303
A;Accession: A40866
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-223 <SHI>
A;Cross-references: GB:M62831; NID:g182260; PIDN:AAA35814.1; PID:g182261

Query Match 26.1%; Score 6; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GQAEGA 17
|||||
DB 165 GQAEGA 170

Search completed: September 11, 2003, 17:57:06
Job time : 8.73262 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:30:37 : Search time 4.42781 Seconds
(without alignments)
244.278 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 23

Sequence: 1 ALAGWLPRPDGGQAGGAELELV 23

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result NO. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 23 | 100.0 | 117 | GHRL_HUMAN | Q9ubj3 homo sapien |
| 2 | 10 | 43.5 | 116 | GHRL_BOVIN | Q9bdj6 bos taurus |
| 3 | 7 | 30.4 | 328 | MPR2_STRCO | Q91127 streptomyce |
| 4 | 7 | 30.4 | 344 | MPRR_STRLI | P43161 streptomyce |
| 5 | 7 | 30.4 | 1239 | V120_EBV | P03189 epstein-bar |
| 6 | 6 | 26.1 | 117 | GHRL_CANFA | Q9bef8 canis famill |
| 7 | 6 | 26.1 | 178 | EFAB_CHICK | P21760 gallus gall |
| 8 | 6 | 26.1 | 198 | HIS5_METTH | O27568 methanobact |
| 9 | 6 | 26.1 | 267 | COLI_PIG | P01192 s corticotr |
| 10 | 6 | 26.1 | 284 | TPM2_DROME | P09491 drosophila |
| 11 | 6 | 26.1 | 288 | PCD1_HUMAN | Q15116 homo sapien |
| 12 | 6 | 26.1 | 289 | OPSD_LIMPA | O42431 limnocottus |
| 13 | 6 | 26.1 | 290 | PARB_HELPJ | Q92k75 helicobacte |
| 14 | 6 | 26.1 | 310 | MTSA_STRP8 | Q8p280 streptococc |
| 15 | 6 | 26.1 | 310 | MTSA_STRPY | Q9a157 streptococc |
| 16 | 6 | 26.1 | 313 | MRWA_XYLEFA | Q9pf88 xylella fas |
| 17 | 6 | 26.1 | 315 | YF56_HAEIN | P45250 haemophilus |
| 18 | 6 | 26.1 | 326 | BSR_BACSU | P36944 bacillus su |
| 19 | 6 | 26.1 | 346 | MRWA_BRUME | Q8y174 brucella me |
| 20 | 6 | 26.1 | 360 | CYS2_MAIZE | Q10717 zea mays (m |
| 21 | 6 | 26.1 | 379 | PURK_BACSU | P12045 bacillus su |
| 22 | 6 | 26.1 | 395 | IF5_SCHPO | Q09689 schizosacch |
| 23 | 6 | 26.1 | 433 | TIG_STAAM | Q99t16 staphylococ |
| 24 | 6 | 26.1 | 436 | CUS1_YEAST | Q02554 saccharomyc |
| 25 | 6 | 26.1 | 497 | RPSD_MYCGE | P47811 mycoplasma |
| 26 | 6 | 26.1 | 499 | RPSD_MYCPN | P78022 mycoplasma |
| 27 | 6 | 26.1 | 511 | SYS_MOUSE | P26638 mus musculu |
| 28 | 6 | 26.1 | 513 | SYS_BOVIN | Q9gmb8 bos taurus |
| 29 | 6 | 26.1 | 513 | SYS_HUMAN | P49591 homo sapien |
| 30 | 6 | 26.1 | 535 | AMYB_HORVU | P16098 hordeum vul |
| 31 | 6 | 26.1 | 539 | Z173_HUMAN | Q12899 homo sapien |
| 32 | 6 | 26.1 | 547 | CH60_BUCTC | Q8kix3 buchnera ap |
| 33 | 6 | 26.1 | 566 | HS60_CANAL | O74261 candida alb |

| | | | | | |
|----|---|------|-----|-------------|--------------------|
| 34 | 6 | 26.1 | 572 | HS60_YEAST | P19882 saccharomyc |
| 35 | 6 | 26.1 | 590 | HS60_AJECA | P50142 ajellomyces |
| 36 | 6 | 26.1 | 620 | SMP_COTJA | Q92154 coturnix co |
| 37 | 6 | 26.1 | 641 | DXS_RHOCA | P26242 rhodobacter |
| 38 | 6 | 26.1 | 650 | HUP1_HUMAN | P51693 homo sapien |
| 39 | 6 | 26.1 | 657 | HUPH_MOUSE | P35492 mus musculu |
| 40 | 6 | 26.1 | 683 | 2263_HUMAN | O14978 homo sapien |
| 41 | 6 | 26.1 | 702 | HELS_AERPE | Q9yfq8 aeropyrum p |
| 42 | 6 | 26.1 | 728 | UVR_C_STRCO | Q92512 streptomyce |
| 43 | 6 | 26.1 | 886 | SM6B_MOUSE | O54951 mus musculu |
| 44 | 6 | 26.1 | 887 | SM6B_RAT | O70141 rattus norv |
| 45 | 6 | 26.1 | 890 | ACOL_ECOLI | P25516 escherichia |

ALIGNMENTS

RESULT 1
GHRL_HUMAN
ID GHRL_HUMAN STANDARD; PRT; 117 AA.
AC Q9UBJ3: Q8TAT9; Q9H3R3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
DE releasing peptide)
GN GHRL OR MTLRP
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
RX MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "ghrelin is a growth-hormone-releasing acylated peptide from stomach.";
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=stomach;
RA Tomasetto C., Karam S.M., Rio M.-C.;
RT "Identification of a novel gastric protein m46.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Wajraich M.P., Ten I.S., Gertner J.M., Leibell R.L.;
RT "Genomic organization of the human Ghrelin gene.";
RL J. Endocrinol. Genet. 1:231-233(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=2388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [6]
 RP SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RL hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RP [7]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RL hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -1- PTM: O-n-octanoylation is essential for activity.
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/GhrelinID327.html".
 CC -----
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 CC -----
 DR EMBL; AB029434; BAA89371.1; -;
 DR EMBL; AB035700; BAB19045.1; -;
 DR EMBL; AJ252278; CAB65733.1; -;
 DR EMBL; AF296558; AAG10300.1; -;
 DR EMBL; BC025791; AAH25791.1; -;
 DR PIR; A59316; A59316.
 DR MIM; 605353; -;
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005825; C:soluble fraction; TAS.
 DR GO; GO:0005131; F:growth hormone receptor ligand activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_ghrelin.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 23
 FT PEPTIDE 24 51 GHRELIN.
 FT PROPEP 52 117 REMOVED IN MATURE FORM.
 FT LIPID 26 26 N-OCTANOATE.
 FT VARSPLIC 37 37 Missing (in isoform 2).
 FT FTId=VSP_003245.
 FT CONFLICT 72 72 L -> M (IN REF. 5).

SQ SEQUENCE 117 AA; 12911 MW; 39C0572BBEACA2755 CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 2
 GHRL_BOVIN STANDARD; PRT; 116 AA.
 ID GHRL_BOVIN
 AC Q9BDJ6; O9GKY6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (growth hormone
 DE releasing peptide).
 GN GHRL.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kita K., Harada K., Yokota H.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 24-99 FROM N.A.
 RA Kojima M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -----
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 DR EMBL; AF350329; AAK18612.1; -;
 DR EMBL; AB035702; BAB19047.1; -;
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR Pfam; PF04643; motilin_ghrelin.
 DR Pfam; PF04644; motilin_assoc; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
 KW SIGNAL 1 23
 KW PEPTIDE 24 50 GHRELIN (BY SIMILARITY).
 KW PROPEP 51 116 REMOVED IN MATURE FORM (BY SIMILARITY).
 KW LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
 KW CONFLICT 34 34 K -> E (IN REF. 2).
 SQ SEQUENCE 116 AA; 12792 MW; F55536DAC5FA59B6 CRC64;
 Query Match 43.5%; Score 10; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 QAEGAEDELE 22

```
DE Small neutral protease regulatory protein.
GN MPRR OR SNPR.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=66 / 1326;
RX MEDLINE=93099553; PubMed=1464066;
RA Butler M.J., Davey C.C., Krygsmann P., Walczyk E., Malek L.T.;
RT "Cloning of genetic loci involved in endoprotease activity in
RT Streptomyces lividans 66: a novel neutral protease gene with an
RT adjacent divergent putative regulatory gene.";
RL Can. J. Microbiol. 38:912-920(1992).
RN [2]
RP SEQUENCE OF 1-305 FROM N.A.
RC STRAIN=TK24;
RX MEDLINE=92192468; PubMed=1547948;
RA Lichenstein H.S., Busse L.A., Smith G.A., Narhi L.O.,
RA McGinley M.O., Rohde M.F., Katowitz J.L., Zukowski M.M.;
RT "Cloning and characterization of a gene encoding extracellular
RT metalloprotease from Streptomyces lividans.";
RL Gene 111:125-130(1992).
CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE GENE (SNPA) FOR THE
CC SMALL NEUTRAL PROTEASE.
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC -----
DR EMBL; M81703; AAA26739.1; -
DR EMBL; M89476; AAA26804.1; ALT_INIT.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW Transcription regulation; DNA-binding; Activator.
FT DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
FT CONFLICT 270 270 G -> AR (IN REF. 2).
SQ SEQUENCE 344 AA; 37415 MW; 485C82C813B52312 CRC64;
Query Match 30.4%; Score 7; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLR 7
DB 104 ALAGWLR 110
RESULT 5
V120_EBV
ID V120_EBV STANDARD; PRT; 1239 AA.
AC P03189;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Capsid assembly protein BOLFI.
GN BOLFI.
OS Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
```

```
DE Complete genome sequence of the model actinomycete Streptomyces
GN coelicolor A3(2).
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- FUNCTION: TRANSCRIPTIONAL TRANS-ACTIVATOR OF THE GENE (MPRA) FOR
CC THE SMALL NEUTRAL PROTEASE.
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
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CC -----
DR EMBL; AL939131; CAB76352.1; -
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; Protease; Transcription regulation; Complete proteome.
FT DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
FT CONFLICT 328 328 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 328 AA; 35885 MW; 2BA97730AE4FA16B CRC64;
Query Match 30.4%; Score 7; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLR 7
DB 104 ALAGWLR 110
RESULT 4
MPRR_STRLI
ID MPRR_STRLI STANDARD; PRT; 344 AA.
AC P43181;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
```

RX MEDLINE=84270667; PubMed=6087149;
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
 RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
 RA Tuffnell P.S., Bartell B.G.;
 RT "Data sequence and expression of the B95-8 Epstein-Barr virus genome.";
 RL Nature 310:207-211(1984).
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,
 CC SHV-1 23, EBV BOLFI, VZV 21, HVS-1 63, AND HCMV UL47.
 CC -----
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 CC -----
 CC EMBL; V01555; CAA24841.1; -;
 DR PIR; A43041; Q0BE10.
 DR Capsid assembly.
 KW SEQUENCE 1239 AA; 132748 MW; 6C5DBFC55F2FF729 CRC64;
 SQ
 Query Match 30.48; Score 7; DB 1; Length 1239;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 AEGAED 20
 DB 596 AEGAED 702
 RESULT 6
 ID GHRL_CANFA STANDARD; PRT; 117 AA.
 AC Q9BEF8; Q9BEF7;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide) (Motilin-related peptide).
 GN GHRL OR MTLRP
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE-Gastric fundus;
 RA Tonasetto C., Wendling C., Rio M.-C., Poitras P.;
 RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
 RT fundus.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing: Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9BEF8-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9BEF8-2; Sequence=VSP_003244;
 CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; AJ298295; CAC29155.1; -;
 DR EMBL; AJ298296; CAC29156.1; -;
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrel.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc.1.
 DR Pfam; PF04644; motilin_ghrel.1.
 DR PRINTS; PRO1624; GHRELIN.
 DR PRODOM; PD332162; Preproghrelin; 1.
 DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 23 BY SIMILARITY
 FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
 FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
 FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
 FT VARSPIC 37 37 Missing (in isoform 2).
 FT /FTid=VSP_003244.
 SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;
 Query Match 26.18; Score 6; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 AEDELE 22
 DB 68 AEDELE 73
 RESULT 7
 ID EFAB_CHICK STANDARD; PRT; 178 AA.
 AC P21760; P21928; Q9PWN9;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Extracellular fatty acid binding protein precursor (Ex-FABP)
 DE (Quiescence-specific protein) (p20K) (Ch21 protein).
 GN EXFABP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89261749; PubMed=2498647;
 RA Badard P.-A., Vannoni Y., Simmons D.L., Erikson R.L.;
 RT "Rapid repression of quiescence-specific gene expression by epidermal
 RT growth factor, insulin, and pp60v-src.";
 RL Mol. Cell. Biol. 9:1371-1375(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92147639; PubMed=1737754;
 RA Dozin B., Descalzi F., Briata L., Hayashi M., Gentili C.,
 RA Hayashi K., Quarto R., Cancedda R.;
 RT "Expression, regulation, and tissue distribution of the Ch21 protein
 RT during chicken embryogenesis.";
 RL J. Biol. Chem. 267:2979-2985(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Leghorn;
 RA Giannoni P., Dozin B., Zambotti A., Neri M., Cancedda R.;
 RT "Differentiation-dependent activation of the extracellular fatty acid
 RT binding protein (EXFABP) gene in chicken embryo chondrocytes.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 25-178 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=91035433; PubMed=2229062;
 RA Cancedda F.D., Dozin B., Rossi F., Molina F., Cancedda R.,
 RA Negri A., Ronchi S.;
 RT "The Ch21 protein, developmentally regulated in chick embryo, belongs

to the superfamily of lipophilic molecule carrier proteins.";
 J. Biol. Chem. 265:19060-19064(1990).
 [5]
 SEQUENCE OF 21-48.
 MEDLINE-90267487; PubMed-2346493;
 Cancedda F.D., Asaro D., Molina F., Cancedda R., Caruso C.,
 Camardella L., Negri A., Ronchi S.;
 "The amino terminal sequence of the developmentally regulated Ch21
 protein shows homology with amino terminal sequences of low molecular
 weight proteins binding hydrophobic molecules.";
 Biochem. Biophys. Res. Commun. 168:933-938(1990).
 [6]
 SEQUENCE OF 103-178 FROM N.A.
 STRAIN-White leghorn; TISSUE-Bone marrow;
 RX MEDLINE-92195690; PubMed-1549365;
 Nakano T., Graf T.;
 "Identification of genes differentially expressed in two types of
 v-myb-transformed avian myelomonocytic cells.";
 Oncogene 7:527-534(1992).
 [7]
 CHARACTERIZATION.
 RX MEDLINE-96355330; PubMed-8702740;
 Cancedda F.D., Malpeli M., Gentili C., Di Marzo V., Bet P.,
 Carlevaro M., Cermelli S., Cancedda R.;
 "The developmentally regulated avian Ch21 lipocalin is an
 extracellular fatty acid-binding protein.";
 J. Biol. Chem. 271:20163-20169(1996).
 [8]
 CHARACTERIZATION.
 RX MEDLINE-20513977; PubMed-11058755;
 Descalzi Cancedda F., Dozin B., Zeraga B., Cermelli S., Cancedda R.;
 "Ex-FABP: a fatty acid binding lipocalin developmentally regulated in
 chicken endochondral bone formation and myogenesis.";
 Biochim. Biophys. Acta 1482:127-135(2000).
 CC -!- FUNCTION: Preferentially binds long-chain unsaturated fatty acids
 such as linoleic acid, oleic acid, arachidonic acid. Also binds
 with a lower affinity long chain saturated fatty acids such as
 stearic acid. May act as survival protein by playing a role in
 maintaining cell viability.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: PREFERENTIALLY SYNTHESIZED IN NONPROLIFERATING
 CELLS.
 CC -!- PTM: Does not seem to be glycosylated.
 CC -!- MISCELLANEOUS: Developmentally regulated in chick embryo.
 CC -!- SIMILARITY: Belongs to the lipocalin family.

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 EMBL: M25784; AAA53371.1; -
 EMBL: M55644; AAA48677.1; -
 EMBL: AF121346; RAD23569.1; -
 EMBL: X61199; -; NOT_ANNOTATED_CDS.
 DR PIR: A30230; A30230.
 DR InterPro: IPR002345; Lipocalin.
 DR InterPro: IPR000566; Lipocalin_cytFABP.
 DR Pfam: PF00061; Lipocalin; 1.
 DR PRINTS: PR00179; LIPOCALIN.
 DR PROSITE: PS00213; LIPOCALIN; 1.
 KW Lipocalin; Transport; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 178 EXTRACELLULAR FATTY ACID BINDING PROTEIN.
 FT MOD_RES 21 21 BLOCKED.
 FT DISULFID 80 173 BY SIMILARITY.
 FT CONFLICT 4 4 L -> S (IN REF. 2).
 FT CONFLICT 27 27 R -> S (IN REF. 2 AND 4).
 FT CONFLICT 45 45 F -> S (IN REF. 2 AND 4).

FT CONFLICT 62 62 F -> S (IN REF. 1).
 FT CONFLICT 96 96 L -> V (IN REF. 1).
 SQ SEQUENCE 178 AA; 20201 MW; 0DDBC33CIA0C6B8 CRC64;
 Query Match 26.1%; Score 6; DB 1; Length 178;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 EDELEV 23
 IIIIII
 Db 65 EDELEV 70
 RESULT 8
 HIS5_METTH
 ID HIS5_METTH STANDARD; PRT; 198 AA.
 AC 027568;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP
 synthase glutamine amidotransferase subunit) (IGP synthase subunit
 hisH) (ImGP synthase subunit hisH) (IGPS subunit hisH).
 DE hisH OR MTH1524.
 GN Methanobacterium thermoautotrophicum.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE-98037514; PubMed-9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 Jiwni N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 "Complete genome sequence of Methanobacterium thermoautotrophicum
 deltaH: functional analysis and comparative genomics.";
 J. Bacteriol. 179:7135-7155(1997).
 CC -!- FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine to
 IGP, AICAR and glutamate. The hisH subunit provides the glutamine
 amidotransferase activity that produces the ammonia necessary to
 hisP for the synthesis of IGP and AICAR (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulose-1-
 ylamino)methylidenemino]-1-(5-phosphoribosyl)imidazole-4-
 carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-
 aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
 CC -!- PATHWAY: Histidine biosynthesis; fifth step.
 CC -!- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.

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 EMBL: AF000912; BAB85999.1; -
 DR PIR: D69070; D69070.
 DR HAMAP: MF_00278; -; 1.
 DR InterPro: IPR000991; GATase_1.
 DR Pfam: PF00117; GATase; 1.
 DR PROSITE: PS00442; GATASE_TYPE1; 1.
 KW Histidine biosynthesis; Transferrase; Glutamine amidotransferase;
 Complete proteome.
 FT ACT_SITE 77 77 BY SIMILARITY.
 FT ACT_SITE 177 177 BY SIMILARITY.

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FT ACT_SITE 179 179 BY SIMILARITY.
SQ SEQUENCE 198 AA; 21348 MW; B8EFA43EC9163AEF CRC64;

Query Match 26.18; Score 6; DB 1; Length 198;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15 EGADE 20
Db 130 EGADE 135

RESULT 9
COLI_PIG STANDARD; PRT; 267 AA.
ID COLI_PIG STANDARD; PRT; 267 AA.
AC P01192; Q95246;
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Corticotropin-lipotropin precursor (Pro-opiomelanocortin) (POMC)
DE [Contains: NPP; Melanotropin gamma (Gamma-MSH); Corticotropin
DE (Adrenocorticotrophic hormone) (ACTH); Melanotropin alpha (Alpha-MSH);
DE Corticotropin-like intermediary peptide (CLIP); Lipotropin beta (Beta-
DE LPH); Lipotropin gamma (Gamma-LPH); Melanotropin beta (Beta-MSH);
DE Beta-endorphin; Met-enkephalin].
GN POMC.
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86131687; PubMed=3753882;
RA Gossard F.J., Chang A.C.Y., Cohen S.N.;
RT "Sequence of the cDNA encoding porcine pro-opiomelanocortin.";
RL Biochim. Biophys. Acta 866:68-74(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84069823; PubMed=6196724;
RA Bolleau G., Barbeau C., Jeannotte L., Chretien M., Drouin J.;
RT "Complete structure of the porcine pro-opiomelanocortin mRNA derived
RT from the nucleotide sequence of cloned cDNA.";
RL Nucleic Acids Res. 11:8063-8071(1983).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95046835; PubMed=7958386;
RA Gen K., Hirai T., Kato T., Kato Y.;
RT "Presence of the same transcript of pro-opiomelanocortin (POMC) genes
RT in the porcine anterior and intermediate pituitary lobes.";
RL Mol. Cell. Endocrinol. 103:101-108(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=84239667; PubMed=6547437;
RA Oates E., Herbert E.;
RT "5' sequence of porcine and rat pro-opiomelanocortin mRNA. One porcine
RT and two rat forms.";
RL J. Biol. Chem. 259:7421-7425(1984).
RN [5]
RP SEQUENCE OF 136-174.
RA Shepherd R.G., Willson S.D., Howard K.S., Bell P.H., Davies D.S.,
RA Davis S.B., Eigner E.A., Shakespear N.E.;
RT "Studies with corticotropin. III. Determination of the structure of
RT beta-corticotropin and its active degradation products.";
RL J. Am. Chem. Soc. 78:5067-5076(1956).
RN [6]
RP REVISIONS TO 160 AND 165.
RX MEDLINE=72114902; PubMed=4334191;
RA Rniker B., Sieber P., Rittel W., Zuber H.;
RT "Revised amino-acid sequences for porcine and human
RT adrenocorticotrophic hormone.";
RL Nature New Biol. 235:114-115(1972).
RN [7]
RP REVISIONS (CORTICOTROPIN).

RX MEDLINE=74306590; PubMed=4369114;
RA Graf L.;
RT "Re-examination of the sequence of the C-terminal tryptic fragment
RT from porcine adrenocorticotrophic hormone.";
RL Acta Biochim. Biophys. Acad. Sci. Hung. 7:293-297(1972).
RN [8]
RP SEQUENCE OF 136-174.
RX MEDLINE=91071194; PubMed=2174774;
RA Volgt K., Stegmaier W., McGregor G.P., Roesch H., Seliger H.;
RT "Isolation and full structural characterisation of six
RT adrenocorticotropin-like peptides from porcine pituitary gland.
RT Identification of three novel fragments of adrenocorticotropin and of
RT two forms of a novel adrenocorticotropin-like peptide.";
RL Eur. J. Biochem. 194:225-236(1990).
RN [9]
RP SEQUENCE OF 136-148.
RX MEDLINE=91071194; PubMed=2174774;
RA Harris J.I., Lerner A.B.;
RT "Amino-acid sequence of the alpha-melanocyte-stimulating hormone.";
RL Nature 179:1346-1347(1957).
RN [10]
RP SEQUENCE OF 177-267.
RX MEDLINE=71111231; PubMed=5543613;
RA Graf L., Barat E., Cseh G., Sajgo M.;
RT "Amino acid sequence of porcine beta-lipotrophic hormone.";
RL Biochim. Biophys. Acta 229:276-278(1971).
RN [11]
RP REVISIONS (LIPOTRIPIN).
RA Gilardeau C., Chretien M.;
RT "Complete amino acid sequence of porcine beta-lipotrophic hormone
RT (beta-LPH).";
RL (In) Meienhofer J. (eds.);
RL Chemistry and biology of peptides, pp.609-611, Ann Arbor Sci. Pub.,
RL Ann Arbor (1972).
RN [12]
RP REVISION TO 211.
RX MEDLINE=73048217; PubMed=4673865;
RA Pankov Y.A., Yudaev N.A.;
RT "Complete amino acid sequence in the molecule of porcine beta-
RT lipotropin.";
RL Biochimia 37:991-1004(1972).
RN [13]
RP SEQUENCE OF 217-234.
RA Harris J.I., Roos P.;
RT "Amino-acid sequence of a melanophore-stimulating peptide.";
RL Nature 178:90-90(1956).
RN [14]
RP SEQUENCE OF 217-234.
RA Geschwind I.I., Li C.H., Barnafi L.;
RT "The structure of the beta-melanocyte-stimulating hormone.";
RL J. Am. Chem. Soc. 79:620-625(1957).
RN [15]
RP SEQUENCE OF 237-241.
RX MEDLINE=76100762; PubMed=1207728;
RA Hughes J., Smith T.W., Kosterlitz H.W., Fothergill L.A., Morgan B.A.,
RA Morris H.R.;
RT "Identification of two related pentapeptides from the brain with
RT potent opiate agonist activity.";
RL Nature 258:577-579(1975).
RN [16]
RP SEQUENCE OF 237-267.
RX MEDLINE=77084500; PubMed=1007884;
RA Graf L., Barat E., Pathy A.;
RT "Isolation of a COOH-terminal beta-lipotropin fragment (residues
RT 61-91) with morphine-like analgesic activity from porcine pituitary
RT glands.";
RL Acta Biochim. Biophys. Acad. Sci. Hung. 11:121-122(1976).
RN [17]
RP REVISIONS TO 160 AND 165.
RX MEDLINE=72114902; PubMed=4334191;
RA Rniker B., Sieber P., Rittel W., Zuber H.;
RT "Revised amino-acid sequences for porcine and human
RT adrenocorticotrophic hormone.";
RL Nature New Biol. 235:114-115(1972).
RN [7]
RP REVISIONS (CORTICOTROPIN).

```

CC GLAND.
CC -I- PTM: SPECIFIC ENZYMATIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
CC THE DIFFERENT ACTIVE PEPTIDES.
CC -I- SIMILARITY: BELONGS TO THE POMC FAMILY.
CC -----
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CC -----
CC EMBL: X03561; CAA27248.1; -
CC DR EMBL: X00135; CAA24968.1; -
CC DR EMBL: S73519; AAB32312.1; -
CC DR EMBL: K01879; AAA31104.1; -
CC DR FIR: A93496; CTPGP.
CC DR InterPro: IPR001941; Mcoitin_ACTH.
CC DR Pfam: PF00976; ACTH_domain; 1.
CC DR PRINTS: PR00383; MELANOCORTIN.
CC KW Endorphin: Hormone: Cleavage on pair of basic residues; Amidation;
CC Glycoprotein; Signal.
CC FT SIGNAL 1 26 BY SIMILARITY.
CC FT PEPTIDE 27 106 NPP.
CC FT PEPTIDE 77 87 MELANOTROPIN GAMMA.
CC FT PEPTIDE 136 174 CORTICOTROPIN.
CC FT PEPTIDE 136 148 MELANOTROPIN ALPHA.
CC FT PEPTIDE 154 174 CORTICOTROPIN-LIKE INTERMEDIARY PEPTIDE.
CC FT PEPTIDE 177 267 LIPOTRONIN BETA.
CC FT PEPTIDE 177 234 LIPOTRONIN GAMMA.
CC FT PEPTIDE 217 234 MELANOTROPIN BETA.
CC FT PEPTIDE 237 267 BETA-ENDOPHIN.
CC FT PEPTIDE 237 241 MET-ENKEPHALIN.
CC FT MOD_RES 87 87 AMIDATION (G-88 PROVIDE AMIDE GROUP).
CC FT MOD_RES 148 148 AMIDATION (G-149 PROVIDE AMIDE GROUP).
CC FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VARIANT 143 143 R -> T.
CC FT CONFLICT 6 6 G -> S (IN REF. 3 AND 4).
CC FT CONFLICT 15 15 T -> A (IN REF. 3 AND 4).
CC FT CONFLICT 23 23 G -> E (IN REF. 3 AND 4).
CC FT CONFLICT 49 49 A -> S (IN REF. 4).
CC SQ SEQUENCE 267 AA; 28894 MW; A6DB487A5032B648 CRC64;

CC Query Match 26.1%; Score 6; DB 1; Length 267;
CC Best Local Similarity 100.0%; Pred. No. 36;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 16 GAEDEL 21
CC DB 161 GAEDEL 166

CC RESULT 10
CC TPW2_DROME STANDARD; PRT; 284 AA.
CC AC P09491; P09490; Q24408; Q24427; Q24428; Q8S265; Q9VF95;
CC DT 01-MAR-1989 (Rel. 10, Created)
CC DT 01-MAR-1989 (Rel. 10, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Tropomyosin 2 (Tropomyosin I).
CC GN TM2 OR TM1 OR CG4843.
CC OS Drosophila melanogaster (Fruit fly).
CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC OC Ephydroidea; Drosophilidae; Drosophila.
CC OX NCBI_Taxid=7227;
CC [1]
CC SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
CC RP TISSUE=Embryo, Larva, and Pupae;
CC RX MEDLINE=84205681; PubMed=6202423;
CC RA Karlik C.C., Mahaffey J.W., Coutu M.D., Fyrberg E.A.;
CC RT "Organization of contractile protein genes within the 88F subdivision

RT of the D. melanogaster third chromosome.";
RL Cell 37:469-481(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
RX MEDLINE=86085920; PubMed=3079761;
RA Basi G.S., Storti R.V.;
RT "Structure and DNA sequence of the tropomyosin I gene from Drosophila
RT melanogaster.";
RL J. Biol. Chem. 261:817-827(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupsky M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [4]
RP REVISIONS.
RC STRAIN=Berkeley;
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM EMBRYONIC).
RC STRAIN=Berkeley; TISSUE=Embryo;
RX PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";

```
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
RN [6]
RP SEQUENCE OF 258-284 FROM N.A. (ISOFORM EMBRYONIC).
RX MEDLINE=85215579; PubMed=4000944;
RA Boardman M., Basi G.S., Storti R.V.;
RT "Multiple polyadenylation sites in a Drosophila tropomyosin gene are
RL used to generate functional mRNAs.";
RL Nucleic Acids Res. 13:1763-1776(1985).
CC -1- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Thoracic; Synonyms=127; t;
CC IsoId=p09491-1; Sequence=displayed;
CC Name=Embryonic; Synonyms=129; A, B, e;
CC IsoId=p09491-2; Sequence=VSP_006616;
CC -1- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE
CC EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
CC -1- SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY.
CC -1- CAUTION: Ref.6 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K02622; AAA28970.1; -
DR EMBL; K02623; AAA28971.1; -
DR EMBL; K02622; AAA28971.1; JOINED.
DR EMBL; K03277; AAA28973.1; -
DR EMBL; K03277; AAA28974.1; -
DR EMBL; AE003708; AAN13652.1; -
DR EMBL; AY071087; AAL48709.1; -
DR EMBL; X02220; CAA26142.1; ALT_SEQ.
DR PIR; A25624; A25624.
DR PIR; B25624; B25624.
DR FlyBase; FBgn004117; Tm2.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS00326; TROPOMYOSIN; 1.
KW Muscle protein; Coiled coil; Repeat; Alternative splicing;
KW Multigene family.
KW VARSPLIC 259 284 RLFNEKEKYKAICDDLDQTFAEITGY -> ELGINKDRYKS
LADMDSTFAELAGY (in isoform Embryonic).
/FTId=VSP_006616
M -> V (IN REF. 1).
Q -> L (IN REF. 1).
I -> T (IN REF. 1).
R -> D (IN REF. 1).
SQ SEQUENCE 284 AA; 32981 MW; 07AD03FDD304EA5F CRC64;
Query Match 26.1%; Score 6; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 18 EDELEV 23
Db 173 EDELEV 178
|||||
RESULT 11
PCD1_HUMAN STANDARD; PRT; 288 AA.
ID Q15116; Q00517;
AC Q15116; Q00517;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Programmed cell death protein 1 precursor (Protein PD-1) (hpd-1).
GN PCD1 OR PDI.
OS Homo sapiens (Human).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95154844; PubMed=7851902;
RA Shinohara T., Taniwaki M., Ishida Y., Kawalch M., Honjo T.;
RT "Structure and chromosomal localization of the human PD-1 gene
RL (PDCD1).";
RL Genomics 23:704-706(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97473511; PubMed=9332365;
RA Finger L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,
RA Burrows P.D., Billips L.D.;
RA Gene 203:253-253(1997).
CC -1- FUNCTION: POSSIBLE CELL DEATH INDUCER, IN ASSOCIATION WITH
CC OTHER FACTORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DEVELOPMENTAL STAGE: INDUCED AT PROGRAMMED CELL DEATH.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC -----
DR EMBL; L27440; AAC41700.1; -
DR EMBL; U64863; AAC51773.1; -
DR PIR; A55737; A55737.
DR HSSP; P01607; IREI.
DR Genew; HGNC:8760; PDCD1.
DR MIM; 600244; -
DR GO; GO:0004871; F:signal transducer activity; TAS.
DR GO; GO:0006915; P:apoptosis; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0006959; P:humoral immune response; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; Apoptosis.
FT SIGNAL 1 288
FT CHAIN 21 288 PROGRAMMED CELL DEATH PROTEIN 1.
FT DOMAIN 21 170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 171 191 POTENTIAL.
FT DOMAIN 192 288 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 35 145 IG-LIKE V-TYPE.
FT DISULFID 54 123 POTENTIAL.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 38 38 F -> S (IN REF. 1).
FT CONFLICT 162 162 P -> S (IN REF. 1).
SQ SEQUENCE 288 AA; 31707 MW; A5210AD50C3046C7 CRC64;
Query Match 26.1%; Score 6; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 6 LRPEDG 11
Db 277 LRPEDG 282

RESULT 12
OPSD_LIMPA
ID OPSD_LIMPA STANDARD; PRT; 289 AA.
AC Q42431;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Rhodopsin (Fragment).
GN RHO.
OS Limnococtus pallidus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoldei; Abyssocottidae; Limnococtus.
OX NCBI_TaxID=61634;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98086781; PubMed=9417898;
RA Hunt D.M., Fitzgibbon J., Slobodyanyuk S.J., Bowmaker J.K.,
RA Dulai K.S.;
RT "Molecular evolution of the cottoid fish endemic to Lake Baikal
RT deduced from nuclear DNA evidence.";
RL Mol. Phylogenet. Evol. 8:415-422(1997).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC LINKED TO CIS-RETINAL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES
CC VISION IN DIM LIGHT.
CC -!- PTH: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U97271; AAB61725.1; -.
CC HSSP: P02699; IBOJ.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC InterPro: IPR001760; Opsin.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS: PR00237; GPCR_RHODPSN.
CC PROSITE: PS00237; G-PROTEIN_RECEPTOR_F1_1; FALSE_NEG.
CC PROSITE: PS00262; G-PROTEIN_RECEPTOR_F1_2; 1.
CC PROSITE: PS00238; OPSIN; 1.
CC Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.
FT NON_TER 1 1
FT DOMAIN <1 7 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 8 32 1 (POTENTIAL).
FT DOMAIN 33 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 69 2 (POTENTIAL).
FT DOMAIN 70 84 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 85 104 3 (POTENTIAL).
FT DOMAIN 105 123 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 124 147 4 (POTENTIAL).
FT DOMAIN 148 173 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 174 201 5 (POTENTIAL).
FT DOMAIN 202 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 247 6 (POTENTIAL).
FT DOMAIN 248 255 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 256 280 7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
RETINAL CHROMOPHORE (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
>289
DOMAIN 281
DISULFID 81
BINDING 158
CARBOHYD 267
NON_TER 171
SEQUENCE 289
MW: 160D08E17E5E1280 CRC64;
Query Match 26.1%; Score 6; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LAGWLR 7
Db 143 LAGWLR 148

RESULT 13
PARB_HELPJ
ID PARB_HELPJ STANDARD; PRT; 290 AA.
AC Q92K75;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable chromosome partitioning protein parB.
GN PARB OR JHP1066.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- FUNCTION: INVOLVED IN CHROMOSOME PARTITION. LOCALIZE TO BOTH POLES
CC OF THE PREDIVISIONAL CELL FOLLOWING COMPLETION OF DNA REPLICATION.
CC BINDS TO THE DNA ORIGIN OF REPLICATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARB FAMILY.
CC -----
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CC -----
CC EMBL: AE001534; AAD06646.1; -.
CC PIR: H71852; H71852.
CC InterPro: IPR004437; ParB_part.
CC InterPro: IPR003115; ParBc.
CC Pfam: PF02195; ParBc; 1.
CC SMART: SM00470; ParB; 1.
CC TIGRFAMs: TIGR00180; parB_part; 1.
CC Chromosome partition; DNA-binding; Complete proteome.
KW Chromosome partition; DNA-binding; Complete proteome.
SQ SEQUENCE 290 AA; 33405 MW; 6709BA0547A55A4F CRC64;
Query Match 26.1%; Score 6; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 AEDELE 22
Db 245 AEDELE 250

RESULT 14
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MTSA_STRP8
ID MTSA_STRP8 STANDARD; PRT; 310 AA.
AC QBP280;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metal ABC transporter substrate-binding lipoprotein precursor.
GN MTSA OR SPYM18_0494.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OC NCBI_TaxID=186103;
RX
RN
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS8232 / Serotype M18;
RX MEDLINE=2197593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC -1- FUNCTION: Part of an ATP-driven transport system for a metal; this
CC protein has affinity for Zn(II), Fe(III) and Cu(II).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC -1- SIMILARITY: Belongs to the bacterial solute-binding protein family
CC 9. Lipoprotein receptor antigen (Lrai) subfamily.
CC -----
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CC -----
DR EMBL; AEO09988; AAL97215.1; -;
DR InterPro: IPR006128; Lipoprotein_4.
DR InterPro: IPR006127; SBP_bac_9.
DR Pfam: PF01297; SBP_bac_9; 1.
DR PRINTS; PR00690; ADHESNFAMILY.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
DR Transport; Zinc transport; Iron transport; Copper; Membrane;
KW Lipoprotein; Signal; Complete proteome.
FT SIGNAL 1 20
FT CHAIN 21 310
FT METAL ABC TRANSPORTER SUBSTRATE-
FT BINDING LIPOPROTEIN.
FT LPID 21 21 N-ACYL DIGLYCERIDE (PROBABLE).
SQ SEQUENCE 310 AA; 34330 MW; 40F613659AAD1768 CRC64;
Query Match 26.1%; Score 6; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 EDGGQA 14
| | | | |
Db 94 EDGGQA 99
RESULT 15
MTSA_STRPY
ID MTSA_STRPY STANDARD; PRT; 310 AA.
AC Q9A157; Q9RNI7; Q9RNJ0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Metal ABC transporter substrate-binding lipoprotein precursor.
GN MTSA OR SPY0453 OR SPYM3_0318 OR SPS1539.
OS Streptococcus pyogenes, and
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.
OX NCBI_TaxID=1314, 198466;
RN
RP SEQUENCE FROM N.A., SEQUENCE OF 30-39, AND CHARACTERIZATION.
RC STRAIN-SF370 / ATCC 700294 / Serotype M1, and API / Serotype M1;
RX MEDLINE=20032372; PubMed=10564500;
RA Janulczyk R., Pallon J., Bjoerck L.;
RT "Identification and characterization of a Streptococcus pyogenes ABC
RT transporter with multiple specificity for metal cations.";
RL Mol. Microbiol. 34:596-606(1999).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes: a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Part of an ATP-driven transport system for a metal; this
CC protein has affinity for Zn(II), Fe(III) and Cu(II).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC -1- SIMILARITY: Belongs to the bacterial solute-binding protein family
CC 9. Lipoprotein receptor antigen (Lrai) subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AFI80520; AAD56936.1; -;
DR EMBL; AFI80521; AAD56939.1; -;
DR EMBL; AE006505; AAK33468.1; -;
DR EMBL; AE014143; AAM78925.1; ALT_INIT.
DR EMBL; AP005145; BAC64634.1; ALT_INIT.
DR HSP; P96116; ITOA.
DR InterPro: IPR006128; Lipoprotein_4.
DR InterPro: IPR006127; SBP_bac_9.
DR Pfam: PF01297; SBP_bac_9; 1.
DR PRINTS; PR00690; ADHESNFAMILY.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Transport; Zinc transport; Iron transport; Copper; Membrane;
KW Lipoprotein; Signal; Complete proteome.
FT SIGNAL 1 20
FT CHAIN 21 310
FT METAL ABC TRANSPORTER SUBSTRATE-
FT BINDING LIPOPROTEIN
FT LPID 21 21 N-ACYL DIGLYCERIDE (PROBABLE).
FT VARIANT 77 77 V -> A (IN STRAIN API).

```

FT CONFLICT 26 26 T -> A (IN REF. 1).
FT CONFLICT 30 30 K -> E (IN REF. 1).
FT CONFLICT 44 44 A -> G (IN REF. 1).
FT CONFLICT 49 50 AI -> VM (IN REF. 1).
SQ SEQUENCE 310 AA: 34358 MW: B0F829EF1C72CADC CRC64;

Query Match 26.1%; Score 6; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 EDGGOA 14
Db 94 EDGGOA 99

```

Search completed: September 11, 2003, 17:52:41
Job time : 4.42781 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:02 ; Search time 22.016 seconds
(without alignments)
269.586 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 23

Sequence: 1 ALAGWLRPDGGQAEDELEV 23

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | ID | Description |
|------------|-------|-------------|---------------|--------------------|
| 1 | 20 | 87.0 | 117 4 Q8TAT9 | Q8tat9 homo sapien |
| 2 | 11 | 47.8 | 117 11 Q8CH53 | Q8ch53 meriones un |
| 3 | 8 | 34.8 | 433 10 Q93ZV7 | Q93zv7 arabidopsis |
| 4 | 8 | 34.8 | 433 10 Q8L7E4 | Q8l7e4 arabidopsis |
| 5 | 8 | 34.8 | 483 10 Q65529 | Q65529 arabidopsis |
| 6 | 7 | 30.4 | 103 16 Q9L063 | Q9l063 streptomyce |
| 7 | 7 | 30.4 | 313 2 Q8VP52 | Q8vp52 streptomyce |
| 8 | 7 | 30.4 | 433 16 Q8CNY4 | Q8cny4 staphylococ |
| 9 | 7 | 30.4 | 887 16 Q8XY49 | Q8xy49 ralstonia s |
| 10 | 7 | 30.4 | 910 16 Q9I3F5 | Q9i3f5 pseudomonas |
| 11 | 7 | 30.4 | 2376 5 Q9V5J0 | Q9v5j0 drosophila |
| 12 | 7 | 30.4 | 2376 5 Q966V1 | Q966v1 drosophila |
| 13 | 6 | 26.1 | 69 16 Q9A542 | Q9a542 caulobacter |
| 14 | 6 | 26.1 | 88 17 Q8ZZR1 | Q8zzr1 pyrobaculum |
| 15 | 6 | 26.1 | 98 5 P91785 | P91785 onchocerca |
| 16 | 6 | 26.1 | 100 16 Q8PBN4 | Q8pbn4 xanthomonas |

| | | | | |
|----|---|------|---------------|---------------------|
| 17 | 6 | 26.1 | 106 10 P93359 | P93359 nicotiana t |
| 18 | 6 | 26.1 | 110 2 Q87801 | Q87801 pseudomonas |
| 19 | 6 | 26.1 | 112 5 Q26847 | Q26847 trypanosoma |
| 20 | 6 | 26.1 | 113 16 Q8G7N5 | Q8g7n5 bifidobacte |
| 21 | 6 | 26.1 | 117 12 Q65548 | Q65548 bovine herp |
| 22 | 6 | 26.1 | 129 4 O43180 | O43180 homo sapien |
| 23 | 6 | 26.1 | 133 13 Q8JFY6 | Q8jfy6 litoria cae |
| 24 | 6 | 26.1 | 137 4 Q8N8H9 | Q8n8h9 homo sapien |
| 25 | 6 | 26.1 | 138 16 Q9RD30 | Q9rd30 streptomyce |
| 26 | 6 | 26.1 | 142 16 Q8ZBU1 | Q8zbu1 yersinia pe |
| 27 | 6 | 26.1 | 147 5 Q25622 | Q25622 onchocerca |
| 28 | 6 | 26.1 | 148 5 Q8WT59 | Q8wt59 onchocerca |
| 29 | 6 | 26.1 | 154 5 Q8WT58 | Q8wt58 onchocerca |
| 30 | 6 | 26.1 | 154 5 Q8WT56 | Q8wt56 litomosolde |
| 31 | 6 | 26.1 | 154 5 Q8WT57 | Q8wt57 onchocerca |
| 32 | 6 | 26.1 | 159 3 Q05697 | Q05697 saccharomyc |
| 33 | 6 | 26.1 | 159 4 Q8N9A4 | Q8n9a4 homo sapien |
| 34 | 6 | 26.1 | 161 10 Q9LWY4 | Q9lwy4 oryza sativ |
| 35 | 6 | 26.1 | 165 2 Q9RNJ3 | Q9rnj3 zymomonas m |
| 36 | 6 | 26.1 | 165 16 Q8XXY6 | Q8xxxy6 ralstonia s |
| 37 | 6 | 26.1 | 171 5 Q25624 | Q25624 onchocerca |
| 38 | 6 | 26.1 | 175 13 Q8JFY7 | Q8jfy7 litoria cae |
| 39 | 6 | 26.1 | 175 16 Q9KQ90 | Q9kq90 vibrio chol |
| 40 | 6 | 26.1 | 177 11 Q8CIQ8 | Q8ciq8 rattus norv |
| 41 | 6 | 26.1 | 178 5 Q25619 | Q25619 onchocerca |
| 42 | 6 | 26.1 | 178 5 Q8WZJ8 | Q8wzj8 acanthochei |
| 43 | 6 | 26.1 | 178 16 Q98IM5 | Q98im5 rhizobium l |
| 44 | 6 | 26.1 | 180 2 O50344 | O50344 lactobacill |
| 45 | 6 | 26.1 | 186 5 Q9UIY0 | Q9uiy0 caenorhabdi |

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY; PRT; 117 AA.
AC Q8TAT9;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Ghrelin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025791; AAH25791.1; -
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
SQ SEQUENCE 117 AA; 12939 MW; 25B0572EBECB7610 CRC64;

Query Match 87.0%; Score 20; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.4e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAEDE 20
|||||
DB 52 ALAGWLRPDGGQAEDE 71

RESULT 2

Q8CH53 PRELIMINARY; PRT; 117 AA.
ID Q8CH53;
AC Q8CH53;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

```

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoka T., Miyazawa M., Anagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AAO06965.1; -;
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 47.8%; Score 11; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 QOAGAEDELE 22
DB |||||
63 QOAGAEDELE 73

RESULT 3
Q932V7 PRELIMINARY; PRT; 433 AA.
AC Q932V7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative RNA-binding protein LAH1.
GN A74G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Koesena E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene AT4g32720 (GI:7270219).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY056237; AAL07086.1; -;
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR PROSITE; PS0102; RRM; 1.
SQ SEQUENCE 433 AA; 48095 MW; E58EBAF51C35A8F7 CRC64;

Query Match 34.8%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAED 20
DB |||||
287 QAEGAED 294

RESULT 4
Q8L7E4 PRELIMINARY; PRT; 433 AA.
AC Q8L7E4
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN AT4G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Shinn P., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
RA Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sekano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY136302; AAM96968.1; -;
DR EMBL; BT000396; AAN15715.1; -;
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR PROSITE; PS0102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 433 AA; 48126 MW; CFFF611A29AA0318 CRC64;

Query Match 34.8%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAED 20
DB |||||
287 QAEGAED 294

RESULT 5
O65529 PRELIMINARY; PRT; 483 AA.
AC O65529
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 54.1 kDa protein.
GN F4D11.80 OR AT4G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoerge W., Hoheisel J.,
RA Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]

```

RP SEQUENCE FROM N.A.
 RA Benes V., Rechmann S., Borkova D., Ansoorge W., Mewes H.W., Lemcke K.,
 RL Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL022537; CAA18589.1; -;
 DR EMBL: AL161582; CAB79989.1; -;
 DR InterPro: IPR002344; Lupus_La.
 DR InterPro: IPR006630; Lupus_La_dom.
 DR InterPro: IPR00504; RNA_rec_mot.
 DR Pfam: PF00076; rrm; 1.
 DR PRINTS: PR00302; LUPUSLA.
 DR SMART: SM00715; LA; 1.
 DR SMART: SM00360; RRM; 1.
 DR PROSITE: PS50102; RRM; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 483 AA; 54125 MW; 20840B34A0BC94E2 CRC64;
 Query Match 34.8%; Score 8; DB 10; Length 483;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 OAEGAEDE 20
 |||||
 DB 302 OAEGAEDE 309

RESULT 6
 Q9L063
 ID Q9L063 PRELIMINARY; PRT; 103 AA.
 AC Q9L063
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein SC02791.
 GN SC02791 OR SC0105.22C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL939114; CAB87228.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 103 AA; 10639 MW; 9316F1F38C1BD492 CRC64;

Query Match 30.4%; Score 7; DB 16; Length 103;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 DGGQAEQ 16
 |||||
 DB 48 DGGQAEQ 54

RESULT 7

Q8VP52
 ID Q8VP52 PRELIMINARY; PRT; 313 AA.
 AC Q8VP52
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE LysR-like transcriptional activator SnpR.
 OS Streptomyces sp. C5.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=45212;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C5;
 RA Desanti C.L., Strohl W.R.;
 RT "Characterization of the Streptomyces sp. strain C5 snp locus and
 development of an snp-derived expression vector family.";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL: AY072041; AAL61992.1; -;
 DR InterPro: IPR000847; HTH_LysR.
 DR InterPro: IPR005119; LysR_subst.
 DR Pfam: PF00126; HTH_1; 1.
 DR Pfam: PF03466; LysR_substrate; 1.
 DR PRINTS: PR00039; HTHLYSR.
 DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
 KW DNA-binding; Transcription; Transcription regulation.
 SQ SEQUENCE 313 AA; 34258 MW; C907C8AF51C3FA13 CRC64;
 Query Match 30.4%; Score 7; DB 23; Length 313;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLR 7
 |||||
 DB 103 ALAGWLR 109

RESULT 8
 Q8CNY4
 ID Q8CNY4 PRELIMINARY; PRT; 433 AA.
 AC Q8CNY4
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Trigger factor.
 GN SEI350.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE016748; AAO04949.1; -;
 KW Complete proteome.
 SQ SEQUENCE 433 AA; 48732 MW; FF249AD097F437D CRC64;
 Query Match 30.4%; Score 7; DB 16; Length 433;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 DGGQAEQ 16
 |||||
 DB 180 DGGQAEQ 186

RESULT 9
 Q8XY49
 ID Q8XY49 PRELIMINARY; PRT; 887 AA.

AC Q8XY49;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Probable phage-related tail transmembrane protein.
 GN RSC1914 OR RS03483.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GMI1000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Canus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646067; CADL5616.1; -;
 KW Complete proteome.
 SQ SEQUENCE 887 AA; 94105 MW; 9A8840E5362E740E CRC64;
 Query Match 30.4%; Score 7; DB 16; Length 887;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 GQAEAG 18
 Db 290 GQAEAG 296
 ID Q913F5 PRELIMINARY; PRT; 910 AA.
 AC Q913F5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Aconitate hydratase 1.
 GN ACNA OR PA1562.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Slover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen";
 RL Nature 406:959-964(2000).
 DR EMBL; AE004584; AAG04951.1; -;
 DR HSSP; P20004; IACO.
 DR InterPro; IPR006249; Aconitase.1.
 DR InterPro; IPR000573; Aconitase.C.
 DR InterPro; IPR001030; Aconitase.N.
 DR Pfam; PF00330; aconitase; 1.
 DR Pfam; PF00694; Aconitase_C; 1.
 DR PRINTS; PR00415; ACONITASE.
 DR ProDom; PD000511; Aconitase.N; 1.
 DR TIGRFAMS; TIGR01341; aconitase.1;
 DR PROSITE; PS00450; ACONITASE_1; 1.
 DR PROSITE; PS01244; ACONITASE_2; 1.

KW Complete proteome.
 SQ SEQUENCE 910 AA; 99147 MW; C65F23CDB6FA0E1C CRC64;
 Query Match 30.4%; Score 7; DB 16; Length 910;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLR 7
 Db 65 ALAGWLR 71
 RESULT 11
 Q9V5J0 PRELIMINARY; PRT; 2376 AA.
 ID Q9V5J0
 AC Q9V5J0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG18408 protein.
 GN REXIN OR CG3451 OR CG18408 OR CG18409.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazej M.R., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Crowley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Fertaz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matteo B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busan D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalaal M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.B., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Brysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Milburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003830; AAF58816.2; -
DR FlyBase; FBgn0033504; rexin.
DR InterPro; IPR001452; SH3.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000066; SH3; 3.
DR SMART; SM00326; SH3; 3.
DR PROSITE; PS50002; SH3; 3.
SQ SEQUENCE 2376 AA; 267666 MW; A5F2D0589B8B695C CRC64;
Query Match 30.4%; Score 7; DB 5; Length 2376;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 QAEGAEED 19
Db 37 QAEGAEED 43
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AC Q966V1
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DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Rexin L1.
GN REXIN OR RXN OR CG3451 OR CG18408 OR CG18409.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydrioides; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki H.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamazaki H., Willert K., Fish M., Nusse R.;
RT "Drosophila Rexin, a Novel SH3 Adaptor Protein of Axin and Arrow that
RT is Essential for Living in Late Stage Embryo.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 3 SH3 DOMAINS.
DR EMBL; AB053478; BAB62017.1; -
DR FlyBase; FBgn0033504; rexin.
DR InterPro; IPR002965; P_Rich_extensn.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 3.
DR PRINTS; PR01217; PRICHEXTENS.
DR ProDom; PD000066; SH3; 3.
DR SMART; SM00326; SH3; 3.
DR PROSITE; PS50002; SH3; 3.
KW SH3 domain.
SQ SEQUENCE 2376 AA; 267657 MW; 9C7BD6C7A705C888 CRC64;
Query Match 30.4%; Score 7; DB 5; Length 2376;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 QAEGAEED 19
Db 37 QAEGAEED 43
RESULT 13
Q9A542 ID Q9A542 PRELIMINARY; PRT; 69 AA.
AC Q9A542
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cold-shock domain family protein.
GN CC2623.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR EMBL; AE005930; AAK24591.1; -
DR HSP; P15277; IMJC.
DR TIGR; CC2623; -
DR InterPro; IPR002059; Cold_shock.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000621; Cold_shock; 1.
DR SMART; SM00357; CSP; 1.
KW Activator; DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 69 AA; 7450 MW; 8EA80BE9EE56853C CRC64;
Query Match 26.1%; Score 6; DB 16; Length 69;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 PEDGGQ 13
Db 20 PEDGGQ 25
RESULT 14
Q8Z2R1 ID Q8Z2R1 PRELIMINARY; PRT; 88 AA.

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AC Q82ZRI; 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PAE0124.
GN PAE0124.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RL aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009752; AAL62578.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 88 AA; 9492 MW; 22091651B45CADD1 CRC64;

Query Match 26.1%; Score 6; DB 17; Length 88;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
DB 45 ALAGWL 50

RESULT 15
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ID P91785 PRELIMINARY; PRT; 98 AA.
AC P91785;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Antigen maltose binding protein (Fragment).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=94336252; PubMed=8058358;
RA Trenholme K.R., Tree T.I., Gillespie A.J., Guderian R., Maizels R.M.,
RA Bradley J.E.;
RT "Heterogeneity of IgG antibody responses to cloned Onchocerca volvulus
RT antigens in microfilariemia positive individuals from Esmeraldas
RT Province, Ecuador.";
RL Parasite Immunol. 16:201-209(1994).
DR EMBL; S71371; AAC60510.2; -
FT NON_TER 1
FT NON_TER 98
SQ SEQUENCE 98 AA; 11165 MW; 221BEFEBFE14DC76 CRC64;

Query Match 26.1%; Score 6; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LRPEDG 11
DB 51 LRPEDG 56
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Search completed: September 11, 2003, 17:55:49
Job time : 22.016 secs

GenCore version 5.1.6
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OM protein ~ protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 23.984 Seconds
(without alignments)
152.215 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 121

Sequence: 1 ALAGWLRPEDGGAGAEDELEV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 121 | 100.0 | 23 | AAE23840 | Human zsig33-linker |
| 2 | 121 | 100.0 | 23 | AAE23841 | Human zsig33-linker |
| 3 | 121 | 100.0 | 23 | AAE15885 | Human zsig33-linker |
| 4 | 121 | 100.0 | 23 | AAE15886 | Human zsig33-linker |
| 5 | 121 | 100.0 | 24 | AAE23839 | Human zsig33-linker |
| 6 | 121 | 100.0 | 24 | AAE15884 | Human zsig33-linker |
| 7 | 121 | 100.0 | 91 | AAE33410 | Human exon 3-delet |
| 8 | 121 | 100.0 | 116 | AAE60517 | Human des-Gln14-gh |
| 9 | 121 | 100.0 | 117 | AAW87991 | Protein designated |

| | | | | | | |
|----|------|-------|------|----|----------|--------------------|
| 10 | 121 | 100.0 | 117 | 21 | AAE87236 | Human signal pepti |
| 11 | 121 | 100.0 | 117 | 22 | AAE38890 | Human polypeptide |
| 12 | 121 | 100.0 | 117 | 22 | AAE62649 | Human zsig33 poly |
| 13 | 121 | 100.0 | 117 | 22 | AAE20101 | zsig33 protein. H |
| 14 | 121 | 100.0 | 117 | 22 | AAE60511 | Human ghrelin prep |
| 15 | 121 | 100.0 | 117 | 23 | AAE78319 | Amino acid sequenc |
| 16 | 121 | 100.0 | 117 | 23 | AAE23838 | Human zsig33 prote |
| 17 | 121 | 100.0 | 117 | 23 | AAE15883 | Human zsig33 prote |
| 18 | 121 | 100.0 | 117 | 24 | AAE6790 | Human PRO polypept |
| 19 | 121 | 100.0 | 117 | 24 | AAE67066 | Human secreted/tr |
| 20 | 121 | 100.0 | 117 | 24 | AAE59871 | Novel secreted and |
| 21 | 121 | 100.0 | 117 | 24 | AAE59124 | Novel human secret |
| 22 | 121 | 100.0 | 117 | 24 | AAE59271 | Human secreted/tr |
| 23 | 121 | 100.0 | 117 | 24 | AAE59420 | Novel human secret |
| 24 | 121 | 100.0 | 117 | 24 | AAE60555 | Human secreted/tr |
| 25 | 121 | 100.0 | 117 | 24 | AAE58046 | Human PRO polypept |
| 26 | 121 | 100.0 | 117 | 24 | AAE58977 | Human secreted/tr |
| 27 | 121 | 100.0 | 117 | 24 | AAE33409 | Human preproghreli |
| 28 | 121 | 100.0 | 117 | 24 | AAE13937 | Human PRO1066 poly |
| 29 | 121 | 100.0 | 117 | 24 | AAE10892 | Human PRO polypept |
| 30 | 121 | 100.0 | 118 | 21 | AAE66708 | Membrane-bound pro |
| 31 | 121 | 100.0 | 118 | 22 | AAE12392 | Human PRO1066 poly |
| 32 | 121 | 100.0 | 118 | 22 | AAE65231 | Human PRO1066 (UNG |
| 33 | 121 | 100.0 | 126 | 22 | AAE40676 | Human polypeptide |
| 34 | 90 | 74.4 | 90 | 23 | ABP08975 | Human ORFX protein |
| 35 | 90 | 74.4 | 116 | 22 | AAE60516 | Rat des-Gln14-ghre |
| 36 | 90 | 74.4 | 117 | 22 | AAE60510 | Rat ghrelin prepro |
| 37 | 87 | 71.9 | 117 | 22 | AAE60521 | Porcine des-Gln14- |
| 38 | 87 | 71.9 | 118 | 22 | AAE60520 | Porcine ghrelin pr |
| 39 | 62.5 | 51.7 | 89 | 22 | AAE60523 | Bovine ghrelin pre |
| 40 | 54 | 44.6 | 200 | 24 | ABP58240 | Xenopus laevis nuc |
| 41 | 50 | 41.3 | 653 | 17 | AAE98903 | Murine APLP1. Mus |
| 42 | 48 | 39.7 | 82 | 22 | AAE73526 | Human colon cancer |
| 43 | 48 | 39.7 | 287 | 22 | AAE15575 | Novel human diagno |
| 44 | 48 | 39.7 | 570 | 22 | ABG20671 | Novel human diagno |
| 45 | 48 | 39.7 | 2836 | 22 | ABE62719 | Drosophila melanog |

ALIGNMENTS

RESULT 1

AAE23840

ID AAE23840 standard; peptide; 23 AA.

XX AAE23840;

AC AAE23840;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human zsig33-linker peptide #2.

XX

KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;

KW growth hormone; digestive enzyme; restorative therapy; gene therapy;

KW protein therapy; gastrolntestinal; endocrine; anabolic.

XX

OS Homo sapiens.

XX

PN US2002055156-A1.

XX

PD 09-MAY-2002.

XX

PF 10-MAY-2001; 2001US-0853253.

XX

PR 11-MAY-2000; 2000US-203300P.

XX

PA (JASP/) JASPERS S R.

PA (SHEP/) SHEPPARD P O.

PA (DEIS/) DEISHER T A.

PA (BISH/) BISHOP P D.

XX

PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX

XX WPI; 2002-443750/47.

DR

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones -
XX
XX
PS Claim 1; Page 28; 34pp; English.
XX
XX The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 121; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. NO. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 2
AAE23841
ID AAE23841 standard; peptide; 23 AA.
XX
AC AAE23841;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human zsig33-linker peptide #3.
XX
KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.
XX
OS Homo sapiens.
XX
PN US200205156-A1.
XX
PD 09-MAY-2002.
XX
PF 10-MAY-2001; 2001US-0853253.
XX
PR 11-MAY-2000; 2000US-203300P.
XX
PA (JASP/) JASPERS S R.
PA (SHEP/) SHEPPARD P O.
PA (DEIS/) DEISHER T A.
PA (BISH/) BISHOP P D.
XX
PI Jaspers SR, Sheppard PO, Delsher TA, Bishop PD;
XX
DR WPI; 2002-443750/47.
XX
XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones -
XX
PS Claim 1; Page 28; 34pp; English.
XX
XX The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 121; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. NO. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
Db 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 3
AAE15885
ID AAE15885 standard; peptide; 23 AA.
XX
AC AAE15885;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human zsig33-linker peptide #2.
XX
KW Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycemic;
KW adsorption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33-linker peptide.
XX
OS Homo sapiens.
XX
PN WO200187933-A2.
XX
PD 22-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-US15091.
XX
PR 11-MAY-2000; 2000US-0569271.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX
DR WPI; 2002-082982/11.
DR N-PSDB; AAD25760.
XX
XX New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and
PT treating gastrointestinal and growth related diseases, comprises

FT XX /note= "Hydrophilic region"

PN US2002055156-A1.

XX 09-MAY-2002.

XX 10-MAY-2001; 2001US-0853253.

XX 11-MAY-2000; 2000US-203300P.

XX (JASP/) JASPERS S. R.

PA (SHEP/) SHEPPARD P. O.

PA (DEIS/) DEISHER T. A.

PA (BISH/) BISHOP P. D.

XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI; 2002-443750/47.

DR N-PSDB; AAD38239.

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

PT contractility, nutrient uptake, growth hormones and/or secretion of

PT digestive/pancreatic enzymes and hormones -

XX Claim 1; Page 28; 34pp; English.

PS The invention relates to zsig33-like peptides and their corresponding

XX nucleic acids and methods for modulating gastric contractility, nutrient

CC uptake, growth hormones, secretion of digestive enzymes and hormones.

CC The sequences of the invention are used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate ZSIG33 expression.

CC The nucleic acids of the invention and their complements are used as

CC DNA probes in diagnostic assays to detect and quantitate the presence

CC of similar nucleic acids in samples, and therefore which patients may be

CC in need of restorative therapy. The ZSIG33 peptides are used as antigens

CC in the production of antibodies against ZSIG33 and in assays to identify

CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies

CC and antagonists are used to down regulate expression and activity. The

CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting

CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent

CC assay (ELISA)). The peptides and nucleic acids of the invention are used

CC to modulate gastric contractility, nutrient uptake, growth hormones, the

CC secretion of digestive enzymes and hormones, and/or secretion of enzymes

CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy

CC and zsig33-like peptide is used in protein therapy. The present sequence

CC is human zsig33-like peptide, zsig33-linker peptide.

XX Sequence 24 AA;

SQ Query Match 100.0%; Score 121; DB 23; Length 24;

Best Local Similarity 100.0%; Pred. No. 3.8e-11;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGGAEGAEDELEV 23

|||||

Db 1 ALAGWLRPDGGGAEGAEDELEV 23

RESULT 6

AAE15884

ID AAE15884 standard; peptide; 24 AA.

XX AC AAE15884;

XX 26-MAR-2002 (first entry)

DT Human zsig33-linker peptide #1.

XX Human; zsig33-like peptide; ZS33LP; immunity; developmental process;

KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;

KW adsorption enhancer; gastrointestinal disease; growth related disease;

KW inflammation; gene therapy; growth regulation; blood vessel formation;

KW HIV; zsig33-linker peptide.

XX Homo sapiens.

OS Key Location/Qualifiers

XX Region 6..22

FT /note= "Hydrophilic antigenic site"

FT Region 7..18

FT /note= "Hydrophilic region"

XX WO200187933-A2.

XX 22-NOV-2001.

XX 10-MAY-2001; 2001WO-US15091.

XX 11-MAY-2000; 2000US-0569271.

XX (ZYMO) ZYMOGENETICS INC.

PA Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

PI WPI; 2002-082982/11.

DR N-PSDB; AAD25760.

XX New polypeptides, useful for modulating gastric contractility, nutrient

PT uptake, pancreatic secretion of hormones, digestive enzymes and

PT treating gastrointestinal and growth related diseases, comprises

PT zsig33-like peptides -

XX Claim 1a; Page 81; 89pp; English.

XX The invention relates to zsig33-like peptides (ZS33LP) including

CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and

CC zsig33-epsilon peptides and nucleic acid molecules encoding such

CC zsig33-like peptides. ZS33LP peptides activate the immune system

CC in boosting immunity to infectious diseases, treating immunocompromised

CC patients such as human immunodeficiency virus (HIV) patients, in

CC improving vaccines and in treatment of bacterial, viral, protozoal and

CC fungal infections. Peptides of the invention are used to identify and

CC isolate receptors involved in growth regulation in the liver, blood

CC vessel formation and other developmental processes. They are useful for

CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate

CC growth and/or differentiation of tumour cells, as additives to anti-

CC hypoglycaemic preparations containing glucose and as adsorption

CC enhancers for oral drugs which require fast nutrient action and to

CC stimulate glucose-induced insulin release. They are also useful as

CC research reagents for the expansion, differentiation, growth factor and

CC hormone secretion and/or cell-cell interactions of tissues associated

CC with gastrointestinal system, brain and central nervous system. These

CC molecules are useful for treating dysfunction associated with contractile

CC tissues or to suppress or enhance contractility in vivo and to treat

CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic

CC acids and/or antibodies are useful for treating disorders associated

CC with gastrointestinal contractility, secretion of digestive enzymes,

CC hormone and acids, secretion of hormones in the pancreas and/or brain,

CC gastrointestinal motility, recruitment of digestive enzymes, inflammation

CC and regulation of nutrient absorption. Sequences of the invention are

CC useful in gene therapy. The present sequence is human zsig33-linker

CC peptide.

XX SQ Sequence 24 AA;

Query Match 100.0%; Score 121; DB 23; Length 24;

Best Local Similarity 100.0%; Pred. No. 3.8e-11;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGGAEGAEDELEV 23

|||||

Db 1 ALAGWLRPDGGGAEGAEDELEV 23

RESULT 7

AAE33410

ID AAE33410 standard; Protein; 91 AA.
 AC AAE33410;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human exon 3-deleted ghrelin protein.
 XX
 KW Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
 KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
 KW cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200290387-A1.
 XX
 PD 14-NOV-2002.
 XX
 PF 10-MAY-2002; 2002WO-AU00582.
 XX
 PR 10-MAY-2001; 2001AU-0004919.
 PR 17-DEC-2001; 2001AU-0009567.
 XX
 PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 PI Choplin LK, Jeffery PL, Herington AC;
 XX
 DR WPI: 2003-111957/10.
 DR N-PSDB; AAD50726.
 XX
 PT Identifying a cancer cell or tissue for treating prostate, ovarian,
 PT breast cancer, or benign prostatic hyperplasia, by detecting the
 PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
 PT 1b proteins or nucleic acids -
 XX
 PS Claim 14; Page 34; 50pp; English.
 XX
 CC The invention relates to a method for identifying a cancer cell or
 CC tissue of the reproductive system by detecting expression of a ghrelin,
 CC an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic
 CC acids. The antibodies, exon 3-deleted form of preproghrelin and
 CC antagonists are useful for treating cancer of the reproductive system
 CC such as prostate, ovarian, breast, cervical or uterine cancer,
 CC choriocarcinoma or benign prostatic hyperplasia. The present sequence
 CC is human exon 3-deleted ghrelin protein.
 XX
 SQ Sequence 91 AA;
 Query Match 100.0%; Score 121; DB 24; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 8
 AAB60517
 ID AAB60517 standard; Protein; 116 AA.
 XX
 AC AAB60517;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
 XX
 KW Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX

PN WO200107475-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-JP04907.
 XX
 PR 23-JUL-1999; 99JP-0210002.
 PR 29-NOV-1999; 99JP-0338841.
 PR 26-APR-2000; 2000JP-0126623.
 XX
 PA (KANG/) KANGAWA K.
 XX
 PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 XX
 DR WPI: 2001-159704/16.
 DR N-PSDB; AAF59647.
 XX
 PT New peptide compounds which induce growth hormone secretion and
 PT elevate cell calcium concentrations, useful in treatment and diagnosis
 PT of infant growth disorders -
 XX
 PS Claim 3; Page 186-187; 210pp; Japanese.
 XX
 CC The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX
 SQ Sequence 116 AA;
 Query Match 100.0%; Score 121; DB 22; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 51 ALAGWLRPEDGGQAGAEDELEV 73
 RESULT 9
 AAW87991
 ID AAW87991 standard; Protein; 117 AA.
 XX
 AC AAW87991;
 XX
 DT 07-APR-1999 (first entry)
 XX
 DE Protein designated zsig33.
 XX
 KW Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
 KW nutrient absorption regulation; obesity; metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 PI Key Location/Qualifiers
 FT Peptide 1..23 /note= "signal peptide"
 FT Protein 24..117 /note= "mature protein"
 XX

PN W09842840-A1.
 XX 01-OCT-1998.
 XX 23-MAR-1998; 98WO-US05620.
 XX 24-MAR-1997; 97US-0822897.
 PR 24-MAR-1997; 97US-0041102.
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Delsher TA, Sheppard PO;
 XX WPI; 1999-070071/06.
 DR N-PSDB; AAX04550.
 XX
 PT Human polypeptide having homology to motilin, zsig33 - useful e.g.
 PT to treat gastrointestinal motility disorders, obesity etc. and to
 PT identify antagonists to treat gastrointestinal hypermotility
 XX
 PS Claim 13; Page 55-56; 69pp; English.
 XX
 CC The present sequence represents a protein designated Zsig33. The nucleic
 CC acids are strongly expressed in stomach tissue. The polypeptide (or
 CC allelic variants/orthologs) can be used to stimulate gastric motility,
 CC measured as increased transit time or gastric emptying of an ingested
 CC substance in mammals. The products are used to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes/acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
 CC absorption regulation. Zsig33 polypeptides may also be important
 CC neurologically, since the family of gut-brain peptides to which the
 CC homologous protein motilin belongs has been associated with neurological
 CC and CNS functions. They may therefore be used e.g. to regulate satiety
 CC or treat obesity and other metabolic disorders where neurological
 CC feedback modulates nutritional absorption. They are useful to identify
 CC zsig33 agonists, antagonists and ligands and to produce antibodies.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 121; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
 |||||
 Db 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 10
 AAY87236
 ID AAY87236 standard; Protein; 117 AA.
 XX
 AC AAY87236;
 XX
 DT 11-MAY-2000 (first entry)
 DE
 DE Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
 XX
 KW Human: signal peptide-containing protein; HSPP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
 KW antisthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 OS Homo sapiens.
 OS
 PN W0200000610-A2.
 XX

PD 06-JAN-2000.
 XX 25-JUN-1999; 99WO-US14484.
 XX 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX (INCYTE) INCYTE PHARM INC.
 XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX WPI; 2000-160673/14.
 DR N-PSDB; AAZ98121.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease -
 XX
 PS Claim 1; Page 168-169; 327pp; English.
 XX
 CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
 CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
 CC neuroprotective, cardiovascular and antisthmatic activities, and can
 CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPP. Antagonists of
 CC HSPP are used to treat or prevent disorders associated with increased
 CC activity or function of HSPP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC ischaemic heart disease, Crohn's disease, microbial or other infections, congestive or
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
 CC nucleic acids can be used for the recombinant production of HSPP, for
 CC detecting HSPP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPP
 CC from natural sources.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 121; DB 21; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
 |||||
 Db 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 11
 AAM38890
 ID AAM38890 standard; Protein; 117 AA.
 XX
 AC AAM38890;
 XX
 DT 22-OCT-2001 (first entry)
 DE
 DE Human polypeptide SEQ ID NO 2035.
 XX
 KW Human: nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

PN 26-JUL-2001.

PD 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-052317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI: 2001-442253/47.

DR N-PSDB; AAI58046.

XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX Example 3; SEQ ID NO 2035; 10078pp; English.
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 117 AA;

Query Match 100.0%; Score 121; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEV 23

DB 52 ALAGWLRPEDGGGAEGAEDELEV 74

RESULT 12

AAB62649

ID AAB62649 standard; Protein; 117 AA.

XX AAB62649;

XX 23-JUL-2001 (first entry)

XX Human zsig33 polypeptide.

XX

KW zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
 KW G-protein coupled receptor.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 24..37
 FT /note= "specifically claimed fragment that binds to
 FT the GHS-R"

XX WO200138355-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US32074.

XX 22-NOV-1999; 99US-0166765.

XX (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

XX WPI: 2001-355879/37.

XX N-PSDB; AAF83678.

XX Forming reversible peptide receptor complex for purifying cell and
 PT peptides, stimulating signal transduction and modulating hormone
 PT secretion, involves contacting a receptor with zsig33 polypeptide -

XX Claim 1; Page 93-94; 111pp; English.

XX The invention relates to a method of forming a reversible peptide-
 CC receptor complex that involves providing an immobilized receptor, and
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
 CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
 CC is useful for purifying cells, purifying a peptide, stimulating signal
 CC transduction in a cell expressing a receptor. It is also useful for
 CC modulating secretion of hormones, neural development and/or utilization,
 CC gastric contractility, nutrient uptake, secretion of digestive and
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
 CC hormone secretion in a mammal having a disease associated with abnormal
 CC levels of growth hormone, such as osteoporosis, bone repair, bone
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,
 CC protein catabolic responses after surgery, cachexia, protein loss,
 CC dwarfism, wound healing and ovulation induction, treating a mammal having
 CC a metabolic disorder requiring neurological feedback, such as satiety
 CC regulation, glucose absorption and metabolism and neuropathy-associated
 CC gastrointestinal disorders, and stimulating glucose-induced insulin
 CC release in a mammal. The present sequence represents the human zsig33
 CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.

XX Sequence 117 AA;

Query Match 100.0%; Score 121; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEV 23

DB 52 ALAGWLRPEDGGGAEGAEDELEV 74

RESULT 13

AAB20101

ID AAB20101 standard; Protein; 117 AA.

XX AAB20101;

XX

DT 23-APR-2001 (first entry)
 XX zsig33 protein.
 DE
 KW SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
 KW nutritional absorption modulator; growth hormone secretagogue;
 KW therapy; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Signal_peptide
 FT Protein 24..117
 FT /label= Mature_protein
 FT Peptide 24..34
 FT /label= SGIP_peptide
 FT /note= "this peptide is claimed in Claim 1"
 XX
 XX WO200100830-A1.
 XX
 XX 04-JAN-2001.
 XX
 XX 30-JUN-2000; 2000WO-US18306.
 XX
 XX 30-JUN-1999; 99US-0345157.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 XX
 XX WPI; 2001-123010/13.
 XX
 XX N-PSDB; AAF30033.
 XX
 XX Novel variants of SGIP peptides for modulating contractility in
 XX duodenum or jejunum tissue, pancreatic secretion of hormones and
 XX digestive enzymes, inducing growth hormone secretion or modulating
 XX gastric emptying -
 XX
 XX Disclosure; 54; 61pp; English.
 XX
 XX The present sequence is that of zsig33, a secreted protein with
 XX homology to motilin (see AAB20102). zsig33 is expressed at high
 XX levels in the stomach, and at lower levels in the small intestine
 XX and pancreas. A novel peptide fragment of zsig33, termed SGIP (see
 XX AAB20100), is claimed. SGIP is a ligand for growth hormone
 XX secretagogue receptor, and is therefore useful for modulating
 XX secretion of growth hormone and insulin like growth factor 1.
 XX SGIP, and variant SGIP peptides, are used in claimed methods for
 XX stimulating contractility in duodenum or jejunum tissue,
 XX modulating pancreatic secretion of hormones and digestive enzymes,
 XX inducing growth hormone secretion, and modulating gastric emptying.
 XX
 XX Sequence 117 AA;
 XX
 XX Query Match 100.0%; Score 121; DB 22; Length 117;
 XX Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 ALAGWLRPEDGGGAEGAEDEV 23
 XX |
 XX 52 ALAGWLRPEDGGGAEGAEDEV 74
 XX
 XX RESULT 14
 XX AAB60511
 XX ID AAB60511 standard; Protein; 117 AA.
 XX
 XX AC AAB60511;
 XX
 XX 24-APR-2001 (first entry)
 XX
 XX Human ghrelin preproprotein, SEQ ID NO:5.

XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX
 XX WO200107475-A1.
 XX
 XX 01-FEB-2001.
 XX
 XX 24-JUL-2000; 2000WO-JP04907.
 XX
 XX 23-JUL-1999; 99JP-0210002.
 XX
 XX 29-NOV-1999; 99JP-0338841.
 XX
 XX 26-APR-2000; 2000JP-0126623.
 XX
 XX (KANG/) KANGAWA K.
 XX
 XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 XX
 XX WPI; 2001-159704/16.
 XX
 XX N-PSDB; AAF59645.
 XX
 XX New peptide compounds which induce growth hormone secretion and
 XX elevate cell calcium concentrations, useful in treatment and diagnosis
 XX of infant growth disorders -
 XX
 XX Claim 3; Page 182; 210pp; Japanese.
 XX
 XX The invention relates to a novel peptide compound or its salt which
 XX induces the secretion of growth hormone and/or elevates calcium ion
 XX concentration in cells. The peptides are ghrelin homologues and are
 XX characterised in that at least one amino acid has been substituted by
 XX a modified amino acid and/or a non-amino acid compound. The invention
 XX also encompasses the unmodified peptides; the DNA encoding the peptides;
 XX vectors and host cells comprising such DNA; a method of producing the
 XX peptides comprising recombinant production, optionally followed by
 XX chemical modification; an antibody specific for a peptide of the
 XX invention; and an assay and kit for detecting the peptides. The peptides
 XX of the invention are useful for treating the peptides. The peptides
 XX caused by a deficiency in growth hormone expression or activity. In
 XX particular, they are useful for promoting infant growth due to growth
 XX hormone deficiency. The compounds of the invention are safe with
 XX no accompanying side effects. The present sequence represents a
 XX ghrelin-type growth hormone secretagogue (GHS) precursor protein
 XX of the invention.
 XX
 XX Sequence 117 AA;
 XX
 XX Query Match 100.0%; Score 121; DB 22; Length 117;
 XX Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 ALAGWLRPEDGGGAEGAEDEV 23
 XX |
 XX 52 ALAGWLRPEDGGGAEGAEDEV 74
 XX
 XX RESULT 15
 XX ABB78319
 XX ID ABB78319 standard; Protein; 117 AA.
 XX
 XX AC ABB78319;
 XX
 XX 05-DEC-2002 (first entry)
 XX
 XX Amino acid sequence of a human zsig33.
 XX
 XX Short gastrointestinal peptide; SGIP; zsig33; motilin.
 XX
 XX Homo sapiens.
 XX

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 6.14973 Seconds
(without alignments)
158.243 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 121

Sequence: 1 ALAGWLRPEDGGQAEGBDELEV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

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- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 121 | 100.0 | 117 | 3 | US-09-046-479-2 |
| 2 | 121 | 100.0 | 117 | 4 | US-08-822-897C-2 |
| 3 | 121 | 100.0 | 117 | 4 | US-09-608-810A-4 |
| 4 | 121 | 100.0 | 117 | 4 | US-09-996-243-268 |
| 5 | 52 | 43.0 | 233 | 4 | US-09-252-991A-27758 |
| 6 | 50 | 41.3 | 634 | 1 | US-08-339-152A-17 |
| 7 | 50 | 41.3 | 653 | 1 | US-08-339-152A-16 |
| 8 | 50 | 41.3 | 653 | 2 | US-08-007-999B-3 |
| 9 | 50 | 41.3 | 653 | 2 | US-08-689-276A-3 |
| 10 | 49 | 40.5 | 139 | 2 | US-08-039-198B-10 |
| 11 | 48 | 39.7 | 518 | 4 | US-09-252-991A-23604 |
| 12 | 47 | 38.8 | 283 | 4 | US-09-252-991A-29700 |
| 13 | 46 | 38.0 | 341 | 4 | US-09-252-991A-27327 |
| 14 | 46 | 38.0 | 428 | 4 | US-09-252-991A-19723 |
| 15 | 46 | 38.0 | 517 | 4 | US-09-252-991A-25921 |
| 16 | 46 | 38.0 | 1044 | 4 | US-09-252-991A-18853 |
| 17 | 45.5 | 37.6 | 579 | 3 | US-08-704-711A-1 |
| 18 | 45.5 | 37.6 | 579 | 4 | US-09-521-220-1 |
| 19 | 45.5 | 37.6 | 582 | 3 | US-08-704-711A-2 |
| 20 | 45.5 | 37.6 | 582 | 3 | US-08-448-489-1 |
| 21 | 45.5 | 37.6 | 582 | 3 | US-09-211-704A-9 |
| 22 | 45.5 | 37.6 | 582 | 4 | US-09-521-220-2 |
| 23 | 45.5 | 37.6 | 582 | 4 | US-09-391-104-28 |
| 24 | 45.5 | 37.6 | 591 | 2 | US-08-889-402-1 |
| 25 | 45 | 37.2 | 174 | 4 | US-09-252-991A-18600 |
| 26 | 45 | 37.2 | 494 | 1 | US-08-464-340A-4 |
| 27 | 45 | 37.2 | 494 | 5 | PCT-US94-08449A-4 |

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| 28 | 45 | 37.2 | 1059 | 4 | US-09-394-272-5 | Sequence 5, Appli |
| 29 | 44 | 36.4 | 405 | 4 | US-09-252-991A-20326 | Sequence 20326, A |
| 30 | 43 | 35.5 | 118 | 3 | US-08-482-304-12 | Sequence 12, Appl |
| 31 | 43 | 35.5 | 118 | 3 | US-08-483-474-12 | Sequence 12, Appl |
| 32 | 43 | 35.5 | 140 | 3 | US-08-482-304-9 | Sequence 9, Appli |
| 33 | 43 | 35.5 | 140 | 3 | US-08-483-474-9 | Sequence 9, Appli |
| 34 | 43 | 35.5 | 162 | 4 | US-09-252-991A-24838 | Sequence 24838, A |
| 35 | 43 | 35.5 | 191 | 4 | US-09-252-991A-21437 | Sequence 21437, A |
| 36 | 43 | 35.5 | 212 | 3 | US-09-154-083-4 | Sequence 4, Appli |
| 37 | 43 | 35.5 | 247 | 4 | US-09-252-991A-27419 | Sequence 27419, A |
| 38 | 43 | 35.5 | 268 | 4 | US-09-252-991A-27950 | Sequence 27950, A |
| 39 | 43 | 35.5 | 311 | 4 | US-09-252-991A-28068 | Sequence 28068, A |
| 40 | 43 | 35.5 | 380 | 3 | US-08-765-743-2 | Sequence 2, Appli |
| 41 | 43 | 35.5 | 380 | 4 | US-09-341-446B-2 | Sequence 2, Appli |
| 42 | 43 | 35.5 | 424 | 4 | US-09-341-446B-6 | Sequence 6, Appli |
| 43 | 43 | 35.5 | 424 | 4 | US-09-341-446B-8 | Sequence 8, Appli |
| 44 | 43 | 35.5 | 427 | 4 | US-09-341-446B-4 | Sequence 4, Appli |
| 45 | 43 | 35.5 | 450 | 4 | US-09-252-991A-25523 | Sequence 25523, A |

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046.479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 100.0%; Score 121; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGADELEV 23
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Db 52 ALAGWLRPEDGGGAEGADELEV 74

RESULT 2

US-08-822-897C-2
; Sequence 2, Application US/08822897C
; Patent No. 6380158
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,897C
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-822-897C-2

Query Match 100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGADELEV 23
|||||
Db 52 ALAGWLRPEDGGGAEGADELEV 74

RESULT 3

US-09-608-810A-4
; Sequence 4, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608,810A
; CURRENT FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
; US-09-608-810A-4

Query Match 100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGADELEV 23
|||||
Db 52 ALAGWLRPEDGGGAEGADELEV 74

RESULT 4

US-09-996-243-268
; Sequence 268, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600

[illegible]

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEV 23
|||||
Db 52 ALAGWLRPEDGGGAEGAEDELEV 74

RESULT 5

US-09-252-991A-27758
; Sequence 27758, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27758
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27758

Query Match 43.0%; Score 52; DB 4; Length 233;
Best Local Similarity 72.7%; Pred. No. 2.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GWLRLPDGGQA 14
|||||
Db 203 GWLRLPDGSGRA 213

RESULT 6

US-08-339-152A-17
; Sequence 17, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzil, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-339-152A-17

Query Match 41.3%; Score 50; DB 1; Length 634;
Best Local Similarity 76.9%; Pred. No. 16;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGOAEGAEDELEV 23
|||||
Db 213 GGRAEGEEDLEV 225

RESULT 7

US-08-339-152A-16
; Sequence 16, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzil, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-152A-16

Query Match 41.3%; Score 50; DB 1; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGOAEGAEDELEV 23
|||||
Db 233 GGRAEGEEDLEV 245

RESULT 8
US-08-007-999B-3
; Sequence 3, Application US/08007999B
; Patent No. 5851787
; GENERAL INFORMATION:
; APPLICANT: Wasco, Wilma
; APPLICANT: Bupp, Keith
; APPLICANT: Magendantz, Margaret
; APPLICANT: Tanzi, Rudolph
; APPLICANT: Solomon, Frank
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/007,999B
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,642
; FILING DATE: 20-APR-1992
; PRIOR APPLICATION NUMBER: US 07/930,022
; FILING DATE: 17-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: 0609.3520002/JAG/GKT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2571
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-007-999B-3
Query Match 41.3%; Score 50; DB 2; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 11 GGOAGAEDELEV 23
||:|||||
Db 233 GGRAEGGEDEEV 245
RESULT 9
US-08-689-276A-3
; Sequence 3, Application US/08689276A
; Patent No. 5891991
; GENERAL INFORMATION:
; APPLICANT: Wasco, Wilma
; APPLICANT: Bupp, Keith
; APPLICANT: Magendantz, Margaret
; APPLICANT: Tanzi, Rudolph
; APPLICANT: Solomon, Frank
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/689,276A
; FILING DATE: 06-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/007,999
; FILING DATE: 21-JAN-1993
; APPLICATION NUMBER: US 07/872,642
; FILING DATE: 20-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,022
; FILING DATE: 17-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.3520003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2571
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-689-276A-3
Query Match 41.3%; Score 50; DB 2; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 11 GGOAGAEDELEV 23
||:|||||
Db 233 GGRAEGGEDEEV 245
RESULT 10
US-08-039-198B-10
; Sequence 10, Application US/08039198B
; Patent No. 5858725
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PREPARATION OF CHIMAERIC ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/039,198B
; FILING DATE: 29-JUL-1993
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01744
; FILING DATE: 08-OCT-91
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-86
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-039-1988-10

Query Match      40.5%; Score 49; DB 2; Length 139;
Best Local Similarity 61.5%; Pred. No. 4.4;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGQAG 16
Db 68 GWIDPEDGGTKY 80

RESULT 11
US-09-252-991A-23604
; Sequence 23604, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23604
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23604

Query Match      39.7%; Score 48; DB 4; Length 518;
Best Local Similarity 47.4%; Pred. No. 26;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 3 AGWLRPEDGGQAGAEDEL 21
Db 412 AGWAQPEPGCGGGAERL 430

RESULT 12
US-09-252-991A-29700
; Sequence 29700, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
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; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29700
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29700

Query Match      38.8%; Score 47; DB 4; Length 283;
Best Local Similarity 58.8%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 AGWLRPEDGGQAGAE 19
Db 86 AAGLRQEDGADGTGAED 102

RESULT 13
US-09-252-991A-27327
; Sequence 27327, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27327
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27327

Query Match      38.0%; Score 46; DB 4; Length 341;
Best Local Similarity 52.4%; Pred. No. 33;
Matches 11; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

Qy 7 RPEDGGQAGAE-----DELEV 23
Db 181 QPEGGGQGEHAQADRPDPLEV 201

RESULT 14
US-09-252-991A-19723
; Sequence 19723, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19723
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19723

Query Match      38.0%; Score 46; DB 4; Length 428;
Best Local Similarity 55.0%; Pred. No. 42;
Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
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QY 2 LAGWLRPEDGGQGAEGADEL 21
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Db 293 LALWSLPEDPRPADWADEL 312

RESULT 15

US-09-252-991A-25921
; Sequence 25921, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25921
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25921

Query Match 38.0%; Score 46; DB 4; Length 517;
Best Local Similarity 47.6%; Pred. No. 52;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQGAEGADELE 22
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Db 338 LAGLDPHPGIQAQCPHOQLQ 358

Search completed: September 11, 2003, 17:27:18
Job time : 7.14973 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:26:32 ; Search time 14.0214 Seconds
(without alignments)
239.348 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 121

Sequence: 1 ALAGWLRPEDGGQAGAEDELEV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications_AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------------|-------------------|
| 1 | 121 | 100.0 | 23 | US-09-853-253-5 | Sequence 5, Appli |
| 2 | 121 | 100.0 | 23 | US-09-853-253-6 | Sequence 6, Appli |
| 3 | 121 | 100.0 | 24 | US-09-853-253-4 | Sequence 4, Appli |
| 4 | 121 | 100.0 | 117 | US-09-794-987-2 | Sequence 2, Appli |
| 5 | 121 | 100.0 | 117 | US-09-853-253-2 | Sequence 2, Appli |
| 6 | 121 | 100.0 | 117 | US-09-989-722-268 | Sequence 268, App |
| 7 | 121 | 100.0 | 117 | US-09-989-723-268 | Sequence 268, App |
| 8 | 121 | 100.0 | 117 | US-09-989-279-268 | Sequence 268, App |
| 9 | 121 | 100.0 | 117 | US-09-989-727-268 | Sequence 268, App |
| 10 | 121 | 100.0 | 117 | US-09-989-731-268 | Sequence 268, App |
| 11 | 121 | 100.0 | 117 | US-09-989-732-268 | Sequence 268, App |
| 12 | 121 | 100.0 | 117 | US-09-991-073-268 | Sequence 268, App |
| 13 | 121 | 100.0 | 117 | US-09-990-442-268 | Sequence 268, App |
| 14 | 121 | 100.0 | 117 | US-09-991-163-268 | Sequence 268, App |
| 15 | 121 | 100.0 | 117 | US-09-993-604-268 | Sequence 268, App |

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|----|-----|-------|-----|----|--------------------|-------------------|
| 16 | 121 | 100.0 | 117 | 10 | US-09-990-456-268 | Sequence 268, App |
| 17 | 121 | 100.0 | 117 | 10 | US-09-989-721-268 | Sequence 268, App |
| 18 | 121 | 100.0 | 117 | 10 | US-09-992-598-268 | Sequence 268, App |
| 19 | 121 | 100.0 | 117 | 10 | US-09-989-293A-268 | Sequence 268, App |
| 20 | 121 | 100.0 | 117 | 10 | US-09-989-735-268 | Sequence 268, App |
| 21 | 121 | 100.0 | 117 | 10 | US-09-990-444-268 | Sequence 268, App |
| 22 | 121 | 100.0 | 117 | 10 | US-09-991-181-268 | Sequence 268, App |
| 23 | 121 | 100.0 | 117 | 10 | US-09-989-730-268 | Sequence 268, App |
| 24 | 121 | 100.0 | 117 | 10 | US-09-990-436-268 | Sequence 268, App |
| 25 | 121 | 100.0 | 117 | 10 | US-09-993-687-268 | Sequence 268, App |
| 26 | 121 | 100.0 | 117 | 11 | US-09-989-734-268 | Sequence 268, App |
| 27 | 121 | 100.0 | 117 | 11 | US-09-997-653-268 | Sequence 268, App |
| 28 | 121 | 100.0 | 117 | 11 | US-09-993-667-268 | Sequence 268, App |
| 29 | 121 | 100.0 | 117 | 11 | US-09-997-428-268 | Sequence 268, App |
| 30 | 121 | 100.0 | 117 | 11 | US-09-997-666-268 | Sequence 268, App |
| 31 | 121 | 100.0 | 117 | 11 | US-09-990-438-268 | Sequence 268, App |
| 32 | 121 | 100.0 | 117 | 11 | US-09-990-562-268 | Sequence 268, App |
| 33 | 121 | 100.0 | 117 | 11 | US-09-990-711-268 | Sequence 268, App |
| 34 | 121 | 100.0 | 117 | 11 | US-09-989-726-268 | Sequence 268, App |
| 35 | 121 | 100.0 | 117 | 11 | US-09-998-156-268 | Sequence 268, App |
| 36 | 121 | 100.0 | 117 | 11 | US-09-990-437-268 | Sequence 268, App |
| 37 | 121 | 100.0 | 117 | 11 | US-09-991-157-268 | Sequence 268, App |
| 38 | 121 | 100.0 | 117 | 11 | US-09-997-514-268 | Sequence 268, App |
| 39 | 121 | 100.0 | 117 | 11 | US-09-997-573-268 | Sequence 268, App |
| 40 | 121 | 100.0 | 117 | 11 | US-09-991-172-268 | Sequence 268, App |
| 41 | 121 | 100.0 | 117 | 11 | US-09-990-726-268 | Sequence 268, App |
| 42 | 121 | 100.0 | 117 | 11 | US-09-997-559-268 | Sequence 268, App |
| 43 | 121 | 100.0 | 117 | 11 | US-09-997-601-268 | Sequence 268, App |
| 44 | 121 | 100.0 | 117 | 11 | US-09-990-443-268 | Sequence 268, App |
| 45 | 121 | 100.0 | 117 | 11 | US-09-991-854-268 | Sequence 268, App |

ALIGNMENTS

RESULT 1
US-09-853-253-5
; Sequence 5, Application US/09853253
; Patent No. US2002005156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-5

Query Match 100.0%; Score 121; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
Db 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 2
US-09-853-253-6
; Sequence 6, Application US/09853253
; Patent No. US2002005156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN

ADDRESS: ZymoGen
STREET: 1201 East

QY 1 ALAGWLRPEDGGQAEGAEDELEV

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/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/794,987
/ FILING DATE: 27-Feb-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/046,479
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sawislak, Deborah A
/ REGISTRATION NUMBER: 37,438
/ REFERENCE/DOCKET NUMBER: 97-04
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6672
/ TELEFAX: 206-442-6678
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 117 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
/
US-09-794-987-2

Query Match          100.0%;   Score 121;   DB 9;   Length 117;
Best Local Similarity 100.0%;   Pred. No. 4.2e-09;
Matches 23;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY 1 ALAGWLRPDGGQGAEGADELEV 23
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DB 52 ALAGWLRPDGGQGAEGADELEV 74

RESULT 5
US-09-853-253-2
/ Sequence 2, Application US/09853253
/ Patent No. US20020055156A1
/ GENERAL INFORMATION:
/ APPLICANT: JASPERS, STEPHEN
/ APPLICANT: SHEPPARD, PAUL
/ APPLICANT: DEISHER, THERESA
/ APPLICANT: BISHOP, PAUL
/ TITLE OF INVENTION: zsig33-like Peptides
/ FILE REFERENCE: 00-30
/ CURRENT APPLICATION NUMBER: US/09/853,253
/ CURRENT FILING DATE: 2001-05-10
/ PRIOR APPLICATION NUMBER: 60/203,300
/ PRIOR FILING DATE: 2000-05-11
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 117
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-853-253-2

Query Match          100.0%;   Score 121;   DB 9;   Length 117;
Best Local Similarity 100.0%;   Pred. No. 4.2e-09;
Matches 23;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Db 52 ALAGWLRPEDGGQAEGBDELIV 74

RESULT 6

US-09-989-722-268

; Sequence 268, Application US/09989722

; Patent No. US20020072067A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730PIC63

; CURRENT APPLICATION NUMBER: US/09/989,722

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/087106

; PRIOR FILING DATE: 1998-05-28

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087609

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087759

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087827

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: 60/088021

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088025

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088026

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088028

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088029

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088030

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088033

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088326

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088167

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/088202

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/088212

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/088217

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/088655

; PRIOR FILING DATE: 1998-06-09

; PRIOR APPLICATION NUMBER: 60/088734

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: 60/088738

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; PRIOR APPLICATION NUMBER: 60/088742

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; PRIOR FILING DATE: 1998-06-11

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; PRIOR APPLICATION NUMBER: 60/089440

; PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: 60/089512

; PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: 60/089514

; PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: 60/089532

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089538

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089598

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089599

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089600

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089653

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089801

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: 60/089907

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: 60/089908

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: 60/089947

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: 60/089948

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: 60/089952

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: 60/090246

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: 60/090252

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: 60/090254

; PRIOR FILING DATE: 1998-06-22
 ; PRIOR APPLICATION NUMBER: 60/090349
 ; PRIOR FILING DATE: 1998-06-23
 ; PRIOR APPLICATION NUMBER: 60/090355
 ; PRIOR FILING DATE: 1998-06-23
 ; PRIOR APPLICATION NUMBER: 60/090429
 ; PRIOR FILING DATE: 1998-06-24
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 ; PRIOR APPLICATION NUMBER: 60/090535
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.2e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEV 23
 Db 52 ALAGWLRPEDGGGAEGAEDELEV 74

RESULT 7
 US-09-989-723-268
 ; Sequence 268, Application US/09989723
 ; Patent No. US20020072092A1

; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C62
 ; CURRENT APPLICATION NUMBER: US/09/989,723
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.2e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 8
 US-09-989-279-268
 ; Sequence 268, Application US/09989279
 ; Patent No. US20020072496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerbitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Napier, Mary A.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEV 23
Db 52 ALAGWLRPEDGGGAEGAEDELEV 74

RESULT 9

US-09-989-727-268
; Sequence 268, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 23; Conservative 0;

Oy 1 ALAGWLRPEDGGQAGAEDELEV 23
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RESULT 10

US-09-989-731-268
; Sequence 268, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAEAGDELEY 23
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 Db 52 ALAGWLRPEDGGQAEAGDELEY 74

RESULT 11

; Sequence 268, Application US/09989732
 ; Patent No. US20020123463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730P1C57

; CURRENT APPLICATION NUMBER: US/09/989,732
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
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| ; | PRIOR FILING DATE: | 1998-06-26 |
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| ; | PRIOR FILING DATE: | 1998-07-01 |
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| ; | PRIOR APPLICATION NUMBER: | 60/091978 |
| ; | PRIOR FILING DATE: | 1998-07-07 |
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| ; | PRIOR FILING DATE: | 1998-07-07 |
| ; | PRIOR APPLICATION NUMBER: | 60/092182 |
| ; | PRIOR FILING DATE: | 1998-07-09 |
| Query Match | | |
| Best Local Similarity | | 100.0%; Score |
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| | | |
| Db | 52 | ALAGWLPRPDGGQAGABDELEV 74 |
| | | |
| RESULT 12 | | |
| US-09-991-073-268 | | |
| Sequence 268, Application US/09991073 | | |
| Patent No. US20030127576A1 | | |
| GENERAL INFORMATION: | | |
| ; | APPLICANT: | Ashkenazi, Avi J. |
| ; | APPLICANT: | Baker, Kevin P. |
| ; | APPLICANT: | Botstein, David |
| ; | APPLICANT: | Desnoyers, Luc |
| ; | APPLICANT: | Eaton, Dan L. |
| ; | APPLICANT: | Ferrara, Napoleone |
| ; | APPLICANT: | Fong, Sherman |
| ; | APPLICANT: | Gerber, Hanspeter |
| ; | APPLICANT: | Gerritsen, Mary E. |
| ; | APPLICANT: | Goddard, Audrey |
| ; | APPLICANT: | Godowski, Paul J. |
| ; | APPLICANT: | Grimaldi, J. Christopher |
| ; | APPLICANT: | Gurney, Austin L. |
| ; | APPLICANT: | Kijavini, Ivar J. |
| ; | APPLICANT: | Napier, Mary A. |
| ; | APPLICANT: | Pan, James |
| ; | APPLICANT: | Pao, Nicholas F. |
| ; | APPLICANT: | Roy, Margaret Ann |
| ; | APPLICANT: | Stewart, Timothy A. |
| ; | APPLICANT: | Tumas, Daniel |
| ; | APPLICANT: | Watanabe, Colin K. |
| ; | APPLICANT: | Williams, P. Mickey |
| ; | APPLICANT: | Wood, William I. |
| ; | APPLICANT: | Zhang, Zemin |
| TITLE OF INVENTION: Secreted and Transferred | | |
| FILE REFERENCE: P2730P1C15 | | |
| CURRENT FILING DATE: 2001-11-14 | | |
| PRIOR APPLICATION NUMBER: 60/049787 | | |
| PRIOR FILING DATE: 1997-06-16 | | |
| PRIOR APPLICATION NUMBER: 60/062250 | | |
| PRIOR FILING DATE: 1997-10-17 | | |
| PRIOR APPLICATION NUMBER: 60/065186 | | |

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| 21 | PRIOR APPLICATION NUMBER: 60/089947 |
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAGAEDELEV 23
Db 52 ALAGWLRPDGGQAGAEDELEV 74

RESULT 13
US-09-990-442-268
; Sequence 268, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25

;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
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;; PRIOR APPLICATION NUMBER: 60/089105
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;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089532
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;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598

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; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score
Best Local Similarity 100.0%; Pred.
Matches 23; Conservative

QY 1 ALAGWLRPDGGQAGAEDELEV 23
|||||
Db 52 ALAGWLRPDGGQAGAEDELEV 74
|||||

RESULT 14
US-09-991-163-268
; Sequence 268, Application US/09991163
; Patent No. US2002013253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerttsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napter, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Trans
; TITLE OF INVENTION: Acids Encoding t
; FILE REFERENCE: P27301C17
; CURRENT APPLICATION NUMBER: US/09/991
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106

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RESULT 14
US-09-991-163-268

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: Sequence 268, Application US/09991163
: Patent No. US20020132253A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grumskil, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmitted
: FILE REFERENCE: P2730PIC17
: CURRENT APPLICATION NUMBER: US/09/991
: CURRENT FILING DATE: 2001-11-14
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
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: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
: PRIOR APPLICATION NUMBER: 60/084600
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic


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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. NO. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ALAGWLRPDGGQGAEGAEDELEV 23
        |||||
Db      52 ALAGWLRPDGGQGAEGAEDELEV 74

RESULT 15
US-09-993-604-268
; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Peoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
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; PRIOR FILING DATE: 1998-06-18
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5 PRIOR FILING DATE: 1998-06-19
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12 PRIOR APPLICATION NUMBER: 60/090349
13 PRIOR FILING DATE: 1998-06-23
14 PRIOR APPLICATION NUMBER: 60/090355
15 PRIOR FILING DATE: 1998-06-23
16 PRIOR APPLICATION NUMBER: 60/090429
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22 PRIOR APPLICATION NUMBER: 60/090444
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62 PRIOR APPLICATION NUMBER: 60/091633
63 PRIOR FILING DATE: 1998-07-02
64 PRIOR APPLICATION NUMBER: 60/091978
65 PRIOR FILING DATE: 1998-07-07
66 PRIOR APPLICATION NUMBER: 60/091982
67 PRIOR FILING DATE: 1998-07-07
68 PRIOR APPLICATION NUMBER: 60/092182
69 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAEDELEV 23
|||||
Db 52 ALAGWLRPEDGGQAEDELEV 74

Search completed: September 11, 2003, 17:48:33
Job time : 15.0214 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 : Search time 3.32086 Seconds
(without alignments)
325.703 Million cell updates/sec

Title: US-09-853-253-6
Perfect score: 121
Sequence: 1 ALAGWLRPEDGGQAEDELEV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|-------|--------|------------|----|--------------------|
| 1 | 121 | 100.0 | 117 | 1 | GHRL_HUMAN | | Q9ubu3 homo sapien |
| 2 | 90 | 74.4 | 117 | 1 | GHRL_RAT | | Q9dyh7 rattus norv |
| 3 | 87 | 71.9 | 118 | 1 | GHRL_PIG | | Q9gky5 sus scrofa |
| 4 | 86 | 71.1 | 117 | 1 | GHRL_MOUSE | | Q9eqx0 mus musculu |
| 5 | 72 | 59.5 | 116 | 1 | GHRL_BOVIN | | Q9bdj6 bos taurus |
| 6 | 68 | 56.2 | 117 | 1 | GHRL_CANFA | | Q9bef8 canis faml |
| 7 | 54 | 44.6 | 200 | 1 | NUPL_XENLA | | P05221 xenopus lae |
| 8 | 51 | 42.1 | 91 | 1 | ACYP_BACSU | | Q35031 bacillus su |
| 9 | 50 | 41.3 | 653 | 1 | APPL_MOUSE | | Q03157 mus musculu |
| 10 | 48 | 39.7 | 300 | 1 | NKX1_BISBI | | O46383 bison bison |
| 11 | 48 | 39.7 | 668 | 1 | SYM_METKA | | O8tx28 methanopyru |
| 12 | 48 | 38.7 | 1216 | 1 | NKX1_BOVIN | | Q28i39 bos taurus |
| 13 | 47 | 38.8 | 380 | 1 | OPRK_CAVPO | | P41144 cavia porce |
| 14 | 47 | 38.8 | 1168 | 1 | DXH8_ARATH | | Q38953 arabidopsis |
| 15 | 45.5 | 37.6 | 580 | 1 | MM14_PIG | | Q9xt90 sus scrofa |
| 16 | 45.5 | 37.6 | 582 | 1 | MM14_HUMAN | | P50281 homo sapien |
| 17 | 45.5 | 37.6 | 582 | 1 | MM14_MOUSE | | P53690 mus musculu |
| 18 | 45.5 | 37.6 | 582 | 1 | MM14_RAT | | Q10739 rattus norv |
| 19 | 45.5 | 37.6 | 591 | 1 | PAXI_HUMAN | | P49023 homo sapien |
| 20 | 45 | 37.2 | 190 | 1 | RS9A_SCHPO | | Q09757 schizosacch |
| 21 | 45 | 37.2 | 242 | 1 | HAP5_YEAST | | Q02516 saccharomyc |
| 22 | 45 | 37.2 | 494 | 1 | KCF1_HUMAN | | Q9h3m0 homo sapien |
| 23 | 45 | 37.2 | 544 | 1 | PRG_DEIRA | | Q9ru23 deinococcus |
| 24 | 45 | 37.2 | 992 | 1 | SNXJ_HUMAN | | Q92543 homo sapien |
| 25 | 45 | 37.2 | 1059 | 1 | SPS_VICFA | | Q43876 vicia faba |
| 26 | 44.5 | 36.8 | 777 | 1 | RGL2_HUMAN | | O15211 homo sapien |
| 27 | 44.5 | 36.8 | 1233 | 1 | VLI2_REOVD | | P15024 reovirus (t |
| 28 | 44 | 36.4 | 115 | 1 | INS_VERMO | | Q9w7r2 verasper mo |
| 29 | 44 | 36.4 | 168 | 1 | TCTP_BRAOL | | Q944w6 brassica ol |
| 30 | 44 | 36.4 | 273 | 1 | NK22_MOUSE | | P42586 mus musculu |
| 31 | 44 | 36.4 | 449 | 1 | CMGA_BOVIN | | P05059 bos taurus |
| 32 | 44 | 36.4 | 4447 | 1 | PKSK_BACSU | | P40803 bacillus su |
| 33 | 43.5 | 36.0 | 525 | 1 | SYK_DEIRA | | Q9rxel deinococcus |

ALIGNMENTS

RESULT 1

| ID | GHRL_HUMAN | STANDARD; | PRT; | 117 AA. |
|----|---|-----------|------|---------|
| AC | Q9UBU3; Q8TAT9; Q9H3R3; | | | |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) | | | |
| DT | 28-FEB-2003 (Rel. 41, Last annotation update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein). | | | |
| DE | releasing peptide) (Motilin-related peptide) (M46 protein). | | | |
| GN | GHRL OR MTLRP. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26. | | | |
| RX | MEDLINE=20067959; PubMed=10604470; | | | |
| RA | Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.; | | | |
| RT | "Ghrelin is a growth-hormone-releasing acylated peptide from stomach." | | | |
| RL | Nature 402:656-660(1999). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). | | | |
| RA | Kojima M.; | | | |
| RL | Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). | | | |
| RC | TISSUE=Stomach; | | | |
| RA | Tomasetto C., Karam S.M., Rio M.-C.; | | | |
| RT | "Identification of a novel gastric protein m46."; | | | |
| RL | Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [4] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). | | | |
| RA | Wajhrach M.P., Ten I.S., Gertner J.M., Leibel R.L.; | | | |
| RT | "Genomic organization of the human Ghrelin gene."; | | | |
| RL | J. Endocrinol. Genet. 1:231-233(2000). | | | |
| RN | [5] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). | | | |
| RC | TISSUE=Blood; | | | |
| RX | MEDLINE=2238857; PubMed=12477932; | | | |
| RA | Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G., | | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., | | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., | | | |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., | | | |
| RA | Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., | | | |
| RA | Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., | | | |
| RA | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., | | | |
| RA | Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | | | |
| RA | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., | | | |
| RA | Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A., | | | |
| RA | Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., | | | |
| RA | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., | | | |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., | | | |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., | | | |
| RA | Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., | | | |

Q95220 oryctolagus
Q9d5v6 mus musculu
P41145 homo sapien
Q8pn25 xanthomonas
P16230 oryctolagus
P96142 thermus the
P29376 homo sapien
P54423 bacillus su
P38631 saccharomyc
P01341 lophius pis
P05019 homo sapien
P27484 nicotiana s

34 43.5 36.0 582 1 MM14_RABIT
35 43 35.5 365 1 SYAP_MOUSE
36 43 35.5 380 1 OPRK_HUMAN
37 43 35.5 579 1 SYQ_XANAC
38 43 35.5 852 1 SRCH_RABIT
39 43 35.5 862 1 SYV_THETH
40 43 35.5 864 1 KLTK_HUMAN
41 43 35.5 894 1 WPRB_BACSU
42 43 35.5 1876 1 GLS1_YEAST
43 42.5 35.1 116 1 INS_LOPPI
44 42.5 35.1 195 1 IGFB_HUMAN
45 42.5 35.1 214 1 GRP2_NICSY

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [7]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 receptor type 1 (GHSR) inducing the release of growth hormone from
 the pituitary. Has an appetite-stimulating effect, induces
 adiposity and stimulates gastric acid secretion. Involved in
 growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -1- PTM: O-n-octanoylation is essential for activity.
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 WWW="http://www.infobiogen.fr/services/chronocancer/Genes/GhrelinID327.html".
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB029434; BAA89371.1; -
 DR EMBL; AB035700; BAB19045.1; -
 DR EMBL; AJ252278; CAB65733.1; -
 DR EMBL; AF296558; AAG10300.1; -
 DR EMBL; BC025791; AAH25791.1; -
 DR PIR; A59316; A59316.
 DR MIM; 605353; -
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005131; F:growth hormone receptor ligand activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaling. . .; TAS.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc; 1.
 DR Pfam; PF04644; motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR PRODOM; PD332162; Preproghrelin; 1.
 KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 FT Alternative splicing.
 FT SIGNAL 1 23
 FT PEPTIDE 24 51 GHRELIN.
 FT PROPEP 52 117 REMOVED IN MATURE FORM.
 FT LIPID 26 26 N-OCTANOATE.
 FT VARSPLIC 37 37 Missing (in isoform 2).
 FT /FTId=VSP_003245.
 FT CONFLICT 72 72 L -> M (IN REF. 5).

SQ SEQUENCE 117 AA; 12911 MW; 39C0572BECA2755 CRC64;
 Query Match 100.0%; Score 121; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
 Db 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 2
 GHRL_RAT
 ID GHRL_RAT STANDARD; PRT; 117 AA.
 AC Q9QYH7; O9ET69;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 releasing peptide).
 GN GHRL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,
 AND ACYLATION OF SER-26.
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
 RX MEDLINE=20067959; PubMed=10604470;
 RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
 RT "Ghrelin is a growth-hormone-releasing acylated peptide from
 stomach.";
 RL Nature 402:656-660(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS
 SPECTROMETRY, AND ACYLATION OF SER-26.
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
 RX MEDLINE=20357315; PubMed=10801861;
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
 RT "Purification and characterization of rat des-Gln14-ghrelin, a second
 endogenous ligand for the growth hormone secretagogue receptor.";
 RL J. Biol. Chem. 275:21995-22000(2000).
 RN [3]
 RP CHARACTERIZATION.
 RP MEDLINE=21092536; PubMed=11162448;
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
 RT "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
 in gastrointestinal tissue.";
 RL Biochem. Biophys. Res. Commun. 279:909-913(2000).
 RN [4]
 RP STRUCTURE-ACTIVITY RELATIONSHIP.
 RX MEDLINE=21433488; PubMed=11549267;
 RA Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
 RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
 RT "Structure-activity relationship of ghrelin: pharmacological study of
 ghrelin peptides.";
 RL Biochem. Biophys. Res. Commun. 287:142-146(2001).
 RN [5]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 receptor type 1 (GHSR) inducing the release of growth hormone from
 the pituitary. Has an appetite-stimulating effect, induces
 adiposity and stimulates gastric acid secretion. Involved in
 growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;


```
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9QYH7-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9QYH7-2; Sequence=VSP_003248;
CC TISSUE SPECIFICITY: Broadly expressed with higher expression in
CC the stomach. Very low levels are detected in the hypothalamus,
CC heart, lung, pancreas, intestine and adipose tissue.
CC -! PTM: O-n-octanoylation is essential for activity. The replacement
CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.
CC -! MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;
CC RANGE=24-51.
CC -! MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;
CC RANGE=24-36, 38-51.
CC -! SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB029433; BAA89370.1; -
CC EMBL; AB035699; BAB11956.1; -
CC PIR; B59316; B59316.
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC InterPro; IPR005441; Preproghrelin.
CC Pfam; PF04643; motilin_assoc; 1.
CC Pfam; PF04644; motilin_ghrelin; 1.
CC PRINTS; PR01624; GHRELIN.
CC ProDom; PD332162; Preproghrelin; 1.
CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
KW SIGNAL 1 23
FT PEPTIDE 24 51 GHRELIN.
FT PROPEP 52 117 REMOVED IN MATURE FORM.
FT LIPID 26 26 N-OCTANOATE.
FT VARSPLIC 37 37 Missing (in isoform 2).
FT /FTID=VSP_003248.
SQ SEQUENCE 117 AA; 13176 MW; 8857546FE51A7691 CRC64;

Query Match 74.4%; Score 90; DB 1; Length 117;
Best Local Similarity 73.9%; Pred. No. 4.1e-06;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
DB 52 ALEGWLHPDRGQAEEAELEI 74

RESULT 3
GHRL_PIG
ID GHRL_PIG STANDARD; PRT; 118 AA.
AC Q9QYH5; Q9BDG8; Q9QYH4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide).
GN GHRL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Stomach;
```

```
RA Rousselle J., Lacroix D., Dubreuil P.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (by similarity).
CC -! SUBCELLULAR LOCATION: Secreted (By similarity).
CC -! ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9GKY5-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9GKY5-2; Sequence=VSP_003247;
CC -! PTM: O-n-octanoylation is essential for activity (By similarity).
CC -! SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB035703; BAB19048.1; -
CC EMBL; AB035704; BAB19049.1; -
CC EMBL; AF308930; AAK19243.1; -
CC EMBL; AY028942; AAK30002.1; -
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC InterPro; IPR005441; Preproghrelin.
CC Pfam; PF04643; motilin_assoc; 1.
CC Pfam; PF04644; motilin_ghrelin; 1.
CC PRINTS; PR01624; GHRELIN.
CC ProDom; PD332162; Preproghrelin; 1.
CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
KW SIGNAL 1 24 BY SIMILARITY.
FT PEPTIDE 25 52 GHRELIN.
FT PROPEP 53 118 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 27 27 N-OCTANOATE (BY SIMILARITY).
FT VARSPLIC 38 38 Missing (in isoform 2).
FT /FTID=VSP_003247.
FT CONFLICT 17 17 L -> P (IN REF. 2; AAK30002).
FT CONFLICT 72 72 K -> E (IN REF. 2; AAK30002).
SQ SEQUENCE 118 AA; 12785 MW; 85603E1D6DAB1A76 CRC64;

Query Match 71.9%; Score 87; DB 1; Length 118;
Best Local Similarity 65.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
DB 53 ALEGWLGPDSGEVEGTEDKLEI 75

RESULT 4
GHRL_MOUSE
ID GHRL_MOUSE STANDARD; PRT; 117 AA.
AC Q9EQX0; Q9WU21;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide) (M46 protein).
GN GHRL OR MTLRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
```

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RC TISSUE=Stomach;
RX MEDLINE=20389976; PubMed=10930375;
RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT "Identification and characterization of a novel gastric peptide
RL hormone: the motilin-related peptide.";
RN Gastroenterology 119:395-405(2000).
RP [2]
RA Kojima M.;
RA "Mouse mRNA for preproghrelin.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RA SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Yunshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
RP [5]
RA REVIEW.
RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RL hormone secretagogue receptor.";
RN Trends Endocrinol Metab 12:118-122(2001).
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC Name=2; Synonyms=del-cln14-ghrelin;
CC IsoId=Q9EQX0-1; Sequence=Displayed;
CC IsoId=Q9EQX0-2; Sequence=VSP_003246;
CC -1- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
CC with higher levels in the stomach, medium levels in the duodenum,
CC jejunum, ileum and colon. Low expression in the testis and brain.
CC Not detected in the salivary gland, pancreas, liver and lung.
CC -1- PTM: O-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
CC
CC EMBL: AJ243503; CAB46500.1; -
CC EMBL: AB035701; BAB19046.1; -
CC EMBL: AB060078; BAB69857.1; -
CC EMBL: AK008658; BAB25814.1; -
CC EMBL: AK008860; BAB25934.1; -
CC MGD; MGI:1930008; Ghrl.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005576; C:extracellular; IDA.
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC InterPro; IPR005441; Preproghrelin.
CC Pfam; PF04643; motilin_assoc; 1.
CC Pfam; PF04644; motilin_ghrelin; 1.
CC PRINTS; PR01624; GHRELIN.
CC PRODOM; PD332162; Preproghrelin; 1.
CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23 GHRELIN
FT PEPTIDE 24 51 REMOVED IN MATURE FORM (BY SIMILARITY).
FT PROPEP 52 117 N-OCTANOATE (BY SIMILARITY).
FT LIPID 26 26 MISSING (In isoform 2).
FT VARSPPLIC 37 37 /FTID=VSP_003246.
SQ SEQUENCE 117 AA; 13207 MW; EACBA49D2E3CA7203 CRC64;
Query Match 71.18; Score 86; DB 1; Length 117;
Best Local Similarity 69.68; Pred. No. 1.5e-05;
Matches 16; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 ALAGWLRPEDGGQAGAEAELEV 23
Db 52 ALEGWLHPEDRGQAEELEELEI 74
RESULT 5
GHRL_BOVIN STANDARD; PRT; 116 AA.
AC Q9BDJ6; Q9GKV6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ghrelin precursor (growth hormone secretagogue) (growth hormone
DE releasing peptide).
GN GHRL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Kita K., Harada K., Yokota H.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 24-99 FROM N.A.
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- PTM: O-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----

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CC -----
DR EMBL: AF350329; AAK18612.1; -.
DR EMBL: AB035702; BAB19047.1; -.
DR InterPro: IPR006737; motilin_ghrelin.
DR InterPro: IPR006737; motilin_ghrelin.
DR Pfam: PF04643; motilin_ghrelin; 1.
DR PRINTS: PR01624; motilin_ghrelin; 1.
DR PRODOM: PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 50 GHRELIN (BY SIMILARITY).
FT PROPEP 51 116 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT CONFLICT 34 34 K -> E (IN REF. 2).
SQ SEQUENCE 116 AA; 12792 MW; F55536DAC5FA59B6 CRC64;

Query Match 59.5%; Score 72; DB 1; Length 116;
Best Local Similarity 68.2%; Pred. No. 0.0015;
Matches 15; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGAEDELEV 23
   | | | | | | | | | | | | | |
Db 52 LEGQFDPEVGSQAEGAEDELEI 73

RESULT 6
GHRL_CANFA
ID GHRL_CANFA STANDARD; PRT; 117 AA.
AC Q9BEF8; Q9BEF7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).
GN GHRL OR MTLRP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Gastric fundus;
RA Tomasetto C., Wendling C., Rio M.-C., Poitras P.;
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog fundus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC isoId=Q9BEF8-1; Sequences=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC isoId=Q9BEF8-2; Sequences=VSP_003244;
CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC EMBL: AJ298295; CAC29155.1; -.

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DR EMBL: AJ298296; CAC29156.1; -.
DR InterPro: IPR006737; motilin_ghrelin.
DR InterPro: IPR006738; motilin_ghrelin.
DR InterPro: IPR005441; Preproghrelin.
DR Pfam: PF04643; motilin_ghrelin; 1.
DR Pfam: PF04644; motilin_ghrelin; 1.
DR PRINTS: PR01624; GHRELIN.
DR PRODOM: PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
KW Alternative splicing.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPIC 37 37 Missing (in isoform 2).
FT CONFLICT 34 34 /FTID=VSP_003244.
SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;

Query Match 56.2%; Score 68; DB 1; Length 117;
Best Local Similarity 65.2%; Pred. No. 0.0058;
Matches 15; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
   | | | | | | | | | | | | | |
Db 52 ALEGLGPRDTSQVBEAEDELEI 74

RESULT 7
NUPL_XENLA
ID NUPL_XENLA STANDARD; PRT; 200 AA.
AC P05221;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nucleoplasmin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218476; PubMed=2884102;
RA Dingwall C., Dillworth S.M., Black S.J., Kearsley S.E., Cox L.S., Laskey R.A.;
RT "Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and a cluster of sequences homologous to putative nuclear localization signals.";
RT signals.";
RL EMBO J. 6:69-74(1987).
RN [2]
RP SEQUENCE OF 7-200 FROM N.A.
RX MEDLINE=88112783; PubMed=3428591;
RA Buergrlin T.R., Mattaj I.W., Newmeyer D.D., Zeller R., de Robertis E.M.;
RT "Cloning of nucleoplasmin from Xenopus laevis oocytes and analysis of its developmental expression.";
RL Genes Dev. 1:97-107(1987).
CC -1- FUNCTION: NUCLEOPLASMIN IS AN ACIDIC, PENTAMERIC, THERMOSTABLE PROTEIN WHICH IS ABLE TO ASSEMBLE NUCLEOSOMES BY BINDING HISTONES AND TRANSFERRING THEM TO DNA.
CC -1- SUBUNIT: Homopentamer.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.
CC -----
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CC EMBL: X04766; CAA28460.1; -.

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RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serrif P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weizenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RA "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RT RT
RL Nature 390:249-256(1997).
CC -1- CATALYTIC ACTIVITY: An acyl phosphate + H2O = a fatty acid anion
CC + phosphate.
CC -----
CC -1- SIMILARITY: BELONGS TO THE ACYLPHOSPHATASE FAMILY.
CC -----
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CC -----
DR EMBL; D86417; BAA223305.1; -
DR EMBL; Z99108; CAB12593.1; -
DR PIR; B69811; B69811.
DR HSSP; P00818; IAPS.
DR Subtilist; BG12947; yfll.
DR InterPro; IPR001792; Acylphosphatase.
DR Pfam; PF00708; Acylphosphatase; 1.
DR PRINTS; PR00112; ACYLPHPTASE.
DR ProDom; PD001884; Acylphosphatase; 1.
DR PROSITE; PS00150; ACYLPHOSPHATASE_1; 1.
DR PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.
KW Hypothetical protein; Hydrolase; Complete proteome.
SQ SEQUENCE 91 AA; 10318 MW; 50795631BF3310F4 CRC64;

Query Match 42.1%; Score 51; DB 1; Length 91;
Best Local Similarity 44.0%; Pred. No. 1;2;
Matches 11; Conservative 5; Mismatches 5; Indels 4; Gaps 1;

QY 2 LAGWLRPEDGGQ----AEGADELE 22
      ||||| : | : ||| : | :
DB 30 LAGWVKNRDDGRVEIIAEGPENALQ 54

RESULT 9
APPL_MOUSE STANDARD; PRT; 653 AA.
ID APPL_MOUSE Q03157; Q8VC38;
AC Q03157; Q8VC38;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP-1) [Contains: C30].
GN APLP1.
GS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RS SEQUENCE FROM N.A.
RP RP
RC TISSUE=Brain;
RX MEDLINE=93066332; PubMed=1279693;
RA Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,
RA Solomon F.;
RT "Identification of a mouse brain cDNA that encodes a protein related
RT to the Alzheimer disease-associated amyloid beta protein precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
```

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Query Match      42.1%; Score 51; DB 1; Length 91;
Best Local Similarity 44.0%; Pred. No. 1.2;
Matches 11; Conservative 5; Mismatches 5; Indels 4; Gaps 1;

QY      2  LAGWLRPEDGQ- ---AEGADELE 22
      ||||:| |: ||| |:| :
DB      30  LAGWVKNRDDGRVEILLAEQPNALQ 54

RESULT 9
APPL_MOUSE
ID APPL_MOUSE STANDARD; PRT; 653 AA.
AC C03157; O8VC38;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
OS APLP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP
RC TISSUE=Brain;
RX MEDLINE=93066322; PubMed=1279693;
RA Wasco W., Bupp K., Megendantz M., Gusella J.F., Tanzi R.E.,
RT Solomon F.;
RT "Identification of a mouse brain cDNA that encodes a protein related
RT to the Alzheimer disease-associated amyloid beta protein precursor.";
RT Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).

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RN [2] SEQUENCE FROM N.A.
 RC TISSUE-Retina;
 RX MEDLINE-22388257; PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [3]
 RN COLLAGEN-BINDING.
 RX MEDLINE-96139497; PubMed-8576160;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and mapping of the binding sites on APP and collagen type I";
 RL J. Biol. Chem. 271:1613-1620(1996).
 RN [4]
 RN INTERACTION WITH DAB1.
 RX MEDLINE-99389880; PubMed-10460257;
 RA Homayouni R., Rice D.S., Sheldon M., Curran T.;
 RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like protein 1";
 RL J. Neurosci. 19:7507-7515(1999).
 RN [5]
 RN INTERACTION WITH MAPK8IP1.
 RX MEDLINE-21408156; PubMed-11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niihara T., Hiraki T., Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T., Kyriakis J.M., Nishimoto I.;
 RA "C-Jun N-terminal kinase (JNK)-interacting protein-1b/Islet-brain-1 scaffolds Alzheimer's amyloid precursor protein with JNK";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [6]
 RN GAMMA-SECRETASE PROCESSING, INTERACTION WITH APPB1, AND MUTAGENESIS OF TYR-641.
 RX MEDLINE-22313598; PubMed-12228233;
 RA Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamo L.;
 RA "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-secretase regulates transcription";
 RL J. Biol. Chem. 277:44195-44201(2002).
 CC -1- FUNCTION: May play a role in postsynaptic function. The C-terminal gamma-secretase processed fragment, ALIDI, activates transcription activation through APPB1 (Re65) binding. Couples to JIP signal transduction through C-terminal binding. May interact with cellular G-protein signaling pathways. Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I.
 CC -1- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of neuronal apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including APPB and APBA family members, MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally processed in the Golgi complex.
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-

CC terminal to the NPXY motif are often required for complete interaction. The NPXY site is also involved in clathrin-mediated endocytosis.
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By similarity).
 CC -1- PTM: N-glycosylated.
 CC -1- PTM: O-glycosylated.
 CC -1- MISCELLANEOUS: Binds zinc and copper in the extracellular domain. Zinc-binding increases heparin binding. No Cu(II) reducing activity with copper-binding.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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 CC -----
 CC EMBL; L04538; AAA37247.1; -;
 CC EMBL; BC021877; AAH21877.1; -;
 CC PIR; A46362; A46362.
 CC HSP; P05067; 1MWP.
 CC MGD; MGI:88046; Ap1p1.
 CC InterPro: IPR001868; A4_APP.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC PRINTS; PR00203; AMYLOIDA4.
 CC SMART; SM00006; A4_EXTRA; 1.
 CC PROSITE; PS00319; A4_EXTRA; 1.
 CC PROSITE; PS00320; A4_INTRA; 1.
 CC Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
 KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
 KW Glycoprotein.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 653 AMYLOID-LIKE PROTEIN 1.
 FT CHAIN 624 653 C30 (BY SIMILARITY).
 FT DOMAIN 38 583 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 584 606 POTENTIAL.
 FT DOMAIN 607 653 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 157 177 COPPER-BINDING.
 FT DOMAIN 203 210 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 313 345 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 413 444 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 445 462 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 263 271 POLY-GLU.
 FT DOMAIN 535 538 POLY-SER.
 FT DOMAIN 601 606 POLY-LEU.
 FT SITE 166 166 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
 FT SITE 607 618 BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
 FT SITE 623 624 CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
 FT SITE 641 644 ENDOCYTOSIS SIGNAL.
 FT SITE 643 646 NPXY MOTIF.
 FT CARBOHYD 464 464 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 554 554 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOTAGEN 641 641 Y->G: REDUCED BINDING OF APB1.
 FT CONFLICT 17 17 P -> PP (IN REF. 2).
 SQ SEQUENCE 653 AA; 72750 MW; 56516DC3EA40E4B0 CRC64;
 Query Match 41.3%; Score 50; DB 1; Length 653;
 Best Local Similarity 76.9%; Pred. No. 12;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 11 GGAGGAEGDELEV 23
 ||:|||||
 Db 233 GGRAGGEDDEEV 245
 RESULT 10
 NKX1_BISBI

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ID NKX1_BISBI STANDARD PRT; 300 AA.
AC O46383;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 (Na(+)/K(+)/Ca(2+)-
DE exchange protein 1) (Retinal rod Na-Ca+K exchanger) (Fragment).
GN SLC24A1 OR NCKX1.
OS Bison bison (American bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bison.
OX NCBI_TaxID=9901;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98138491; PubMed=9478004;
RA Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.;
RT "cDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison
RT with a revised bovine sequence.";
RL Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
CC -1- FUNCTION: Critical component of the visual transduction cascade,
CC controlling the calcium concentration of outer segments during
CC light and darkness. Light causes a rapid lowering of cytosolic
CC free calcium in the outer segment of both retinal rod and cone
CC photoreceptors and the light-induced lowering of calcium is caused
CC by extrusion via this protein which plays a key role in the
CC process of light adaptation. Transports one Ca(2+) and one K(+) in
CC exchange for four Na(+) (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
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DR EMBL; AF025480; AAC13320.1; -
KW Vision; transport; Antiport; Symport; Calcium transport;
KW Potassium transport; Sodium transport; Transmembrane.
FT NON_TER 1
FT TRANSMEM 259 275 POTENTIAL.
FT DOMAIN 218 242 POLY-GLU.
FT NON_TER 300 300
FT SEQUENCE 300 AA; 31671 MW; 2BE592DA5AB9781E CRC64;
Query Match 39.7%; Score 48; DB 1; Length 300;
Best Local Similarity 45.0%; Pred. No. 11;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Qy 4 GWLPEGGGAGAEDELEV 23
I :: :||: || ||| :|
Db 84 GEIQAGEGEGVEGDEGEI 103
RESULT 11
SYM_METKA STANDARD PRT; 668 AA.
AC Q8TX28;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methionyl-trna synthetase (EC 6.1.1.10) (Methionine--trna ligase)
DE (MetrS).
OS Methanopyrus kandleri.
OS Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natile D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozayavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC -1- FUNCTION: Is required not only for elongation of protein synthesis
CC but also for the initiation of all mRNA translation through
CC initiator tRNA(fMet) aminoacylation (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) -> AMP +
CC diphosphate + L-methionyl-tRNA(Met).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC MetG subfamily 1.
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
-----
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-----
DR EMBL; AE010375; AAM02063.1; -
DR HAMAP; MF_00098; fused; 1.
DR InterPro; IPR004495; MetG_Cterm.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002304; tRNA-synt_met.
DR InterPro; IPR002547; tRNA_bind.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR Pfam; PF01588; tRNA_bind; 1.
DR Pfam; PIRSF001528; MetRS_dimerising; 1.
DR TIGRFAMs; TIGR00398; metg; 1.
DR TIGRFAMs; TIGR00399; metg_Cterm; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
DR PROSITE; PS00886; TRBD; 1.
DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW RNA-binding; tRNA-binding; Metal-binding; Zinc; Complete proteome.
FT SITE 11 21 "HIGH" REGION.
FT SITE 332 336 "KMSKS" REGION.
FT DOMAIN 567 668 tRNA-BINDING.
FT METAL 146 146 ZINC (BY SIMILARITY).
FT METAL 149 149 ZINC (BY SIMILARITY).
FT METAL 159 159 ZINC (BY SIMILARITY).
FT METAL 162 162 ZINC (BY SIMILARITY).
SQ SEQUENCE 668 AA; 77386 MW; FBC5734FF5FEF015 CRC64;
Query Match 39.7%; Score 48; DB 1; Length 668;
Best Local Similarity 53.3%; Pred. No. 24;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 6 LRPEGGGAGAEDE 20
I ||: ||: ||: ||
Db 547 LLPESGEGEQDDE 561
RESULT 12
NKX1_BOVIN STANDARD PRT; 1216 AA.
ID NKX1_BOVIN
AC Q28139; O46384;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+) -
DE exchange protein 1) (Retinal rod Na-Ca+K exchanger).
GN SLC24A1 OR NCKX1.

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CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U04092; AAA67171.1; -.
CC PIR; A55259;
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN
CC PROSITE; PS00237; G_PROTEIN_RECIP_FL_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECIP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC phosphorylation; Lipoprotein; Palmitate.
CC DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 59 85 1 (POTENTIAL).
CC DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 96 117 2 (POTENTIAL).
CC DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 133 154 3 (POTENTIAL).
CC DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 174 196 4 (POTENTIAL).
CC DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 223 247 5 (POTENTIAL).
CC DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 276 299 6 (POTENTIAL).
CC DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 312 333 7 (POTENTIAL).
CC DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
CC DISULFID 131 210 BY SIMILARITY.
CC LIPID 345 345 PALMITATE (POTENTIAL).
CC FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 380 AA; 42736 MW; 4FF053834DBBA623 CRC64;

Query Match 38.8%; Score 47; DB 1; Length 380;
Best Local Similarity 38.1%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGAEDELE 22
| | | | | | | | | | | | | | | | | | | | | |
Db 30 LPGAEPDGNAGAGPQDEQLE 50

RESULT 14
DDX8_ARATH DDX8_ARATH STANDARD; PRT; 1168 AA.
AC Q38953; Q9LRV0;
DT 18-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative pre-mRNA splicing factor ATP-dependent RNA helicase.
GN AT3G26560 OR MPE16.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RA Quigley F., Dao P., Cottet A., Mache R.;
RT "Sequence analysis of an 81 kb contig from Arabidopsis thaliana
RL chromosome III.";
RL Nucleic Acids Res. 24:4313-4318(1996).
RN [2]
```

```
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
CC -1- FUNCTION: COULD ACT LATE IN THE SPLICING OF PRE-MRNA AND MEDIATE
CC THE RELEASE OF THE SPLICED MRNA FROM SPLICEOSOMES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. DEAH
CC SUBFAMILY. DDX8/PRP22 ORTHOLOG.
CC -1- SIMILARITY: Contains 1 S1 motif domain.
CC -1- CAUTION: Ref.1 sequences differ from that shown due to a
CC frameshift in position 57.
CC -----
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CC -----
CC EMBL; X98130; CAA66825.1; ALT_FRAME.
CC EMBL; X97970; CAA66613.1; ALT_FRAME.
CC EMBL; AB028611; BAB01838.1; -.
CC HSP; P05055; 1SRO.
CC InterPro; IPR001410; DEAD.
CC InterPro; IPR002464; DEAH_box.
CC InterPro; IPR001650; Helicase_C.
CC InterPro; IPR003029; S1.
CC Pfam; PF00271; helicase_C; 1.
CC Pfam; PF00575; S1; 1.
CC SMART; SM00487; DEXDC; 1.
CC SMART; SM00490; HELICC; 1.
CC SMART; SM00316; S1; 1.
CC PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
CC PROSITE; PS00126; S1; 1.
CC Hypothetical protein; mRNA processing; mRNA splicing; Helicase;
KW ATP-binding; Nuclear protein.
FT DOMAIN 214 283 S1 MOTIF.
FT NP_BIND 538 545 ATP (POTENTIAL).
FT SITE 635 638 DEAH BOX.
FT DOMAIN 777 780 POLY-PRO.
FT SQ SEQUENCE 1168 AA; 134156 MW; B3632DE4A7A7690C CRC64;

Query Match 38.8%; Score 47; DB 1; Length 1168;
Best Local Similarity 57.9%; Pred. No. 59;
Matches 11; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

QY 9 EDGG----QAEGAEDELEV 23
| | | | | | | | | | | | | | | | | | | | | |
Db 372 EDGGDMLYQBEGAELEEI 390

RESULT 15
MM14_PIG MM14_PIG STANDARD; PRT; 580 AA.
AC Q9XT90;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Matrix metalloproteinase-14 precursor (EC 3.4.24.-) (MMP-14)
DE (Membrane-type matrix metalloproteinase 1) (MT-MMP 1) (MTMMP1)
DE (Membrane-type-1 matrix metalloproteinase) (MT1-MMP) (MT1MMP).
GN MMP14.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
```


RP SEQUENCE FROM N.A.
RX MEDLINE=9905929; PubMed=9881602;
RA Caron C., Xue J., Bartlett J.D.;
RT "Expression and localization of membrane type 1 matrix
RT metalloproteinase in tooth tissues";
RL Matrix Biol. 17:501-511(1998).
CC -!- FUNCTION: SEEMS TO SPECIFICALLY ACTIVATE OF PRO-
CC THUS TRIGGER INVASION BY TUMOR CELLS BY ACTIVATING PRO-
CC A ON THE TUMOR CELL SURFACE (BY SIMILARITY). MAY PLAY A ROLE IN
CC THE BIOMINERALIZATION OF ENAMEL AND DENTIN.
CC -!- COFACTOR: Binds 1 zinc ion per subunit, calcium (By similarity).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein (potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN DEVELOPING TOOTH TISSUES
CC AND MAY PLAY A ROLE IN THE BIOMINERALIZATION OF ENAMEL AND DENTIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC -----
DR EMBL; AF067419; AAD38324.1; -.
DR HSSP; P08254; 1HFS.
DR MEROPS; M10.014; -.
DR InterPro; IPR000595; Hemopexin.
DR InterPro; IPR001818; Matrixin.
DR InterPro; IPR006026; Zn_MTpeptdse.
DR InterPro; IPR006025; Zn_MTpeptdse.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolyase; Metalloprotease; Zinc; zymogen; Calcium; Signal;
KW Transmembrane.
FT SIGNAL 1 28 POTENTIAL.
FT PROPEP 29 109 ACTIVATION PEPTIDE.
FT CHAIN 110 580 MATRIX METALLOPROTEINASE-14.
FT DOMAIN 110 539 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 540 560 POTENTIAL.
FT DOMAIN 561 580 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 314 509 HEMOPEXIN-LIKE.
FT SITE 91 91 CYSTEINE SWITCH (POTENTIAL).
FT METAL 237 237 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 238 238 BY SIMILARITY.
FT METAL 241 241 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 247 247 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 317 506 BY SIMILARITY.
SQ SEQUENCE 580 AA; 65934 MW; B7B2C2C569A96CAC CRC64;

Query Match 37.6%; Score 45.5; DB 1; Length 580;
Best Local Similarity 45.8%; Pred. No. 48;
Matches 11; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 ALAGNLRPEDGGA-EGAEDELEY 23
|| | : || : || : ||
Db 499 ALRDMWGPCSGGRPDGTEETEY 522

Search completed: September 11, 2003, 17:21:45
Job time : 4.32086 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 21.893 seconds
(without alignments)
271.100 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 121

Sequence: 1 ALAGWLRPDGGQAGAEDELEV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|--------|--------------------|
| 1 | 119 | 98.3 | 117 | Q8TAT9 | Q8tat9 homo sapien |
| 2 | 92 | 76.0 | 117 | Q8CH53 | Q8ch53 meriones un |
| 3 | 59 | 48.8 | 1208 | Q8I5T3 | Q8i5t3 plasmodium |
| 4 | 59 | 48.8 | 1264 | Q9U445 | Q9u445 plasmodium |
| 5 | 55 | 45.5 | 183 | Q8LNL6 | Q8lnl6 oryza sativ |
| 6 | 53 | 43.8 | 202 | Q90P58 | Q90p58 human immun |
| 7 | 53 | 43.8 | 1228 | Q27724 | Q27724 plasmodium |
| 8 | 52 | 43.0 | 201 | Q90P50 | Q90p50 human immun |
| 9 | 52 | 43.0 | 232 | Q9I6L1 | Q9i6l1 pseudomonas |
| 10 | 52 | 43.0 | 249 | Q82036 | Q82036 hirame rhab |
| 11 | 52 | 43.0 | 392 | Q9QL89 | Q9ql89 hirame rhab |
| 12 | 52 | 43.0 | 977 | Q9S169 | Q9s169 capra hircu |
| 13 | 51.5 | 42.6 | 436 | Q9N638 | Q9n638 caenorhabdi |
| 14 | 51 | 42.1 | 158 | Q8XW90 | Q8xw90 raistonia s |
| 15 | 51 | 42.1 | 201 | Q90NL5 | Q90nl5 human immun |
| 16 | 51 | 42.1 | 604 | Q8UFA5 | Q8ufa5 agrobacteri |

| | | | | | | |
|----|------|------|-----|----|--------|--------------------|
| 17 | 51 | 42.1 | 609 | 2 | Q9RH77 | Q9rh77 bradyrhizob |
| 18 | 50 | 41.3 | 131 | 16 | Q9RV90 | Q9rv90 deinococcus |
| 19 | 50 | 41.3 | 202 | 15 | Q90P76 | Q90p76 human immun |
| 20 | 50 | 41.3 | 202 | 15 | Q90P77 | Q90p77 human immun |
| 21 | 50 | 41.3 | 472 | 10 | Q8LRD5 | Q8lrd5 oryza sativ |
| 22 | 50 | 41.3 | 582 | 6 | Q9XSP0 | Q9xsp0 capra hircu |
| 23 | 50 | 41.3 | 582 | 6 | Q9GLE4 | Q9gle4 bos taurus |
| 24 | 49.5 | 40.9 | 484 | 16 | Q9R2L7 | Q9r2l7 deinococcus |
| 25 | 49 | 40.5 | 201 | 15 | Q90P55 | Q90p55 human immun |
| 26 | 49 | 40.5 | 201 | 15 | Q90N48 | Q90n48 human immun |
| 27 | 49 | 40.5 | 286 | 12 | Q8QRU5 | Q8qr5 chimpanzee |
| 28 | 48.5 | 40.1 | 110 | 10 | Q93VB3 | Q93vb3 oryza sativ |
| 29 | 48.5 | 40.1 | 172 | 2 | Q9RBY2 | Q9rby2 pseudomonas |
| 30 | 48.5 | 40.1 | 172 | 2 | Q9R2S2 | Q9r2s2 pseudomonas |
| 31 | 48.5 | 40.1 | 269 | 2 | Q9FTM8 | Q9ftm8 pseudomonas |
| 32 | 48 | 39.7 | 106 | 16 | Q8ELH4 | Q8elh4 oceanobacil |
| 33 | 48 | 39.7 | 115 | 10 | Q8LI79 | Q8li79 oryza sativ |
| 34 | 48 | 39.7 | 120 | 15 | Q78494 | Q78494 human immun |
| 35 | 48 | 39.7 | 201 | 15 | Q90P53 | Q90p53 human immun |
| 36 | 48 | 39.7 | 201 | 15 | Q90NL3 | Q90nl3 human immun |
| 37 | 48 | 39.7 | 201 | 15 | Q90NL6 | Q90nl6 human immun |
| 38 | 48 | 39.7 | 201 | 15 | Q90NL0 | Q90nl0 human immun |
| 39 | 48 | 39.7 | 201 | 15 | Q90NL1 | Q90nl1 human immun |
| 40 | 48 | 39.7 | 201 | 15 | Q90NM1 | Q90nm1 human immun |
| 41 | 48 | 39.7 | 201 | 15 | Q90NM2 | Q90nm2 human immun |
| 42 | 48 | 39.7 | 201 | 15 | Q90NL9 | Q90nl9 human immun |
| 43 | 48 | 39.7 | 202 | 15 | Q90P31 | Q90p31 human immun |
| 44 | 48 | 39.7 | 202 | 15 | Q90P37 | Q90p37 human immun |
| 45 | 48 | 39.7 | 211 | 10 | Q943L4 | Q943l4 oryza sativ |

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY; PRT; 117 AA.
AC Q8TAT9;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Ghrelin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025791; AAH25791.1; -
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_assoc.1.
DR Pfam; PF04644; motilin_ghrelin.1.
SQ SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;

Query Match 98.3%; Score 119; DB 4; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.6e-09;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAGAEDELEV 23
|||||
DB 52 ALAGWLRPDGGQAGAEDEMEV 74

RESULT 2

Q8CH53 PRELIMINARY; PRT; 117 AA.
ID Q8CH53;
AC Q8CH53;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

```

DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones
ON NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoaka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AA006965.1; -.
SQ SEQUENCE 117 AA; 27657687FC026A74 CRC64;

Query Match 76.0%; Score 92; DB 11; Length 117;
Best Local Similarity 73.9%; Pred. No. 1.3e-05;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEV 23
Db 52 ALEGWLRPDGGRGAEGAEDELEI 74

RESULT 3
Q815T3 PRELIMINARY; PRT; 1208 AA.
AC Q815T3;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE P-type ATPase, putative.
GN PfL0590C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
ON NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., K.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014846; AAN36207.1; -.
SQ SEQUENCE 1208 AA; 133873 MW; 25AA7752E707E621 CRC64;

Query Match 48.8%; Score 59; DB 5; Length 1208;
Best Local Similarity 52.6%; Pred. No. 8.2;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGGAEGAEDELE 22
Db 1072 GWCRPKDNKTSQGYNDELE 1090

RESULT 4
Q90445 PRELIMINARY; PRT; 1264 AA.
ID Q90445
AC Q90445;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE P-type ATPase4.

```

```

GN ATPASE4.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
ON NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21179120; PubMed=11145964;
RA Krishna S., Woodrow C., Webb R., Penny J., Takeyasu K., Kimura M.,
RA East J.M.;
RT "Expression and Functional Characterization of a Plasmodium falciparum
Ca2+-ATPase (PfATP4) Belonging to a Subclass Unique to Apicomplexan
Organisms.";
RL J. Biol. Chem. 276:10782-10787(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
ATPASES).
DR EMBL; AF203980; AAF17245.1; -.
DR HSP; P04191; IEUL.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 5.
DR PROSITE; PS00154; ATPASE_E1-E2; 1.
KW ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SQ SEQUENCE 1264 AA; 140261 MW; 638142BB1B433640 CRC64;

Query Match 48.8%; Score 59; DB 5; Length 1264;
Best Local Similarity 52.6%; Pred. No. 8.6;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGGAEGAEDELE 22
Db 1128 GWCRPKDNKTSQGYNDELE 1146

RESULT 5
Q8LNL6 PRELIMINARY; PRT; 183 AA.
ID Q8LNL6
AC Q8LNL6;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OSJNBA0071120.2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
ON NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA McCombie W.R., Spiegel L., de la Bastide M., Preston R., Ferraro K.,
RA Kuit K., Nascimento L., Zutavern T., Ballja V., Bell M., Baker J.,
RA Miller B., Katzenberger F., Muller S., King L., Sullivan P., Yang C.,
RA Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone
OSJNBA0071120, from chromosome 10, complete sequence.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC074355; AAM74240.1; -.
DR Gramene; Q8LNL6; -.
KW Hypothetical protein.
SQ SEQUENCE 183 AA; 20492 MW; DE73BD8607292D7B CRC64;

Query Match 45.5%; Score 55; DB 10; Length 183;
Best Local Similarity 47.6%; Pred. No. 4.2;
Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

```

DR pfam; PF00702; Hydrolase; 1.

| RA | Sm i |
|----|------|
| RA | Sm i |

| RA | Sm i |
|----|------|
| RA | Sm i |

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."
 RL Nature 406:959-964(2000).
 CC -1- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
 CC EMBL: AE004466; AAC03668.1; -
 DR InterPro: IPR001845; HTH_ArsR.
 DR Pfam: PF01022; HTH_5; 1.
 DR PRINTS: PR00778; HTHARSR.
 DR SMART: SM00418; HTH_ArsR; 1.
 KW DNA-binding; Transcription regulation; Complete proteome.
 SQ SEQUENCE 232 AA; 24440 MW; E3C29187694CF936 CRC64;

Query Match 43.0%; Score 52; DB 16; Length 232;
 Best Local Similarity 72.7%; Pred. No. 15;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GWLRPEDGGQA 14

Db 202 GWLRPDGSGRA 212

RESULT 10

Q82036 PRELIMINARY; PRT; 249 AA.
 ID Q82036
 AC Q82036;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Nucleocapsid protein.
 GN N.
 OS Hirame rhabdovirus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Novirhabdovirus.
 OX NCBI_TaxID=38142;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8401-H;
 RA Nishizawa T.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D45422; BAA08261.1; -
 DR InterPro: IPR004902; Rhabdo_ncap_2.
 DR Pfam: PF03216; Rhabdo_ncap_2; 1.
 SQ SEQUENCE 249 AA; 26936 MW; 62FF2BFA5D47DB89 CRC64;

Query Match 43.0%; Score 52; DB 12; Length 249;
 Best Local Similarity 75.0%; Pred. No. 16;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 EDGGQAEAGDE 20

Db 235 EDGGEDEGE 246

RESULT 11

Q9QL89 PRELIMINARY; PRT; 392 AA.
 ID Q9QL89
 AC Q9QL89;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Nucleocapsid protein.
 GN N.
 OS Hirame rhabdovirus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Novirhabdovirus.
 OX NCBI_TaxID=38142;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CA 9703;
 RA Oh H.K., Choi T.J.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF104985; ANF14116.1; -

DR InterPro: IPR004902; Rhabdo_ncap_2.
 DR Pfam: PF03216; Rhabdo_ncap_2; 1.
 SQ SEQUENCE 392 AA; 42465 MW; CSA282238FC7A638 CRC64;

Query Match 43.0%; Score 52; DB 12; Length 392;
 Best Local Similarity 75.0%; Pred. No. 26;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 EDGGQAEAGDE 20

Db 378 EDGGEDEGE 389

RESULT 12

Q95169 PRELIMINARY; PRT; 977 AA.
 ID Q95169
 AC Q95169;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Skeletal muscle voltage-gated chloride channel gCLC-1 (Fragment).
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97008165; PubMed=8855341;
 RA Beck C.L., Fahlike C., George A.L.;
 RT "Molecular basis for decreased muscle chloride conductance in the myotonic goat."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:11248-11252(1996).
 DR EMBL: U60275; AAC48666.1; -
 DR InterPro: IPR000644; CBS_domain.
 DR InterPro: IPR001807; Cl-channel_volt.
 DR InterPro: IPR005829; Sug_transporter.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00654; voltage_CLC; 1.
 DR PRINTS: PR00762; CLCHANNEL.
 DR PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 977 AA; 107894 MW; 1E462B3CB307A148 CRC64;

Query Match 43.0%; Score 52; DB 6; Length 977;
 Best Local Similarity 62.5%; Pred. No. 67;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GWLRPEDGGQAEAGD 19

Db 895 GWSLPEDGAGATCAGD 910

RESULT 13

Q9N638 PRELIMINARY; PRT; 436 AA.
 ID Q9N638
 AC Q9N638;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE F37D6.6 protein.
 GN F37D6.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilkenson J.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;

RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT Investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA McMurray A.A.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z79600; CAB70221.1; -;
 DR EMBL; Z75540; CAB70221.1; JOINED.
 DR EMBL; Z75540; CAB70215.1; -;
 DR EMBL; Z79600; CAB70215.1; JOINED.
 DR WormPep; F37D6.6; CE24960.
 DR InterPro: IPR001132; DwarfIn.
 DR InterPro: IPR003619; DwarfIn_A.
 DR Pfam; PF03166; MH2; 1.
 DR SMART; SM00523; DWA; 1.
 DR SMART; SM00524; DWA; 1.
 SQ SEQUENCE 436 AA; 49496 MW; E0C71263BC580EEE CRC64;

Query Match 42.6%; Score 51.5; DB 5; Length 436;
 Best Local Similarity 52.9%; Pred. No. 34;
 Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 5 WLRPE-DGGQAEDE 20
 I:III :II :I:II:
 Db 169 WIRPETNGGDDGSEDK 185

RESULT 14

Q8XW90
 ID Q8XW90 PRELIMINARY; PRT; 158 AA.
 AC Q8XW90;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein RSC2585.
 GN RSC2585 OR RS00797.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OX NCBI_Taxid=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choigne N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646070; CAD16292.1; -;
 DR InterPro: IPR002145; HTH_CopG.
 DR Pfam; PF01402; HTH 4; 1
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 158 AA; 17814 MW; C9BA42BF9C10E1BC CRC64;

Query Match 42.1%; Score 51; DB 16; Length 158;
 Best Local Similarity 58.8%; Pred. No. 14;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAECA 17
 III I I I I I
 Db 36 ALASWLSPDAGDQREAA 52

RESULT 15

Q90NL5
 ID Q90NL5 PRELIMINARY; PRT; 201 AA.
 AC Q90NL5;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nickle D.C.;
 RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF371104; AAK66503.1; -;
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR AIDS; Coat protein; Glycoprotein.
 KW NON_TER 1
 FT NON_TER 201 201
 SQ SEQUENCE 201 AA; 22470 MW; E1993A2A412EC118 CRC64;

Query Match 42.1%; Score 51; DB 15; Length 201;
 Best Local Similarity 40.9%; Pred. No. 18;
 Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAEDELEV 23
 I:III :II :I:II:
 Db 179 ITGLLTRDGGGGNGTNETEI 200

Search completed: September 11, 2003, 17:30:28
 Job time : 21.893 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:48:42 ; Search time 40.0428 Seconds
(without alignments)
123.627 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 117

Sequence: 1 MPSPGTWCSLLLLGLMLDL.....LGKFLQDILWEKEAPADK 117

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA.*

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- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 117 | 100.0 | 117 | 3 | US-09-046-479-2 |
| 2 | 117 | 100.0 | 117 | 4 | US-08-822-897C-2 |
| 3 | 117 | 100.0 | 117 | 4 | US-09-608-810A-4 |
| 4 | 117 | 100.0 | 117 | 4 | US-09-996-243-268 |
| 5 | 11 | 9.4 | 11 | 4 | US-09-608-810A-2 |
| 6 | 7 | 6.0 | 442 | 4 | US-09-134-001C-3033 |
| 7 | 7 | 6.0 | 502 | 2 | US-08-481-337A-8 |
| 8 | 7 | 6.0 | 502 | 3 | US-09-382-256-18 |
| 9 | 7 | 6.0 | 502 | 3 | US-09-395-115-18 |
| 10 | 7 | 6.0 | 502 | 3 | US-08-123-934A-4 |
| 11 | 7 | 6.0 | 502 | 4 | US-08-436-265-18 |
| 12 | 7 | 6.0 | 502 | 4 | US-09-679-187-18 |
| 13 | 7 | 6.0 | 502 | 5 | PCT-US94-10080-4 |
| 14 | 7 | 6.0 | 502 | 5 | PCT-US95-05467-8 |
| 15 | 7 | 6.0 | 552 | 4 | US-09-252-991A-27032 |
| 16 | 7 | 6.0 | 599 | 4 | US-09-252-991A-20368 |
| 17 | 7 | 6.0 | 662 | 4 | US-09-252-991A-22861 |
| 18 | 7 | 6.0 | 981 | 4 | US-09-252-991A-16798 |
| 19 | 7 | 6.0 | 3165 | 2 | US-08-459-146-3 |
| 20 | 7 | 6.0 | 3165 | 2 | US-08-459-085-3 |
| 21 | 6 | 5.1 | 15 | 1 | US-08-434-705B-18 |
| 22 | 6 | 5.1 | 15 | 2 | US-09-086-201-18 |
| 23 | 6 | 5.1 | 24 | 3 | US-08-948-782-1 |
| 24 | 6 | 5.1 | 24 | 3 | US-09-482-612-1 |
| 25 | 6 | 5.1 | 24 | 4 | US-09-677-554-1 |
| 26 | 6 | 5.1 | 30 | 2 | US-08-995-927-9 |
| 27 | 6 | 5.1 | 30 | 4 | US-09-582-096-9 |

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|----|---|-----|-----|---|----------------------|-------------------|
| 28 | 6 | 5.1 | 39 | 1 | US-08-428-488-13 | Sequence 13, Appl |
| 29 | 6 | 5.1 | 43 | 3 | US-08-981-739-104 | Sequence 104, App |
| 30 | 6 | 5.1 | 43 | 4 | US-09-128-026-104 | Sequence 104, App |
| 31 | 6 | 5.1 | 45 | 3 | US-08-975-080-11 | Sequence 11, Appl |
| 32 | 6 | 5.1 | 64 | 4 | US-09-328-352-5646 | Sequence 5646, Ap |
| 33 | 6 | 5.1 | 67 | 2 | US-08-511-485-14 | Sequence 14, Appl |
| 34 | 6 | 5.1 | 67 | 4 | US-09-201-936-14 | Sequence 14, Appl |
| 35 | 6 | 5.1 | 80 | 4 | US-09-252-991A-21677 | Sequence 21677, A |
| 36 | 6 | 5.1 | 81 | 4 | US-09-489-847-325 | Sequence 325, App |
| 37 | 6 | 5.1 | 82 | 4 | US-09-489-847-234 | Sequence 234, App |
| 38 | 6 | 5.1 | 89 | 4 | US-09-048-502-2 | Sequence 2, Appl |
| 39 | 6 | 5.1 | 89 | 4 | US-09-048-502-3 | Sequence 3, Appl |
| 40 | 6 | 5.1 | 97 | 2 | US-08-403-852D-31 | Sequence 31, Appl |
| 41 | 6 | 5.1 | 97 | 3 | US-08-510-646B-32 | Sequence 32, Appl |
| 42 | 6 | 5.1 | 97 | 3 | US-09-231-818-31 | Sequence 31, Appl |
| 43 | 6 | 5.1 | 98 | 4 | US-09-107-532A-6022 | Sequence 6022, Ap |
| 44 | 6 | 5.1 | 102 | 4 | US-09-048-502-1 | Sequence 1, Appl |
| 45 | 6 | 5.1 | 103 | 4 | US-09-634-238-275 | Sequence 275, App |

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 100.0%; Score 117; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 1e-109;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MPSPGTVCSSLLGLMLDLAMAGSFLSPHQRVQQRKSKPPAKLQPRALAGWLRLPE 60
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Oy 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSQLGKFLQDILWEAKEAPADK 117
Db 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSQLGKFLQDILWEAKEAPADK 117

RESULT 2

US-08-822-897C-2

; Sequence 2, Application US/08822897C

; Patent No. 6380158

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Delsher, Theresa A.

; TITLE OF INVENTION: MOTILIN HOMOLOGS

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ZymoGenetics, Inc.

; STREET: 1201 Eastlake Avenue East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/822.897C

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sawislak, Deborah A.

; REGISTRATION NUMBER: 37,438

; REFERENCE/DOCKET NUMBER: 97-04

; TELEPHONE: 206-442-6672

; TELEFAX: 206-442-6678

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-822-897C-2

Query Match 100.0%; Score 117; DB 4; Length 117;

Best Local Similarity 100.0%; Pred. No. 1e-109;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MPSPGTVCSSLLGLMLDLAMAGSFLSPHQRVQQRKSKPPAKLQPRALAGWLRLPE 60
Db 1 MPSPGTVCSSLLGLMLDLAMAGSFLSPHQRVQQRKSKPPAKLQPRALAGWLRLPE 60

Oy 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSQLGKFLQDILWEAKEAPADK 117
Db 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSQLGKFLQDILWEAKEAPADK 117

RESULT 3

US-09-608-810A-4

; Sequence 4, Application US/09608810A

; Patent No. 6420521

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Delsher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608.810A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4

LENGTH: 117

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: (1)...(23)

US-09-608-810A-4

Query Match

100.0%; Score 117; DB 4; Length 117;

Best Local Similarity 100.0%; Pred. No. 1e-109;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSQLGKFLQDILWEAKEAPADK 117
Db 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSQLGKFLQDILWEAKEAPADK 117

RESULT 4

US-09-996-243-268

; Sequence 268, Application US/09996243

; Patent No. 6478825

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gottlieb, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: Acids Encoding the Same

; FILE REFERENCE: P2730P1C13

; CURRENT APPLICATION NUMBER: US/09/996.243

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

1 PRIOR FILING DATE: 1997-11-12
2 PRIOR APPLICATION NUMBER: 60/065311
3 PRIOR FILING DATE: 1997-11-13
4 PRIOR APPLICATION NUMBER: 60/066770
5 PRIOR FILING DATE: 1997-11-24
6 PRIOR APPLICATION NUMBER: 60/075945
7 PRIOR FILING DATE: 1998-02-25
8 PRIOR APPLICATION NUMBER: 60/078910
9 PRIOR FILING DATE: 1998-03-20
10 PRIOR APPLICATION NUMBER: 60/083322
11 PRIOR FILING DATE: 1998-04-28
12 PRIOR APPLICATION NUMBER: 60/084600
13 PRIOR FILING DATE: 1998-05-07
14 PRIOR APPLICATION NUMBER: 60/087106
15 PRIOR FILING DATE: 1998-05-28
16 PRIOR APPLICATION NUMBER: 60/087607
17 PRIOR FILING DATE: 1998-06-02
18 PRIOR APPLICATION NUMBER: 60/087609
19 PRIOR FILING DATE: 1998-06-02
20 PRIOR APPLICATION NUMBER: 60/087759
21 PRIOR FILING DATE: 1998-06-02
22 PRIOR APPLICATION NUMBER: 60/087827
23 PRIOR FILING DATE: 1998-06-03
24 PRIOR APPLICATION NUMBER: 60/088021
25 PRIOR FILING DATE: 1998-06-04
26 PRIOR APPLICATION NUMBER: 60/088025
27 PRIOR FILING DATE: 1998-06-04
28 PRIOR APPLICATION NUMBER: 60/088026
29 PRIOR FILING DATE: 1998-06-04
30 PRIOR APPLICATION NUMBER: 60/088028
31 PRIOR FILING DATE: 1998-06-04
32 PRIOR APPLICATION NUMBER: 60/088029
33 PRIOR FILING DATE: 1998-06-04
34 PRIOR APPLICATION NUMBER: 60/088030
35 PRIOR FILING DATE: 1998-06-04
36 PRIOR APPLICATION NUMBER: 60/088033
37 PRIOR FILING DATE: 1998-06-04
38 PRIOR APPLICATION NUMBER: 60/088326
39 PRIOR FILING DATE: 1998-06-04
40 PRIOR APPLICATION NUMBER: 60/088167
41 PRIOR FILING DATE: 1998-06-05
42 PRIOR APPLICATION NUMBER: 60/088202
43 PRIOR FILING DATE: 1998-06-05
44 PRIOR APPLICATION NUMBER: 60/088212
45 PRIOR FILING DATE: 1998-06-05
46 PRIOR APPLICATION NUMBER: 60/088217
47 PRIOR FILING DATE: 1998-06-05
48 PRIOR APPLICATION NUMBER: 60/088655
49 PRIOR FILING DATE: 1998-06-09
50 PRIOR APPLICATION NUMBER: 60/088734
51 PRIOR FILING DATE: 1998-06-10
52 PRIOR APPLICATION NUMBER: 60/088738
53 PRIOR FILING DATE: 1998-06-10
54 PRIOR APPLICATION NUMBER: 60/088742
55 PRIOR FILING DATE: 1998-06-10
56 PRIOR APPLICATION NUMBER: 60/088810
57 PRIOR FILING DATE: 1998-06-10
58 PRIOR APPLICATION NUMBER: 60/088824
59 PRIOR FILING DATE: 1998-06-10
60 PRIOR APPLICATION NUMBER: 60/088826
61 PRIOR FILING DATE: 1998-06-10
62 PRIOR APPLICATION NUMBER: 60/088858
63 PRIOR FILING DATE: 1998-06-11
64 PRIOR APPLICATION NUMBER: 60/088861
65 PRIOR FILING DATE: 1998-06-11
66 PRIOR APPLICATION NUMBER: 60/088876
67 PRIOR FILING DATE: 1998-06-11
68 PRIOR APPLICATION NUMBER: 60/089105
69 PRIOR FILING DATE: 1998-06-12
70 PRIOR APPLICATION NUMBER: 60/089440
71 PRIOR FILING DATE: 1998-06-16
72 PRIOR APPLICATION NUMBER: 60/089512
73 PRIOR FILING DATE: 1998-06-16

74 PRIOR APPLICATION NUMBER: 60/089514
75 PRIOR FILING DATE: 1998-06-16
76 PRIOR APPLICATION NUMBER: 60/089532
77 PRIOR FILING DATE: 1998-06-17
78 PRIOR APPLICATION NUMBER: 60/089538
79 PRIOR FILING DATE: 1998-06-17
80 PRIOR APPLICATION NUMBER: 60/089598
81 PRIOR FILING DATE: 1998-06-17
82 PRIOR APPLICATION NUMBER: 60/089599
83 PRIOR FILING DATE: 1998-06-17
84 PRIOR APPLICATION NUMBER: 60/089600
85 PRIOR FILING DATE: 1998-06-17
86 PRIOR APPLICATION NUMBER: 60/089653
87 PRIOR FILING DATE: 1998-06-17
88 PRIOR APPLICATION NUMBER: 60/089801
89 PRIOR FILING DATE: 1998-06-18
90 PRIOR APPLICATION NUMBER: 60/089907
91 PRIOR FILING DATE: 1998-06-18
92 PRIOR APPLICATION NUMBER: 60/089908
93 PRIOR FILING DATE: 1998-06-18
94 PRIOR APPLICATION NUMBER: 60/089947
95 PRIOR FILING DATE: 1998-06-19
96 PRIOR APPLICATION NUMBER: 60/089948
97 PRIOR FILING DATE: 1998-06-19
98 PRIOR APPLICATION NUMBER: 60/089952
99 PRIOR FILING DATE: 1998-06-19
100 PRIOR APPLICATION NUMBER: 60/090246
101 PRIOR FILING DATE: 1998-06-22
102 PRIOR APPLICATION NUMBER: 60/090252
103 PRIOR FILING DATE: 1998-06-22
104 PRIOR APPLICATION NUMBER: 60/090254
105 PRIOR FILING DATE: 1998-06-22
106 PRIOR APPLICATION NUMBER: 60/090349
107 PRIOR FILING DATE: 1998-06-23
108 PRIOR APPLICATION NUMBER: 60/090355
109 PRIOR FILING DATE: 1998-06-23
110 PRIOR APPLICATION NUMBER: 60/090429
111 PRIOR FILING DATE: 1998-06-24
112 PRIOR APPLICATION NUMBER: 60/090431
113 PRIOR FILING DATE: 1998-06-24
114 PRIOR APPLICATION NUMBER: 60/090435
115 PRIOR FILING DATE: 1998-06-24
116 PRIOR APPLICATION NUMBER: 60/090444
117 PRIOR FILING DATE: 1998-06-24
118 PRIOR APPLICATION NUMBER: 60/090445
119 PRIOR FILING DATE: 1998-06-24
120 PRIOR APPLICATION NUMBER: 60/090472
121 PRIOR FILING DATE: 1998-06-24
122 PRIOR APPLICATION NUMBER: 60/090535
123 PRIOR FILING DATE: 1998-06-24
124 PRIOR APPLICATION NUMBER: 60/090540
125 PRIOR FILING DATE: 1998-06-24
126 PRIOR APPLICATION NUMBER: 60/090542
127 PRIOR FILING DATE: 1998-06-24
128 PRIOR APPLICATION NUMBER: 60/090557
129 PRIOR FILING DATE: 1998-06-24
130 PRIOR APPLICATION NUMBER: 60/090676
131 PRIOR FILING DATE: 1998-06-25
132 PRIOR APPLICATION NUMBER: 60/090678
133 PRIOR FILING DATE: 1998-06-25
134 PRIOR APPLICATION NUMBER: 60/090690
135 PRIOR FILING DATE: 1998-06-25
136 PRIOR APPLICATION NUMBER: 60/090694
137 PRIOR FILING DATE: 1998-06-25
138 PRIOR APPLICATION NUMBER: 60/090695
139 PRIOR FILING DATE: 1998-06-25
140 PRIOR APPLICATION NUMBER: 60/090696
141 PRIOR FILING DATE: 1998-06-25
142 PRIOR APPLICATION NUMBER: 60/090862
143 PRIOR FILING DATE: 1998-06-26
144 PRIOR APPLICATION NUMBER: 60/090863
145 PRIOR FILING DATE: 1998-06-26
146 PRIOR APPLICATION NUMBER: 60/091360

; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 117; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 1e-109;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSGTVCSLLLLLMLDLAMAGSSFLSPHQVQQRKSKPPAKLQPRALAGWLRPE 60
Db 1 MPSGTVCSLLLLLMLDLAMAGSSFLSPHQVQQRKSKPPAKLQPRALAGWLRPE 60
Qy 61 DGGQAEAGDELEVRNAPFDVGTKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAEAGDELEVRNAPFDVGTKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117

RESULT 5

US-09-608-810A-2
; Sequence 2, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Delsher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608.810A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-810A-2

Query Match 9.4%; Score 11; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 GSSFLSPHQH 34
Db 1 GSSFLSPHQH 11

RESULT 6

US-09-134-001C-3033
; Sequence 3033, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C

; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3033
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3033

Query Match 6.0%; Score 7; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 DGGQAEQ 67
Db 189 DGGQAEQ 195

RESULT 7

US-08-481-337A-8
; Sequence 8, Application US/08481337A
; Patent No. 5863738
; GENERAL INFORMATION:
; APPLICANT: TEN DIJKE, Peter
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: MIYAZONO, Kohel
; APPLICANT: SAMPATH, Kuber T.
; TITLE OF INVENTION: Morphogenic Protein-Specific Cell
; TITLE OF INVENTION: Surface Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/481.337A
; APPLICATION NUMBER: US/08/481.337A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: CRP-097CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-481-337A-8

Query Match 6.0%; Score 7; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVCSLLL 12
Db 133 TVCSLLL 139

RESULT 8

US-09-382-256-18
; Sequence 18, Application US/09382256A
; Patent No. 6207814
; GENERAL INFORMATION:
; APPLICANT: MIYAZONO, Kohel
; TEN DIJKE, Peter
; FRANZEN, Petra
; YAMASHITA, Hidetoshi
; HELDIN, Carl-Henrik
; TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
; HAVING SERINE THREONINE KINASE DOMAINS,
; AND THEIR USE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/382,256A
; FILING DATE: 24-Aug-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: NO. 6207814ember 17, 1993
; APPLICATION NUMBER: GB 9224057.1
; FILING DATE: NO. 6207814ember 17, 1992
; APPLICATION NUMBER: GB 9304677.9
; FILING DATE: March 8, 1993
; APPLICATION NUMBER: GB 9304680.3
; FILING DATE: March 8, 1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: May 28, 1993
; APPLICATION NUMBER: 9313763.6
; FILING DATE: July 2, 1993
; APPLICATION NUMBER: 9316099.2
; FILING DATE: August 3, 1993
; APPLICATION NUMBER: 321344.5
; FILING DATE: October 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 6207814man D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5298.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-382-256-18

Query Match 6.0%; Score 7; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVCSLLL 12
Db 133 TVCSLLL 139

RESULT 9

US-09-395-115-18
; Sequence 18, Application US/09395115
; Patent No. 6271365
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohel; Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/395,115
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,265
; FILING DATE: 30-October-1995
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-NO. 6271365ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-NO. 6271365ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-395-115-18

Query Match 6.0%; Score 7; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVCSLLL 12
Db 133 TVCSLLL 139

RESULT 10
US-08-123-934A-4
; Sequence 4, Application US/08123934A
; Patent No. 6291206
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; APPLICANT: CELESTE, Anthony J.
; APPLICANT: THIES, R. Scott
; APPLICANT: YAMAJI, No. 6291206oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123.934A
; FILING DATE: 17-SEP-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-123-934A-4

Query Match 6.0%; Score 7; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVCSLLL 12
Db 133 TVCSLLL 139

RESULT 11
US-08-436-265-18
; Sequence 18, Application US/08436265
; Patent No. 6316217
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohsei; Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436.265
; FILING DATE: 30-October-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. 6316217ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. 6316217ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-265-18

Query Match 6.0%; Score 7; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVCSLLL 12
Db 133 TVCSLLL 139

RESULT 12
US-09-679-187-18
; Sequence 18, Application US/09679187
; Patent No. 6331621
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohsei; Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/679,187
;; FILING DATE: 03-OCT-2000
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/436,265
;; FILING DATE: 30-October-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB93/02367
;; FILING DATE: 17-NO. 6331621ember-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9224057.1
;; FILING DATE: 17-NO. 6331621ember-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9304677.9
;; FILING DATE: 8-March-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9304680.3
;; FILING DATE: 8-March-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9311047.6
;; FILING DATE: 28-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9313763.6
;; FILING DATE: 2-July-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9136099.2
;; FILING DATE: 3-August-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9321344.5
;; FILING DATE: 15-October-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kohlei, Vineet
;; REGISTRATION NUMBER: 37,003
;; REFERENCE/DOCKET NUMBER: LUD 5298
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 502 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-679-187-18

Query Match 6.0%; Score 7; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVCSLLL 12
Db 133 TVCSLLL 139

RESULT 13
PCT-US94-10080-4
;; Sequence 4. Application PC/TUS9410080
;; GENERAL INFORMATION:
;; APPLICANT: GENETICS INSTITUTE, INC.
;; TITLE OF INVENTION: RECEPTOR PROTEINS
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
;; STREET: 87 Cambridgepark Drive
;; CITY: Cambridge
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02140
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/10080
;; FILING DATE: HERewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/123,934
;; FILING DATE: 17-SEP-1993
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: LAZAR, Steven R
;; REGISTRATION NUMBER: 32,618
;; REFERENCE/DOCKET NUMBER: 5203-PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 498-8260
;; TELEFAX: (617) 876-5851
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 502 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US94-10080-4
Query Match 6.0%; Score 7; DB 5; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 TVCSLLL 12
Db 133 TVCSLLL 139
RESULT 14
PCT-US95-05467-8
;; Sequence 8. Application PC/TUS9505467
;; GENERAL INFORMATION:
;; APPLICANT:
;; APPLICANT:
;; TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
;; ADDRESS: THIBEAULT
;; STREET: 53 STATE STREET
;; CITY: BOSTON
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/05467
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: PITCHER, EDMUND R.
;; REGISTRATION NUMBER: 27,829
;; REFERENCE/DOCKET NUMBER: CRP-097PC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 248-7000
;; TELEFAX: (617) 248-7100
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 502 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US95-05467-8

Query Match 6.0%; Score 7; DB 5; Length 502;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVCSLLL 12
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 Db 133 TVCSLLL 139

RESULT 15
 US-09-252-991A-27032
 ; Sequence 27032, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 27032
 ; LENGTH: 552
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-27032

Query Match 6.0%; Score 7; DB 4; Length 552;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 DGGQAE 67
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 Db 22 DGGQAE 28

Search completed: September 11, 2003, 17:58:12
 Job time : 41.0428 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:27:22 ; Search time 123.257 Seconds
(without alignments)
150.669 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 117

Sequence: 1 MPSPTGVCVSLLLGLMLDL.....LGKFLQDLWEAKEAPADK 117

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 117 | 100.0 | 117 | 20 | AAW87991 Protein designated |
| 2 | 117 | 100.0 | 117 | 21 | AA187236 Human signal pepti |
| 3 | 117 | 100.0 | 117 | 22 | AAAM38890 Human polypeptide |
| 4 | 117 | 100.0 | 117 | 22 | AAAB62649 Human zsig33 polyp |
| 5 | 117 | 100.0 | 117 | 22 | AAAB20101 zsig33 protein. H |
| 6 | 117 | 100.0 | 117 | 22 | AAAB60511 Human ghrelin prep |
| 7 | 117 | 100.0 | 117 | 23 | ABH78319 Amino acid sequenc |
| 8 | 117 | 100.0 | 117 | 23 | AAE23838 Human zsig33 prote |
| 9 | 117 | 100.0 | 117 | 23 | AAE15883 Human zsig33 prote |

| | | | | | |
|----|-----|-------|-----|----|------------------------------|
| 10 | 117 | 100.0 | 117 | 24 | ABU66790 Human PRO polypept |
| 11 | 117 | 100.0 | 117 | 24 | ABU67066 Human secreted/tra |
| 12 | 117 | 100.0 | 117 | 24 | ABU59871 Novel secreted and |
| 13 | 117 | 100.0 | 117 | 24 | ABU59124 Novel human secret |
| 14 | 117 | 100.0 | 117 | 24 | ABU59271 Human secreted/tra |
| 15 | 117 | 100.0 | 117 | 24 | ABU59420 Novel human secret |
| 16 | 117 | 100.0 | 117 | 24 | ABU60555 Human secreted/tra |
| 17 | 117 | 100.0 | 117 | 24 | ABU58046 Human PRO polypept |
| 18 | 117 | 100.0 | 117 | 24 | ABU58977 Human secreted/tr |
| 19 | 117 | 100.0 | 117 | 24 | AAE33409 Human preprohrell |
| 20 | 117 | 100.0 | 117 | 24 | ABU13937 Human PRO1066 poly |
| 21 | 117 | 100.0 | 117 | 24 | ABU10892 Human PRO polypept |
| 22 | 117 | 100.0 | 118 | 21 | AA166708 Membrane-bound pro |
| 23 | 117 | 100.0 | 118 | 22 | AAU12392 Human PRO1066 poly |
| 24 | 117 | 100.0 | 118 | 22 | AAE55231 Human PRO1066 (UNQ |
| 25 | 117 | 100.0 | 126 | 22 | AAW40676 Human polypeptide |
| 26 | 81 | 69.2 | 116 | 22 | AAAB60517 Human des-Gln14-gh |
| 27 | 75 | 64.1 | 91 | 24 | AAE33410 Human exon 3-delet |
| 28 | 28 | 23.9 | 28 | 22 | AAAB60509 Human ghrelin, SEQ |
| 29 | 28 | 23.9 | 28 | 23 | ABB09532 Human ghrelin. Ho |
| 30 | 28 | 23.9 | 28 | 23 | AAE19032 Human ghrelin pept |
| 31 | 26 | 22.2 | 28 | 23 | AAE19039 Human ghrelin pept |
| 32 | 25 | 21.4 | 25 | 23 | AAE23842 Human zsig33-beta |
| 33 | 25 | 21.4 | 25 | 23 | AAE15887 Human zsig33-beta |
| 34 | 25 | 21.4 | 28 | 23 | AAE19021 Human ghrelin pept |
| 35 | 25 | 21.4 | 28 | 23 | AAE19027 Human ghrelin pept |
| 36 | 25 | 21.4 | 28 | 23 | AAE19028 Human ghrelin pept |
| 37 | 25 | 21.4 | 28 | 23 | AAE19029 Human ghrelin pept |
| 38 | 25 | 21.4 | 28 | 23 | AAE19030 Human ghrelin pept |
| 39 | 25 | 21.4 | 28 | 23 | AAE19031 Human ghrelin pept |
| 40 | 25 | 21.4 | 28 | 23 | AAE19033 Human ghrelin pept |
| 41 | 25 | 21.4 | 28 | 23 | AAE19034 Human ghrelin pept |
| 42 | 25 | 21.4 | 28 | 23 | AAE19035 Human ghrelin pept |
| 43 | 25 | 21.4 | 28 | 23 | AAE19036 Human ghrelin pept |
| 44 | 25 | 21.4 | 28 | 23 | AAE19037 Human ghrelin pept |
| 45 | 25 | 21.4 | 28 | 23 | AAE19038 Human ghrelin pept |

ALIGNMENTS

RESULT 1
AAW87991
ID AAW87991 standard; Protein; 117 AA.
XX
AC AAW87991;
XX
DT 07-APR-1999 (first entry)
XX
DE Protein designated zsig33.
XX
KW Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
KW nutrient absorption regulation; obesity; metabolic disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23 "signal peptide"
FT Protein 24..117
FT /note= "mature protein"
XX
PN WO9842840-A1.
XX
PD 01-OCT-1998.
XX
PF 23-MAR-1998; 98WO-US05620.
XX
PR 24-MAR-1997; 97US-0822897.
PR 24-MAR-1997; 97US-0041102.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX


```
XX OS Homo sapiens.
XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000WO-US34263.
XX PR 21-JAN-2000; 2000US-0488725.
XX PR 23-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.
XX PR 29-NOV-2000; 2000US-0727344.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX PI
XX DR WPI: 2001-442253/47.
XX DR N-PSDB; AAI58046.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries -
XX PS Example 3; SEQ ID NO 2035; 10078pp; English.
XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
XX CC the encoded polypeptides (AAI38642-AAI42213) with nootropic,
XX CC immunosuppressant and cytosolic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression,
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX CC C.N.S disorders.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification.
XX SQ Sequence 117 AA:
Query Match 100.0%; Score 117; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MFSPTVCSLLLLGLMLDLAMAGSFLSPFHQRVQQRKESKPPAKLPRLAGWLRLPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEAKAPADK 117
DB 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEAKAPADK 117
RESULT 4
AAB62649
ID AAB62649 standard; Protein; 117 AA.
XX AC AAB62649;
XX DT 23-JUL-2001 (first entry)
XX DE Human zsig33 polypeptide.
```

```
XX KW zsig33; signal transduction; hormone; enzyme; neural development;
XX KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
XX KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
XX KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
XX OS G-protein coupled receptor.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT 24..37
XX FT Peptide
XX FT /note= "specifically claimed fragment that binds to
XX FT the GHS-R"
XX PN WO200138355-A2.
XX PD 31-MAY-2001.
XX PF 22-NOV-2000; 2000WO-US32074.
XX PR 22-NOV-1999; 99US-0166765.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX PI WPI: 2001-355879/37.
XX DR N-PSDB; AAF83678.
XX PT Forming reversible peptide receptor complex for purifying cell and
XX PT peptides, stimulating signal transduction and modulating hormone
XX PT secretion, involves contacting a receptor with zsig33 polypeptide -
XX PS Claim 1; Page 93-94; 111pp; English.
XX CC The invention relates to a method of forming a reversible peptide-
XX CC receptor complex that involves providing an immobilized receptor, and
XX CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
XX CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
XX CC is useful for purifying cells, purifying a peptide, stimulating signal
XX CC transduction in a cell expressing a receptor. It is also useful for
XX CC modulating secretion of hormones, neural development and/or utilization,
XX CC gastric contractility, nutrient uptake, secretion of digestive and
XX CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
XX CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
XX CC hormone secretion in a mammal having a disease associated with abnormal
XX CC levels of growth hormone, such as osteoporosis, bone repair, bone
XX CC remodeling, low osteoblast levels, cartilage repair and remodeling,
XX CC skeletal dysplasia, immune suppression, obesity, growth retardation,
XX CC protein catabolic responses after surgery, cachexia, protein loss,
XX CC dwarfism, wound healing and ovulation induction, treating a mammal having
XX CC a metabolic disorder requiring neurological feedback, such as satiety
XX CC regulation, glucose absorption and metabolism and neuropathy-associated
XX CC gastrointestinal disorders, and stimulating glucose-induced insulin
XX CC release in a mammal. The present sequence represents the human zsig33
XX CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
XX SQ Sequence 117 AA;
Query Match 100.0%; Score 117; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEAKAPADK 117
RESULT 5
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AAB20101
ID AAB20101 standard; Protein; 117 AA.
XX AAB20101;
AC AAB20101;
XX 23-APR-2001 (first entry)
DT 23-APR-2001 (first entry)
XX zsig33 protein.
DE zsig33 protein.
XX SGP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
KW nutritional absorption modulator; growth hormone secretagogue;
KW therapy; human.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..23
FT /label= Signal_peptide
FT Protein 24..117
FT /label= Mature_protein
FT Peptide 24..34
FT /label= SGP_peptide
FT /note= "this peptide is claimed in Claim 1"
XX
XX WO200100830-A1.
XX
XX 04-JAN-2001.
XX
XX 30-JUN-2000; 2000WO-US18306.
XX
XX 30-JUN-1999; 99US-0345157.
XX (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX WPI; 2001-123010/13.
XX N-PSDB; AAF30033.
XX Novel variants of SGP peptides for modulating contractility in
PT duodenum or jejunum tissue, pancreatic secretion of hormones and
PT digestive enzymes, inducing growth hormone secretion or modulating
PT gastric emptying -
XX
XX Disclosure; 54; 61pp; English.
XX
XX The present sequence is that of zsig33, a secreted protein with
CC homology to motilin (see AAB20102). zsig33 is expressed at high
CC levels in the stomach, and at lower levels in the small intestine
CC and pancreas. A novel peptide fragment of zsig33, termed SGP (see
CC AAB20100), is claimed. SGP is a ligand for growth hormone
CC secretagogue receptor, and is therefore useful for modulating
CC secretion of growth hormone and insulin like growth factor 1.
CC SGP, and variant SGP peptides, are used in claimed methods for
CC stimulating contractility in duodenum or jejunum tissue,
CC modulating pancreatic secretion of hormones and digestive enzymes,
CC inducing growth hormone secretion, and modulating gastric emptying.
XX
XX Sequence 117 AA;
SQ

Query Match 100.0%; Score 117; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPDHQVQQRKESKPPAKLQPRALAGWLRLPE 60
Oy 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117

RESULT 6
AAB60511
ID AAB60511 standard; Protein; 117 AA.
XX AAB60511;
AC AAB60511;
XX 24-APR-2001 (first entry)
DT 24-APR-2001 (first entry)
XX Human ghrelin preproprotein, SEQ ID NO:5.
DE Human ghrelin preproprotein, SEQ ID NO:5.
XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
KW calcium concentration elevation; infant growth disorder;
KW growth hormone deficiency.
XX Homo sapiens.
OS Homo sapiens.
XX WO200107475-A1.
XX 01-FEB-2001.
XX 24-JUL-2000; 2000WO-JP04907.
XX 23-JUL-1999; 99JP-0210002.
XX 29-NOV-1999; 99JP-0338841.
XX 26-APR-2000; 2000JP-0126623.
XX (KANG/) KANGAWA K.
XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
PI WPI; 2001-159704/16.
XX N-PSDB; AAF59645.
XX New peptide compounds which induce growth hormone secretion and
PT elevate cell calcium concentrations, useful in treatment and diagnosis
PT of infant growth disorders -
XX
XX Claim 3; Page 182; 210pp; Japanese.
XX
XX The invention relates to a novel peptide compound or its salt which
CC induces the secretion of growth hormone and/or elevates calcium ion
CC concentration in cells. The peptides are ghrelin homologues and are
CC characterised in that at least one amino acid has been substituted by
CC a modified amino acid and/or a non-amino acid compound. The invention
CC also encompasses the unmodified peptides: the DNA encoding the peptides;
CC vectors and host cells comprising such DNA; a method of producing the
CC peptides comprising recombinant production, optionally followed by
CC chemical modification; an antibody specific for a peptide of the
CC invention; and an assay and kit for detecting the peptides. The peptides
CC of the invention are useful for treating and/or diagnosing diseases
CC caused by a deficiency in growth hormone expression or activity. In
CC particular, they are useful for promoting infant growth due to growth
CC hormone deficiency. The compounds of the invention are safe with
CC no accompanying side effects. The present sequence represents a
CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
CC of the invention.
XX
XX Sequence 117 AA;
SQ

Query Match 100.0%; Score 117; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPDHQVQQRKESKPPAKLQPRALAGWLRLPE 60
Oy 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117
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RESULT 7

ABB78319
ID ABB78319 standard; Protein; 117 AA.

XX AC ABB78319;
XX DT 05-DEC-2002 (first entry)
XX DE Human zsig33 protein.
XX KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
XX KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
XX KW protein therapy; gastrointestinal; endocrine; anabolic.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Peptide 1..23
XX FT /note= "signal peptide"
XX FT Protein 24..119
XX FT /note= "mature protein"

XX US6420521-B1.
XX PN 16-JUL-2002.
XX PD 30-JUN-2000; 2000US-0608810.
XX PF 30-JUN-1999; 99US-141592P.
XX PR (ZYMO) ZYMOGENETICS INC.
XX PA Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX PI WPI; 2002-634794/68.
XX DR N-PSDB; ABV72214.

XX PT New Short Gastrointestinal Peptide, which has homology to motilin,
XX PT useful for preventing, diagnosing and treating gastrointestinal
XX PT disorders -
XX PS Disclosure; Columns 39-40; 23pp; English.

XX CC The present sequence represents human zsig33. The specification describes
XX CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.
XX CC SGIP has homology to motilin. The SGIP peptide may be used in the
XX CC prevention, diagnosis and treatment of diseases associated with
XX CC inappropriate SGIP expression. For example, SGIP may be used to treat
XX CC disorders associated with decreased expression by rectifying mutations
XX CC or deletions in a patient's genome that affect the activity of SGIP by
XX CC expressing inactive proteins or to supplement the patients own production
XX CC of SGIP. SGIP may also be used as an antigen in the production of
XX CC antibodies against SGIP and in assays to identify modulators of SGIP
XX CC expression and activity. The anti-SGIP antibodies, agonists and
XX CC antagonists may also be used to regulate expression and activity. The
XX CC anti-SGIP antibodies may also be used as diagnostic agents for detecting
XX CC the presence of SGIP in samples.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 117; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPTVCSLLLLGLMLDLAMAGSFLSPHEHQVQQRKSKPPAKLPQPRALAGWLRLPE 60
DB 1 MPSPTVCSLLLLGLMLDLAMAGSFLSPHEHQVQQRKSKPPAKLPQPRALAGWLRLPE 60

QY 61 DGGQAEAGDELEVRNAPFDVGIKLSGVQYQHQHQAALGKFLQDILWEEAKAPADK 117
DB 61 DGGQAEAGDELEVRNAPFDVGIKLSGVQYQHQHQAALGKFLQDILWEEAKAPADK 117

RESULT 8
AAE23838
ID AAE23838 standard; Protein; 117 AA.

XX AC

AAE23838;

XX DT 10-SEP-2002 (first entry)

XX DE Human zsig33 protein.

XX KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
XX KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
XX KW protein therapy; gastrointestinal; endocrine; anabolic.

XX OS Homo sapiens.

XX PN US2002055156-A1.

XX PD 09-MAY-2002.

XX PF 10-MAY-2001; 2001US-0853253.

XX PR 11-MAY-2000; 2000US-203300P.

XX PA (JASP/) JASPERS S R.

XX PA (SHEP/) SHEPPARD P O.

XX PA (DEIS/) DEISHER T A.

XX PA (BISH/) BISHOP P D.

XX PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI; 2002-443750/47.

XX DR N-PSDB; AAD38238.

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
XX PT contractility, nutrient uptake, growth hormones and/or secretion of
XX PT digestive/pancreatic enzymes and hormones -
XX PS Disclosure; Page 27; 34pp; English.

XX CC The invention relates to zsig33-like peptides and their corresponding
XX CC nucleic acids and methods for modulating gastric contractility, nutrient
XX CC uptake, growth hormones, secretion of digestive enzymes and hormones.
XX CC The sequences of the invention are used in the prevention, diagnosis and
XX CC treatment of diseases associated with inappropriate zsig33 expression.
XX CC The nucleic acids of the invention and their complements are used as
XX CC DNA probes in diagnostic assays to detect and quantitate the presence
XX CC of similar nucleic acids in samples, and therefore which patients may be
XX CC in need of restorative therapy. The zsig33 peptides are used as antigens
XX CC in the production of antibodies against zsig33 and in assays to identify
XX CC modulators of zsig33 expression and activity. The anti-zsig33 antibodies
XX CC and antagonists are used to down regulate expression and activity. The
XX CC anti-zsig33 antibodies are also used as diagnostic agents for detecting
XX CC the presence of zsig33 in samples (e.g. by enzyme linked immunosorbent
XX CC assay (ELISA)). The peptides and nucleic acids of the invention are used
XX CC to modulate gastric contractility, nutrient uptake, growth hormones, the
XX CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
XX CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
XX CC and zsig33-like peptide is used in protein therapy. The present sequence
XX CC is human zsig33 protein.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 117; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPTVCSLLLLGLMLDLAMAGSFLSPHEHQVQQRKSKPPAKLPQPRALAGWLRLPE 60
DB 1 MPSPTVCSLLLLGLMLDLAMAGSFLSPHEHQVQQRKSKPPAKLPQPRALAGWLRLPE 60

QY 61 DGGQAEAGDELEVRNAPFDVGIKLSGVQYQHQHQAALGKFLQDILWEEAKAPADK 117
DB 61 DGGQAEAGDELEVRNAPFDVGIKLSGVQYQHQHQAALGKFLQDILWEEAKAPADK 117

| | | | | | | | |
|-----------|--|---|-----------------------|-----------------|---------------------|-----------|-------------|
| XX | Sequence | 117 AA; | Query Match | 100.0%; | Score 117; | DB 23; | Length 117; |
| SQ | | | Best Local Similarity | 100.0%; | Pred. No. 2.3e-101; | | |
| | | | Matches 117; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | MPSPCTVCSLLLLGMLWLDLAMAGSSFLSPESHQVRVQQRKESKPPAKLQPRALAGWLRLPE 60 | | | | | |
| Db | 1 | MPSPCTVCSLLLLGMLWLDLAMAGSSFLSPESHQVRVQQRKESKPPAKLQPRALAGWLRLPE 60 | | | | | |
| QY | 61 | DGGOAEGAEDLEVRFNAPEDVGKLSGVQYQHSQALGKFLQDILWEEAKEAPADK 117 | | | | | |
| Db | 61 | DGGOAEGAEDLEVRFNAPEDVGKLSGVQYQHSQALGKFLQDILWEEAKEAPADK 117 | | | | | |
| RESULT 10 | | | | | | | |
| ABU66790 | | | | | | | |
| ID | ABU66790 | standard; Protein; 117 AA. | | | | | |
| XX | | | | | | | |
| AC | ABU66790; | | | | | | |
| XX | | | | | | | |
| DT | 23-MAY-2003 | (first entry) | | | | | |
| XX | | | | | | | |
| DE | Human PRO polypeptide #221. | | | | | | |
| XX | | | | | | | |
| KW | Human; PRO polypeptide; secreted and transmembrane protein; | | | | | | |
| KW | tumour necrosis factor-alpha; TNF-alpha; blood; proliferation; | | | | | | |
| KW | differentiation; chondrocyte; tumour; genetic disorder; | | | | | | |
| KW | cytostatic. | | | | | | |
| XX | | | | | | | |
| OS | Homo sapiens. | | | | | | |
| XX | | | | | | | |
| PN | US2003036180-A1. | | | | | | |
| XX | | | | | | | |
| PD | 20-FEB-2003. | | | | | | |
| XX | | | | | | | |
| PF | 09-MAY-2002; 2002US-0143114. | | | | | | |
| XX | | | | | | | |
| PR | 31-MAR-1997; 97WO-US05230. | | | | | | |
| PR | 12-JUN-1998; 98WO-US12456. | | | | | | |
| PR | 14-JUL-1998; 98WO-US14552. | | | | | | |
| PR | 28-AUG-1998; 98WO-US17888. | | | | | | |
| PR | 10-SEP-1998; 98WO-US18824. | | | | | | |
| PR | 14-SEP-1998; 98WO-US19093. | | | | | | |
| PR | 14-SEP-1998; 98WO-US19177. | | | | | | |
| PR | 16-SEP-1998; 98WO-US19330. | | | | | | |
| PR | 17-SEP-1998; 98WO-US19437. | | | | | | |
| PR | 07-OCT-1998; 98WO-US21141. | | | | | | |
| PR | 29-OCT-1998; 98WO-US22991. | | | | | | |
| PR | 29-OCT-1998; 98WO-US22992. | | | | | | |
| PR | 20-NOV-1998; 98WO-US24855. | | | | | | |
| PR | 01-DEC-1998; 98WO-US25108. | | | | | | |
| PR | 05-JAN-1999; 99WO-US00106. | | | | | | |
| PR | 08-MAR-1999; 99WO-US05028. | | | | | | |
| PR | 10-MAR-1999; 99WO-US05190. | | | | | | |
| PR | 20-APR-1999; 99WO-US08615. | | | | | | |
| PR | 14-MAY-1999; 99WO-US10733. | | | | | | |
| PR | 02-JUN-1999; 99WO-US12252. | | | | | | |
| PR | 01-SEP-1999; 99WO-US20111. | | | | | | |
| PR | 08-SEP-1999; 99WO-US20594. | | | | | | |
| PR | 13-SEP-1999; 99WO-US20944. | | | | | | |
| PR | 15-SEP-1999; 99WO-US21090. | | | | | | |
| PR | 15-SEP-1999; 99WO-US21547. | | | | | | |
| PR | 05-OCT-1999; 99WO-US23089. | | | | | | |
| PR | 29-NOV-1999; 99WO-US28214. | | | | | | |
| PR | 30-NOV-1999; 99WO-US28313. | | | | | | |
| PR | 30-NOV-1999; 99WO-US28409. | | | | | | |
| PR | 01-DEC-1999; 99WO-US28301. | | | | | | |
| PR | 01-DEC-1999; 99WO-US28634. | | | | | | |
| PR | 02-DEC-1999; 99WO-US28551. | | | | | | |
| PR | 02-DEC-1999; 99WO-US28564. | | | | | | |

PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 98WO-US00106.
PR 08-MAR-1999; 98WO-US05028.
PR 10-MAR-1999; 98WO-US05190.
PR 20-APR-1999; 98WO-US08615.
PR 14-MAY-1999; 98WO-US10733.
PR 02-JUN-1999; 98WO-US12252.
PR 01-SEP-1999; 98WO-US20111.
PR 08-SEP-1999; 98WO-US20594.
PR 13-SEP-1999; 98WO-US20944.
PR 15-SEP-1999; 98WO-US21090.
PR 15-SEP-1999; 98WO-US21547.
PR 05-OCT-1999; 98WO-US23089.
PR 29-NOV-1999; 98WO-US28214.
PR 30-NOV-1999; 98WO-US28313.
PR 30-NOV-1999; 98WO-US28409.
PR 01-DEC-1999; 98WO-US28301.
PR 01-DEC-1999; 98WO-US28634.
PR 02-DEC-1999; 98WO-US28551.
PR 02-DEC-1999; 98WO-US28564.
PR 02-DEC-1999; 98WO-US28564.
PR 16-DEC-1999; 98WO-US30095.
PR 20-DEC-1999; 98WO-US30911.
PR 20-DEC-1999; 98WO-US30999.
PR 22-DEC-1999; 98WO-US30720.
PR 30-DEC-1999; 98WO-US31243.
PR 30-DEC-1999; 98WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04114.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23322.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.

PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX (GETH) GENENTECH INC.
PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-331925/31.
DR N-PSDB; ACA04244.
XX
XX New secreted and transmembrane nucleic acids and polypeptides,
PT designated as PRO, useful for treating inflammation, organ failure,
PT atherosclerosis, cardiac injury, infertility, birth defects, premature
PT aging, AIDS, or cancer -
XX
PS Claim 12; Fig 442; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid
CC further comprises the full-length coding sequence of the DNA deposited
CC under American Type Culture Collection (ATCC) accession number in a list
CC given in the specification. Also included are vectors and host
CC cells for producing PRO proteins. PRO fusion proteins, anti-PRO
CC antibodies, PRO extracellular domains and mature sequences, methods
CC of detecting PRO proteins, methods for stimulating the release of
CC TNF-alpha (tumour necrosis factor alpha) from human blood,
CC and the proliferation of differentiation of chondrocyte cells, the
CC proliferation of, or gene expression in pericyte cells, the release or
CC proteoglycans from cartilage, proliferation of inner ear utricular
CC supporting cells, the proliferation of T-lymphocyte cells, the release
CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
CC proliferation of endothelial cells), a method for modulating the uptake
CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
CC a method for inhibiting the binding of A-peptide to factor VIIa,
CC or the differentiation of adipocyte cells, a method for detecting the
CC presence of a tumour in a mammal and an oligonucleotide probe derived
CC from any of the nucleotide sequences cited above. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
CC diabetic complications. The nucleic acids are useful as hybridisation
CC probes, in chromosome and gene mapping, and in generating antisense RNA
CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors. Both are useful in tissue typing.
CC
XX The present sequence represents a PRO protein of the invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 117; DB 24; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPSCTVCSLLLLGLMLDLAMAGSSFLSPHEQVQQRKESKPKLQPRALAGWLRLPE 60
 Db 1 MPSCTVCSLLLLGLMLDLAMAGSSFLSPHEQVQQRKESKPKLQPRALAGWLRLPE 60

OY 61 DGGQGAEGADELVEFRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
 Db 61 DGGQGAEGADELVEFRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 12

ABU59871
 ID ABU59871 standard; Protein; 117 AA.

XX AC ABU59871;

XX DT 13-MAY-2003 (first entry)

XX DE Novel secreted and transmembrane protein PRO1066.

XX KW Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.

XX OS Homo sapiens.

XX PN US2003017563-A1.

XX PD 23-JAN-2003.

XX PF 07-MAY-2002; 2002US-0140808.

XX PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US22089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 10-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806869.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.

XX (GETH) GENENTECH INC.

XX PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX

DR WPI; 2003-148238/14.
XX N-PSDB; ABX89361.
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
XX treatments -
XX
PS Claim 12; Fig 442; 659pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical insufficiency disorders. PRO1154 and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC is the amino acid sequence of a novel human PRO protein.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 117; DB 24; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHEHQVQQRKESKPPAKLPRLAGWLRLPE 60
Db 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHEHQVQQRKESKPPAKLPRLAGWLRLPE 60

QY 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQHQSHQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQHQSHQALGKFLQDILWEEAKEAPADK 117

RESULT 13
ABU59124
ID ABU59124 standard; Protein; 117 AA.
XX
AC ABU59124;
XX
XX 28-APR-2003 (first entry)
XX
XX Novel human secreted or transmembrane protein PRO1066.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;

KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW -chondrocyte redifferentiation; sports injury; arthritis.
XX Homo sapiens.
OS
XX US2002132252-A1.
XX
XX 19-SEP-2002.
XX
XX 14-NOV-2001; 2001US-0990442.
XX
XX 05-NOV-1997; 97WO-US20069.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 06-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
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PR 28-FEB-2001; 2001WO-US06520.
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PR 13-NOV-1997; 97US-065186P.
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 PR 28-AUG-2001; 2001US-0941992.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber K, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kijavir IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;
 PI Zhang Z;
 XX
 DR WPI: 2003-247083/24.
 DR N-PSDB; ABX80294.
 XX
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments -
 XX
 PS Claim 12: Fig 186; 648pp: English.
 XX
 CC The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with

CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and
 CC are thus useful for treating sports injuries, and arthritis. This
 CC is the amino acid sequence of a novel human PRO protein.
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 DT 22-APR-2003 (first entry)
 XX
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 KW diagnostic; biosensor; bioeffector; tumour; therapeutic;
 KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;
 KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.
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 OS Homo sapiens.
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 PD 06-FEB-2003.
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 PF 15-NOV-2001; 2001US-0997428.
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Query Match      100.0%; Score 117; DB 24; Length 117;
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RESULT 15
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ID ABU59420 standard; Protein; 117 AA.
XX AC ABU59420;
XX DT 22-APR-2003 (first entry)
XX DE Novel human secreted or transmembrane protein PRO1184.
XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disease;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX OS Homo sapiens.
XX PN US200307985-A1.
XX PD 06-FEB-2003.
XX PF 14-NOV-2001; 2001US-0990562.
XX PR 05-NOV-1997; 97WO-US20069.
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| PR | 20-JUL-1998 | 98US-0933399 |
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| PR | 20-AUG-1998 | 98US-0972189 |
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 17:55:57 ; Search time 71.9519 Seconds
(without alignments)
237.266 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 117

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Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 117 | 100.0 | 117 | 9 US-09-853-253-2 | Sequence 2, Appli |
| 3 | 117 | 100.0 | 117 | 9 US-09-989-722-268 | Sequence 268, App |
| 4 | 117 | 100.0 | 117 | 9 US-09-989-723-268 | Sequence 268, App |
| 5 | 117 | 100.0 | 117 | 9 US-09-989-279-268 | Sequence 268, App |
| 6 | 117 | 100.0 | 117 | 9 US-09-989-727-268 | Sequence 268, App |
| 7 | 117 | 100.0 | 117 | 10 US-09-989-731-268 | Sequence 268, App |
| 8 | 117 | 100.0 | 117 | 10 US-09-989-732-268 | Sequence 268, App |
| 9 | 117 | 100.0 | 117 | 10 US-09-991-073-268 | Sequence 268, App |
| 10 | 117 | 100.0 | 117 | 10 US-09-990-442-268 | Sequence 268, App |
| 11 | 117 | 100.0 | 117 | 10 US-09-991-163-268 | Sequence 268, App |
| 12 | 117 | 100.0 | 117 | 10 US-09-993-604-268 | Sequence 268, App |
| 13 | 117 | 100.0 | 117 | 10 US-09-990-456-268 | Sequence 268, App |
| 14 | 117 | 100.0 | 117 | 10 US-09-989-721-268 | Sequence 268, App |
| 15 | 117 | 100.0 | 117 | 10 US-09-992-598-268 | Sequence 268, App |

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| 19 | 117 | 100.0 | 117 | 10 US-09-991-181-268 | Sequence 268, App |
| 20 | 117 | 100.0 | 117 | 10 US-09-989-730-268 | Sequence 268, App |
| 21 | 117 | 100.0 | 117 | 10 US-09-990-436-268 | Sequence 268, App |
| 22 | 117 | 100.0 | 117 | 10 US-09-993-687-268 | Sequence 268, App |
| 23 | 117 | 100.0 | 117 | 11 US-09-989-734-268 | Sequence 268, App |
| 24 | 117 | 100.0 | 117 | 11 US-09-997-653-268 | Sequence 268, App |
| 25 | 117 | 100.0 | 117 | 11 US-09-993-667-268 | Sequence 268, App |
| 26 | 117 | 100.0 | 117 | 11 US-09-997-428-268 | Sequence 268, App |
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| 29 | 117 | 100.0 | 117 | 11 US-09-990-562-268 | Sequence 268, App |
| 30 | 117 | 100.0 | 117 | 11 US-09-990-711-268 | Sequence 268, App |
| 31 | 117 | 100.0 | 117 | 11 US-09-989-726-268 | Sequence 268, App |
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| 35 | 117 | 100.0 | 117 | 11 US-09-997-514-268 | Sequence 268, App |
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| 38 | 117 | 100.0 | 117 | 11 US-09-990-726-268 | Sequence 268, App |
| 39 | 117 | 100.0 | 117 | 11 US-09-997-559-268 | Sequence 268, App |
| 40 | 117 | 100.0 | 117 | 11 US-09-997-601-268 | Sequence 268, App |
| 41 | 117 | 100.0 | 117 | 11 US-09-990-443-268 | Sequence 268, App |
| 42 | 117 | 100.0 | 117 | 11 US-09-991-854-268 | Sequence 268, App |
| 43 | 117 | 100.0 | 117 | 11 US-09-997-628-268 | Sequence 268, App |
| 44 | 117 | 100.0 | 117 | 11 US-09-997-683-268 | Sequence 268, App |
| 45 | 117 | 100.0 | 117 | 11 US-09-989-729A-268 | Sequence 268, App |

ALIGNMENTS

RESULT 1

US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. US20010041791A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 117 amino acids
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

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Best Local Similarity 100.0%; Pred. No. 7.5e-104;
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; Sequence 2, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: 2sig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
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; ORGANISM: Homo sapiens
US-09-853-253-2

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; Sequence 268, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey

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; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 117; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.5e-104;
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; Sequence 268, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zenin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C62
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PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-06-05
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Query Match 100.0%; Score 117; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 7.5e-104; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5

US-09-989-279-268

; Sequence 268, Application US/09989279

; Patent No. US20020072496A1

GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Pan, James

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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
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 ; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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Query Match 100.0%; Score 117; DB 9; Length 117;
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RESULT 7
 ; Sequence 268, Application US/09989731
 ; Patent No. US20020103125A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
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 ; APPLICANT: Tumas, Daniel
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 ; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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; APPLICANT: Zhang, Zemin
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| : | PRIOR FILING DATE: | 1998-06-24 |
| : | PRIOR APPLICATION NUMBER: | 60/090472 |
| : | PRIOR FILING DATE: | 1998-06-24 |
| : | PRIOR APPLICATION NUMBER: | 60/090535 |
| : | PRIOR FILING DATE: | 1998-06-24 |
| : | PRIOR APPLICATION NUMBER: | 60/090540 |
| : | PRIOR FILING DATE: | 1998-06-24 |
| : | PRIOR APPLICATION NUMBER: | 60/090542 |
| : | PRIOR FILING DATE: | 1998-06-24 |
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| : | PRIOR FILING DATE: | 1998-06-24 |
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| : | PRIOR APPLICATION NUMBER: | 60/090690 |
| : | PRIOR FILING DATE: | 1998-06-25 |
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| : | PRIOR FILING DATE: | 1998-06-25 |
| : | PRIOR APPLICATION NUMBER: | 60/090696 |

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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 117; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.5e-104;
Matches 117; Conservative 0; Mismatches 0; Gaps 0;

QY      1  MPSPGTVCSLLLLGLMLWLDLAMAGSSFLSPHEHQRVQQRKSKPPAKLQPRALAGWLRPE 60
Db      1  MPSPGTVCSLLLLGLMLWLDLAMAGSSFLSPHEHQRVQQRKSKPPAKLQPRALAGWLRPE 60

QY      61  DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSOALGKFLQDILWEEAKEAPADK 117
Db      61  DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSOALGKFLQDILWEEAKEAPADK 117

RESULT 10
US-09-990-442-268
; Sequence 268, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

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| 1 | PRIOR FILING DATE: 1998-06-16 | |
| 2 | PRIOR APPLICATION NUMBER: 60/089512 | |
| 3 | PRIOR FILING DATE: 1998-06-16 | |
| 4 | PRIOR APPLICATION NUMBER: 60/089514 | |
| 5 | PRIOR FILING DATE: 1998-06-16 | |
| 6 | PRIOR APPLICATION NUMBER: 60/089532 | |
| 7 | PRIOR FILING DATE: 1998-06-17 | |
| 8 | PRIOR APPLICATION NUMBER: 60/089538 | |
| 9 | PRIOR FILING DATE: 1998-06-17 | |
| 10 | PRIOR APPLICATION NUMBER: 60/089598 | |
| 11 | PRIOR FILING DATE: 1998-06-17 | |
| 12 | PRIOR APPLICATION NUMBER: 60/089599 | |
| 13 | PRIOR FILING DATE: 1998-06-17 | |
| 14 | PRIOR APPLICATION NUMBER: 60/089600 | |
| 15 | PRIOR FILING DATE: 1998-06-17 | |
| 16 | PRIOR APPLICATION NUMBER: 60/089653 | |
| 17 | PRIOR FILING DATE: 1998-06-17 | |
| 18 | PRIOR APPLICATION NUMBER: 60/089801 | |
| 19 | PRIOR FILING DATE: 1998-06-18 | |
| 20 | PRIOR APPLICATION NUMBER: 60/089907 | |
| 21 | PRIOR FILING DATE: 1998-06-18 | |
| 22 | PRIOR APPLICATION NUMBER: 60/089908 | |
| 23 | PRIOR FILING DATE: 1998-06-18 | |
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| 25 | PRIOR FILING DATE: 1998-06-19 | |
| 26 | PRIOR APPLICATION NUMBER: 60/089948 | |
| 27 | PRIOR FILING DATE: 1998-06-19 | |
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| 29 | PRIOR FILING DATE: 1998-06-19 | |
| 30 | PRIOR APPLICATION NUMBER: 60/090246 | |
| 31 | PRIOR FILING DATE: 1998-06-22 | |
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| 36 | PRIOR APPLICATION NUMBER: 60/090349 | |
| 37 | PRIOR FILING DATE: 1998-06-23 | |
| 38 | PRIOR APPLICATION NUMBER: 60/090355 | |
| 39 | PRIOR FILING DATE: 1998-06-23 | |
| 40 | PRIOR APPLICATION NUMBER: 60/090429 | |
| 41 | PRIOR FILING DATE: 1998-06-24 | |
| 42 | PRIOR APPLICATION NUMBER: 60/090431 | |
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| 44 | PRIOR APPLICATION NUMBER: 60/090435 | |
| 45 | PRIOR FILING DATE: 1998-06-24 | |
| 46 | PRIOR APPLICATION NUMBER: 60/090444 | |
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| 48 | PRIOR APPLICATION NUMBER: 60/090445 | |
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| 50 | PRIOR APPLICATION NUMBER: 60/090472 | |
| 51 | PRIOR FILING DATE: 1998-06-24 | |
| 52 | PRIOR APPLICATION NUMBER: 60/090542 | |
| 53 | PRIOR FILING DATE: 1998-06-24 | |
| 54 | PRIOR APPLICATION NUMBER: 60/090557 | |
| 55 | PRIOR FILING DATE: 1998-06-24 | |
| 56 | PRIOR APPLICATION NUMBER: 60/090540 | |
| 57 | PRIOR FILING DATE: 1998-06-24 | |
| 58 | PRIOR APPLICATION NUMBER: 60/090542 | |
| 59 | PRIOR FILING DATE: 1998-06-25 | |
| 60 | PRIOR APPLICATION NUMBER: 60/090678 | |
| 61 | PRIOR FILING DATE: 1998-06-25 | |
| 62 | PRIOR APPLICATION NUMBER: 60/090690 | |
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| 64 | PRIOR APPLICATION NUMBER: 60/090696 | |
| 65 | PRIOR FILING DATE: 1998-06-25 | |
| 66 | PRIOR APPLICATION NUMBER: 60/090862 | |
| 67 | PRIOR FILING DATE: 1998-06-26 | |

; PRIOR APPLICATION NUMBER: 60/090863
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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 117; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 7.5e-104; Indels 0; Gaps 0;
Matches 117; Conservative 0; Mismatches 0;

QY 1 MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQRVQQRKESKKPPAKLQPRALAGWL RPE 60

||||| 1 MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQRVQQRKESKKPPAKLQPRALAGWL RPE 60

QY 61 DGGQGAEGADELEVRFNAPFDVGIKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117

||||| 61 DGGQGAEGADELEVRFNAPFDVGIKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117

RESULT 11

US-09-991-163-268
; Sequence 268, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1997-11-24
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;; PRIOR FILING DATE: 1998-06-17
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;; PRIOR FILING DATE: 1998-06-18
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;; PRIOR APPLICATION NUMBER: 60/090862
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;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360

;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;;
Query Match 100.0%; Score 117; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.5e-104;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;;
QY 1 MPSPGTVCSSLLGLMLWLDLDMAGSSFLSPHQRVQQRKSKPPAKLQPRALAGWLRPE 60
Db 1 MPSPGTVCSSLLGLMLWLDLDMAGSSFLSPHQRVQQRKSKPPAKLQPRALAGWLRPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVYQOQHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAGAEDELEVRNAPFDVGIKLSGVYQOQHSQALGKFLQDILWEEAKEAPADK 117
;;
RESULT 12
US-09-993-604-268
;; Sequence 268, Application US/09993604
;; Patent No. US20020137075A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerlitsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC25
;; CURRENT APPLICATION NUMBER: US/09/993,604
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13

[illegible]

;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 117; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.5e-104;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPGTVCSLLGLMLDLAMAGSFLSPHQRVOORKESKKPPAKLQPRALAGWLRE 60
Db 1 MSPGTVCSLLGLMLDLAMAGSFLSPHQRVOORKESKKPPAKLQPRALAGWLRE 60

QY 61 DGGQAGAEDELEVRNPFVDYGIKLSGVYQHQHSQLGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAGAEDELEVRNPFVDYGIKLSGVYQHQHSQLGKFLQDILWEEAKEAPADK 117

RESULT 13

US-09-990-456-268
; Sequence 268, Application US/09990456
; Patent No. US20020137890A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC22
;; CURRENT APPLICATION NUMBER: US/09/990,456
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
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Query Match 100.0%; Score 117; DB 10; Length 117;
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; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PLC55
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; PRIOR FILING DATE: 1998-07-09

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RESULT 15

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
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;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978

;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 117; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.5e-104;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFSPGTVCSSLLLLGLMLWLDLWAGSSFLSPFHQRVQQRKESKPPAKLQPRALAGWLRPE 60
|||||
DB 1 MFSPGTVCSSLLLLGLMLWLDLWAGSSFLSPFHQRVQQRKESKPPAKLQPRALAGWLRPE 60
|||||
QY 61 DGGQAEAGAELEVRFNAPFDVGIKLSGVQYQOHSOALGKFLQDILWEEAKEAPADK 117
|||||
DB 61 DGGQAEAGAELEVRFNAPFDVGIKLSGVQYQOHSOALGKFLQDILWEEAKEAPADK 117
|||||

Search completed: September 11, 2003, 18:16:17
Job time : 72.9519 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:37 ; Search time 44.4225 Seconds
(without alignments)
253.289 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 117

Sequence: 1 MPSPGTGCSLLLLGLMLDL.....LCKFLQDILWEAKEAPADK 117

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|-------|-------|--------|----------|--------------------|
| 1 | 117 | 100.0 | 117 | 1 A59316 | ghrelin precursor |
| 2 | 18 | 15.4 | 117 | 1 B59316 | ghrelin precursor |
| 3 | 8 | 6.8 | 23 | 2 A4221 | 14K aggregative ad |
| 4 | 8 | 6.8 | 302 | 2 JH0572 | hypothetical prote |
| 5 | 8 | 6.8 | 344 | 2 A48990 | transcription regu |
| 6 | 8 | 6.8 | 483 | 2 T04453 | hypothetical prote |
| 7 | 7 | 6.0 | 22 | 2 PH1333 | Ig heavy chain DJ |
| 8 | 7 | 6.0 | 138 | 2 F83841 | hypothetical prote |
| 9 | 7 | 6.0 | 207 | 2 B83523 | hypothetical prote |
| 10 | 7 | 6.0 | 216 | 2 B73469 | hypothetical prote |
| 11 | 7 | 6.0 | 247 | 2 F82101 | DNA polymerase III |
| 12 | 7 | 6.0 | 256 | 2 B64050 | DNA-directed DNA p |
| 13 | 7 | 6.0 | 406 | 2 AG0548 | probable ABC-trans |
| 14 | 7 | 6.0 | 435 | 2 A86195 | hypothetical prote |
| 15 | 7 | 6.0 | 443 | 2 F87488 | prolyl-tRNA synth |
| 16 | 7 | 6.0 | 444 | 2 D87296 | multidrug resistan |
| 17 | 7 | 6.0 | 464 | 2 A47655 | spliceosome-associ |
| 18 | 7 | 6.0 | 493 | 2 S77612 | amidophosphoribos |
| 19 | 7 | 6.0 | 502 | 2 A53444 | activin receptor-1 |
| 20 | 7 | 6.0 | 502 | 2 JC2491 | serine/threonine k |
| 21 | 7 | 6.0 | 562 | 2 T34319 | hypothetical prote |
| 22 | 7 | 6.0 | 633 | 2 G71026 | hypothetical prote |
| 23 | 7 | 6.0 | 662 | 2 E82991 | probable O-antigen |
| 24 | 7 | 6.0 | 698 | 2 D90541 | atp synthase beta |
| 25 | 7 | 6.0 | 809 | 2 A12747 | conserved hypothet |
| 26 | 7 | 6.0 | 873 | 2 H97528 | hypothetical prote |
| 27 | 7 | 6.0 | 904 | 2 D90772 | sensor protein tor |
| 28 | 7 | 6.0 | 904 | 2 H85634 | sensor protein tor |
| 29 | 7 | 6.0 | 904 | 2 G64840 | protein-histidine |

| | | | | | |
|----|---|-----|------|----------|---------------------|
| 30 | 7 | 6.0 | 910 | 2 B83451 | aconitate hydratase |
| 31 | 7 | 6.0 | 1239 | 1 Q0BE10 | BOLFI protein - hu |
| 32 | 7 | 6.0 | 1970 | 2 T03284 | myoblast city prot |
| 33 | 7 | 6.0 | 3165 | 2 S15010 | hypothetical prote |
| 34 | 6 | 5.1 | 52 | 2 C83241 | hypothetical prote |
| 35 | 6 | 5.1 | 59 | 2 G97930 | hypothetical prote |
| 36 | 6 | 5.1 | 69 | 2 C87574 | cold-shock domain |
| 37 | 6 | 5.1 | 72 | 2 S48790 | troponin T, cardia |
| 38 | 6 | 5.1 | 80 | 1 PCCG | pancreatic hormone |
| 39 | 6 | 5.1 | 84 | 2 AH3402 | hypothetical cytos |
| 40 | 6 | 5.1 | 89 | 2 E83141 | hypothetical prote |
| 41 | 6 | 5.1 | 103 | 2 F82266 | conserved hypothet |
| 42 | 6 | 5.1 | 104 | 2 T48688 | hypothetical prote |
| 43 | 6 | 5.1 | 106 | 2 A71193 | hypothetical prote |
| 44 | 6 | 5.1 | 106 | 2 AE2124 | hypothetical prote |
| 45 | 6 | 5.1 | 108 | 2 T04117 | SEC18 protein homo |

ALIGNMENTS

RESULT 1

A59316

ghrelin precursor - human

N:Alternate names: preproghrelin

C:Species: Homo sapiens (man)

C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000

C:Accession: A59316

R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

Nature 402, 656-660, 1999

A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A:Reference number: A59316; MUID:20067959; PMID:10604470

A:Accession: A59316

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-117 <KOJ>

A:Cross-references: GB:AB029434; NID:g6691571; PIDN:BAA89371.1; PID:g6691572

A:Experimental source: tissue stomach endocrine cells

A:Note: submitted to GenBank, June 1999

C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (gr

C:Superfamily: motilin

C:Keywords: hormone; lipoprotein; stomach

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-51/Product: ghrelin #status predicted <MAT>

F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 117; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.2e-109;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPGTVCSSLLLLGLMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWL RPE 60

DB 1 MPSPGTVCSSLLLLGLMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWL RPE 60

QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSOALGKFLQDILWEAKEAPADK 117

DB 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSOALGKFLQDILWEAKEAPADK 117

RESULT 2

B59316

ghrelin precursor - rat

N:Alternate names: preproghrelin

C:Species: Rattus norvegicus (Norway rat)

C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000

C:Accession: B59316

R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

Nature 402, 656-660, 1999

A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A:Reference number: A59316; MUID:20067959; PMID:10604470

A:Accession: B59316

A:Status: not compared with conceptual translation

A:Molecule type: mRNA; protein
A:Residues: 1-117 <KOJ>
A:Cross-references: GB:AB029433; NID:g6691569; PIDN:BA089370.1; PID:g6691570
A:Experimental source: strain SD; tissue stomach endocrine cells
A:Note: submitted to GenBank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth hormone) from the pituitary gland.
C:Superfamily: motilin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <MAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 15.4%; Score 18; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 QQRKSKPPAKLOPRAL 53
|||||
DB 36 QQRKSKPPAKLOPRAL 53

RESULT 3
A49221
14k aggregative adherence fimbriae I protein - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995
C:Accession: A49221
R:Nataro, J.P.; Yikang, D.; Giron, J.A.; Savarino, S.J.; Kothary, M.H.; Hall, R.
Infect. Immun. 61, 1126-1131, 1993
A:Title: Aggregative adherence fimbria I expression in enteroaggregative Escherichia coli
A:Reference number: A49221; MUID:93162805; PMID:8094379
A:Accession: A49221
A:Contents: 17-2, serotype O3:H2
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <NAT>
A:Note: sequence extracted from NCBI backbone (NCBIP:125179)

Query Match 6.8%; Score 8; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 IKLSGVQY 91
|||||
DB 16 IKLSGVQY 23

RESULT 4
JH0572
hypothetical protein - Streptomyces lividans (fragment)
C:Species: Streptomyces lividans
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-1999
C:Accession: JH0572
R:Lichenstein, H.S.; Busse, L.A.; Smith, G.A.; Narhi, L.O.; McGinley, M.O.; Rohde, M.F.; Gene 111, 125-130, 1992
A:Title: Cloning and characterization of a gene encoding extracellular metalloprotease from Streptomyces lividans
A:Reference number: JH0571; MUID:92192468; PMID:1547948
A:Accession: JH0572
A:Molecule type: DNA
A:Residues: 1-302 <LIC>
A:Cross-references: GB:M09476; NID:g153411; PIDN:AAA26804.1; PID:g153412
A:Experimental source: strain TK24
A:Note: the authors translated the codon GTA for residue 260 as Asp
A:Note: this protein has a strong similarity to LysR family of transcriptional regulators
C:Superfamily: Pseudomonas putida regulatory protein catr

Query Match 6.8%; Score 8; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RALAGWLR 58
|||||

Db 99 RALAGWLR 106

RESULT 5
A48990
transcription regulator LysR family homolog SnpR - Streptomyces lividans
C:Species: Streptomyces lividans
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C:Accession: A48990
R:Butler, M.J.; Davey, C.C.; Krygsman, P.; Walczyk, E.; Malek, L.T.
Can. J. Microbiol. 38, 912-920, 1992
A:Title: Cloning of genetic loci involved in endoprotease activity in Streptomyces lividans
A:Reference number: A48990; MUID:93099553; PMID:1464066
A:Contents: 66
A:Accession: A48990
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-344 <BUT>
A:Note: sequence extracted from NCBI backbone (NCBIN:121210, NCBIP:121213)
C:Superfamily: Pseudomonas putida regulatory protein catr

Query Match 6.8%; Score 8; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RALAGWLR 58
|||||
DB 103 RALAGWLR 110

RESULT 6
T04453
hypothetical protein F4D11.80 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C:Accession: T04453
R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Hohelsel, J.; Mewes, F.
submitted to the Protein Sequence Database, April 1998
A:Reference number: 215360
A:Accession: T04453
A:Molecule type: DNA
A:Residues: 1-483 <BEV>
A:Cross-references: EMBL:AL022537
A:Experimental source: cultivar Columbia; BAC clone F4D11
C:Genetics:
A:Map position: 4
A:Introns: 17/3; 44/1; 141/3; 206/2; 247/2; 345/3; 395/1; 434/2
A:Note: F4D11.80

Query Match 6.8%; Score 8; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 QAEGAED 71
|||||
DB 302 QAEGAED 309

RESULT 7
PH1333
Ig heavy chain DJ region (clone C238-133) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1333
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1333
A:Molecule type: DNA
A:Residues: 1-22 <WAS>
C:Keywords: heterotetramer; immunoglobulin

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Query Match      6.0%; Score 7; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VCSLLLLL 13
DB 6 VCSLLLLL 12

RESULT 8
F83841
hypothetical protein BH1534 [Imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: F83841
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: F83841
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <STO>
A:Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05253.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1534
C:Superfamily: Bacillus subtilis hypothetical protein yndB

Query Match      6.0%; Score 7; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 EVRFNAP 79
DB 10 EVRFNAP 16

RESULT 9
B83523
hypothetical protein PA0981 [Imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83523
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83523
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <STO>
A:Cross-references: GB:AE004531; GB:AE004091; NID:g9946882; PIDN:AAG04370.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0981

Query Match      6.0%; Score 7; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPGTV 7
DB 84 MPSPGTV 90

RESULT 10
B75469
hypothetical protein - Deinococcus radiodurans (strain RL)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
```

```
C:Accession: B75469
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RL.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: B75469
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-216 <WHI>
A:Cross-references: GB:AE001938; GB:AE000513; NID:g6458553; PIDN:AAF10422.1; PID:9645
A:Experimental source: strain RL
C:Genetics:
A:Gene: DR0838
A:Map position: 1

Query Match      6.0%; Score 7; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 LDLAMAG 24
DB 50 LDLAMAG 56

RESULT 11
F82101
DNA polymerase III, epsilon chain VC2233 [Imported] - Vibrio cholerae (strain N16961)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82101
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.
; Chardson, D.; Emolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: F82101
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <HEI>
A:Cross-references: GB:AE004295; GB:AE003852; NID:g9656789; PIDN:AAF95377.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2233
A:Map position: 1
C:Superfamily: dnaQ protein

Query Match      6.0%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 NAPFDVG 83
DB 104 NAPFDVG 110

RESULT 12
B64050
DNA-directed DNA polymerase (EC 2.7.7.7) III epsilon chain - Haemophilus influenzae (
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 21-Jul-2000
C:Accession: B64050
R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: B64050
A:Status: nucleic acid sequence not shown; translation not shown
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A:Molecule type: DNA

A:Residues: 1-256 <TIGR>

A:Cross-references: GB:U32699; GB:L42023; NID:g3212180; PIDN:AAC21808.1; PID:g1573090; T

C:Genetics:

A:Gene: dnaQ

C:Function:

A:Pathway: DNA biosynthesis

C:Superfamily: dnaQ protein

C:Keywords: DNA biosynthesis; DNA replication initiation; nucleotidyltransferase

Query Match 6.0%; Score 7; DB 2; Length 256;

Best Local Similarity 100.0%; Pred. No. 36;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 NAFPDVG 83

|||||||

Db 98 NAFPDVG 104

RESULT 13

AG0548

probable ABC-transporter inner membrane protein SbmA [imported] - Salmonella enteri

C:Species: Salmonella enterica subsp. enterica serovar typhi

A:Note: This species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AG0548

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AG0548

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-406 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD08831.1; PID:g16501645; GSPDB:GN00176

C:Genetics:

A:Gene: sbmA

C:Superfamily: probable inner membrane transport protein bacA

Query Match 6.0%; Score 7; DB 2; Length 406;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 VGKILSG 88

|||||||

Db 261 VGKILSG 267

RESULT 14

A86195

hypothetical protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: A86195

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A86195

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-435 <STO>

A:Cross-references: GB:AE005172; NID:g8810462; PIDN:AAF80123.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

C:Superfamily: flavonol O3-glucosyltransferase

Query Match 6.0%; Score 7; DB 2; Length 435;

Best Local Similarity 100.0%; Pred. No. 56;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 GSSFLSP 30

|||||||

Db 123 GSSFLSP 129

RESULT 15

F87488

prolyl-tRNA synthetase [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002

C:Accession: F87488

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A>Title: Complete genome sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: F87488

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-443 <STO>

A:Cross-references: GB:AE005673; NID:gl34233386; PIDN:AAK23906.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC1931

C:Superfamily: proline-tRNA ligase pros

Query Match 6.0%; Score 7; DB 2; Length 443;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 APFDVGI 84

|||||||

Db 344 APFDVGI 350

Search completed: September 11, 2003, 17:57:03

Job time : 47.4225 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:30:37 : Search time 22.5241 Seconds
(without alignments)
244.278 Million cell updates/sec

Title: US-09-853-253-2
Perfect score: 117
Sequence: 1 MPSPGTGCSLLLLGLMLDL.....LCKFLQDILWEEAKEAPADK 117

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 117 | 100.0 | 117 | 1 | GHRL_HUMAN |
| 2 | 18 | 15.4 | 117 | 1 | GHRL_CANFA |
| 3 | 18 | 15.4 | 117 | 1 | GHRL_MOUSE |
| 4 | 18 | 15.4 | 117 | 1 | GHRL_RAT |
| 5 | 15 | 12.8 | 116 | 1 | GHRL_BOVIN |
| 6 | 15 | 12.8 | 118 | 1 | GHRL_PIG |
| 7 | 8 | 6.8 | 328 | 1 | MPR2_STRCO |
| 8 | 8 | 6.8 | 344 | 1 | MPRR_STRLI |
| 9 | 7 | 6.0 | 253 | 1 | DP3E_PASMU |
| 10 | 7 | 6.0 | 256 | 1 | DP3E_HAEIN |
| 11 | 7 | 6.0 | 286 | 1 | CHM1_BRARE |
| 12 | 7 | 6.0 | 327 | 1 | NAS1_HORVU |
| 13 | 7 | 6.0 | 464 | 1 | S3A2_HUMAN |
| 14 | 7 | 6.0 | 475 | 1 | S3A2_MOUSE |
| 15 | 7 | 6.0 | 493 | 1 | PUR1_SYNP7 |
| 16 | 7 | 6.0 | 502 | 1 | BMRB_HUMAN |
| 17 | 7 | 6.0 | 502 | 1 | BMRB_MOUSE |
| 18 | 7 | 6.0 | 914 | 1 | TORS_ECO57 |
| 19 | 7 | 6.0 | 914 | 1 | TORS_ECOLI |
| 20 | 7 | 6.0 | 1142 | 1 | SPK_HUMAN |
| 21 | 7 | 6.0 | 1239 | 1 | V120_EBV |
| 22 | 6 | 5.1 | 80 | 1 | PAHO_CHICK |
| 23 | 6 | 5.1 | 105 | 1 | RL36_TRIHM |
| 24 | 6 | 5.1 | 112 | 1 | RBFA_MYCPU |
| 25 | 6 | 5.1 | 112 | 1 | SVS4_RAT |
| 26 | 6 | 5.1 | 112 | 1 | SY27_HUMAN |
| 27 | 6 | 5.1 | 116 | 1 | CART_HUMAN |
| 28 | 6 | 5.1 | 117 | 1 | NUSM_PROWI |
| 29 | 6 | 5.1 | 125 | 1 | MSP1_GLORO |
| 30 | 6 | 5.1 | 125 | 1 | MSP2_GLORO |
| 31 | 6 | 5.1 | 125 | 1 | MSP3_GLORO |
| 32 | 6 | 5.1 | 127 | 1 | ACPS_SHEON |
| 33 | 6 | 5.1 | 129 | 1 | CART_MOUSE |

| | | | | | |
|----|---|-----|-----|---|------------|
| 34 | 6 | 5.1 | 129 | 1 | CART_RAT |
| 35 | 6 | 5.1 | 140 | 1 | LCA_MACEU |
| 36 | 6 | 5.1 | 144 | 1 | CSF2_HUMAN |
| 37 | 6 | 5.1 | 149 | 1 | TTHY_MONDO |
| 38 | 6 | 5.1 | 154 | 1 | PFDA_HALNI |
| 39 | 6 | 5.1 | 154 | 1 | RNS6_BOVIN |
| 40 | 6 | 5.1 | 156 | 1 | PSPN_MOUSE |
| 41 | 6 | 5.1 | 162 | 1 | MUG_SERMA |
| 42 | 6 | 5.1 | 165 | 1 | SSPB_ECOLI |
| 43 | 6 | 5.1 | 168 | 1 | IAO3_WHEAT |
| 44 | 6 | 5.1 | 170 | 1 | NU6M_XENLA |
| 45 | 6 | 5.1 | 178 | 1 | EFAB_CHICK |

P49192 rattus norv
Q06655 macropus eu
P04141 homo sapien
P49141 monodelphis
Q9hnm2 halobacteri
P08904 bos taurus
O70300 mus musculu
P43343 serrattia ma
P25663 escherichia
P17314 triticum ae
P03927 xenopus lae
P21760 gallus gall

RESULT 1
GHRL_HUMAN
ID GHRL_HUMAN STANDARD; Q9H3R3; PRT; 117 AA.
AC Q9UBU3: Q8TAT9; Q9H3R3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
GN GHRL OR WTLRP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
RX MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach.";
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Stomach;
RA Tomasetto C., Karam S.M., Rio M.-C.;
RT "Identification of a novel gastric protein m46.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Wajnarajch M.P., Ten I.S., Gertner J.M., Leibell R.L.;
RT "Genomic organization of the human Ghrelin gene.";
RL J. Endocrinol. Genet. 1:231-233(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.J., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Hellton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

ALIGNMENTS

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [6]
 RP SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RL hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [7]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RL hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -!- PTM: O-n-octanoylation is essential for activity.
 CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobogen.fr/services/chromocancer/Genes/GhrelinID327.html".
 CC -----
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 CC -----
 DR EMBL; AB029434; BAA89371.1; -;
 DR EMBL; AB035700; BAB19045.1; -;
 DR EMBL; AJ252278; CAB57733.1; -;
 DR EMBL; AF296538; AAG10300.1; -;
 DR EMBL; BC025791; AAH25791.1; -;
 DR PIR; A59316; A59316.
 DR MIM; 605353; -;
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005131; P:growth hormone receptor ligand activity; TAS.
 DR GO; GO:0007287; P:cell-cell signaling; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc; 1.
 DR Pfam; PF04644; motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR PRODOM; PD332162; Preproghrelin; 1.
 DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 23
 FT PEPTIDE 24 51 GHRELIN.
 FT PROPEP 52 117 REMOVED IN MATURE FORM.
 FT LIPID 26 26 N-OCTANOATE.
 FT VARSPLIC 37 37 Missing (in Isoform 2).
 FT FTID=VSP_003245.
 FT CONFLICT 72 72 L -> M (IN REF. 5).
 FT

SQ SEQUENCE 117 AA; 12911 MW; 39C0572EBE2A2755 CRC64;
 Query Match 100.0%; Score 117; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8e-111;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPTGCSLLGLMLDLAMAGSSFLSPHQRVQQRKSKPKPKLQPRALAGWLRLPE 60
 Db 1 MPSPTGCSLLGLMLDLAMAGSSFLSPHQRVQQRKSKPKPKLQPRALAGWLRLPE 60
 QY 61 DGGQAEAGAEDELEVRFNAPFDVGKLSGVQVQHQISQALGKFLQDILWEEAEAPDK 117
 Db 61 DGGQAEAGAEDELEVRFNAPFDVGKLSGVQVQHQISQALGKFLQDILWEEAEAPDK 117
 RESULT 2
 GHRL_CANFA
 ID GHRL_CANFA STANDARD; PRT; 117 AA.
 AC Q9BEF8; Q9BEF7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide) (Motilin-related peptide).
 GN GHRL OR MTLRP.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Gastric fundus;
 RA Tomasetto C., Wendling C., Rio M.-C., Poltras P.;
 RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
 RT fundus.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation (by similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9BEF8-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9BEF8-2; Sequence=VSP_003244;
 CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; AJ298295; CAC29155.1; -;
 DR EMBL; AJ298296; CAC29156.1; -;
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc; 1.
 DR Pfam; PF04644; motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR PRODOM; PD332162; Preproghrelin; 1.
 DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
 FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
 FT

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FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPLIC 37 37 Missing (in isoform 2).
FT /FTID-VSP_003244
SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;

Query Match 15.4%; Score 18; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 QQRKSKPPAKLPAL 53
DB 36 QQRKSKPPAKLPAL 53

RESULT 3
GHRM_MOUSE
ID GHRM_MOUSE STANDARD; PRT; 117 AA.
AC Q9EQX0; Q9WU21;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
releasing peptide) (Motilin-related peptide) (M46 protein).
GN GHRM OR MTLRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
RC TISSUE=Stomach;
RX MEDLINE=20389976; PubMed=10930375;
RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT "Identification and characterization of a novel gastric peptide
hormone: the motilin-related peptide.";
RL Gastroenterology 119:395-405(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Kojima M.;
RT "Mouse mRNA for preproghrelin.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336;

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RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
receptor type 1 (GHSR) inducing the release of growth hormone from
the pituitary. Has an appetite-stimulating effect, induces
adiposity and stimulates gastric acid secretion. Involved in
growth regulation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9EQX0-1; Sequence=VSP_003246;
CC IsoId=Q9EQX0-2; Sequence=VSP_003246;
CC -!- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
with higher levels in the stomach, medium levels in the duodenum,
jejunum, ileum and colon. Low expression in the testis and brain.
CC Not detected in the salivary gland, pancreas, liver and lung.
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
CC EMBL; AJ243503; CAB46500.1; -
CC EMBL; AB035701; BAB19046.1; -
CC EMBL; AB060078; BAB69857.1; -
CC EMBL; AK008658; BAB25814.1; -
CC EMBL; AK008860; BAB25934.1; -
CC MGD; MGI:1930008; Ghrl.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005576; C:extracellular; IDA.
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC InterPro; IPR005441; Preproghrelin.
CC Pfam; PF04643; motilin_assoc. 1.
CC Pfam; PF04644; motilin_ghrelin; 1.
CC PRINTS; PR01624; GHRELIN
CC ProDom; PD321262; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23
FT PEPTIDE 24 51 GHRELIN.
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPLIC 37 37 MISSING (in isoform 2).
FT /FTID-VSP_003246.
SQ SEQUENCE 117 AA; 13207 MW; EACB49D2E3CA7203 CRC64;

Query Match 15.4%; Score 18; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 QQRKSKPPAKLPAL 53
DB 36 QQRKSKPPAKLPAL 53

RESULT 4
GHRM_RAT
ID GHRM_RAT STANDARD; PRT; 117 AA.
AC Q9QYH7; Q9ET69;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone

```

DE releasing peptide).

GN GHRL.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,

RP AND ACRYLATION OF SER-26.

RC STRAIN=Sprague-Dawley; TISSUE=Stomach;

RX MEDLINE=20067959; PubMed=10604470;

RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;

RT "Ghrelin is a growth-hormone-releasing acylated peptide from

RL stomach.";

RL Nature 402:656-660(1999).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS

RP SPECTROMETRY, AND ACRYLATION OF SER-26.

RC STRAIN=Sprague-Dawley; TISSUE=Stomach;

RX MEDLINE=20357315; PubMed=10801861;

RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;

RT "Purification and characterization of rat des-Gln14-ghrelin, a second

RT endogenous ligand for the growth hormone secretagogue receptor.";

RL J. Biol. Chem. 275:21995-22000(2000).

RN [3]

RP CHARACTERIZATION.

RP MEDLINE=21092536; PubMed=11162448;

RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;

RT "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide

RT in gastrointestinal tissue.";

RL Biochem. Biophys. Res. Commun. 279:909-913(2000).

RN [4]

RP STRUCTURE-ACTIVITY RELATIONSHIP.

RP MEDLINE=21433488; PubMed=11549267;

RA Matsunoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,

RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;

RT "Structure-activity relationship of ghrelin: pharmacological study of

RT ghrelin peptides.";

RL Biochem. Biophys. Res. Commun. 287:142-146(2001).

RN [5]

RP REVIEW.

RP MEDLINE=21203998; PubMed=11306336;

RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;

RT "Ghrelin: discovery of the natural endogenous ligand for the growth

RT hormone secretagogue receptor.";

RL Trends Endocrinol. Metab. 12:118-122(2001).

CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue

CC receptor type 1 (GHSR) inducing the release of growth hormone from

CC the pituitary. Has an appetite-stimulating effect, induces

CC adiposity and stimulates gastric acid secretion. Involved in

CC growth regulation.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Name=1; Synonyms=Ghrelin;

CC IsoId=Q9QYH7-1; Sequence=Displayed;

CC Name=2; Synonyms=del-Gln14-ghrelin;

CC IsoId=Q9QYH7-2; Sequence=VSP_003248;

CC -1- TISSUE SPECIFICITY: Broadly expressed with higher expression in

CC the stomach. Very low levels are detected in the hypothalamus,

CC heart, lung, pancreas, intestine and adipose tissue.

CC -1- PTM: O-n-octanoylation is essential for activity. The replacement

CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.

CC -1- MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;

CC RANGE=24-51.

CC -1- MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;

CC RANGE=24-36, 38-51.

CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.

CC -----

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CC -----

CC EMBL; AB029433; BAA89370.1; -;

DR EMBL; AB035699; BAB11956.1; -;

DR PIR; B59316; B59316.

DR InterPro; IPR006737; motilin_assoc.

DR InterPro; IPR006738; motilin-ghrelin.

DR InterPro; IPR005441; Preproghrelin.

DR Pfam; PF04643; motilin_assoc; 1.

DR Pfam; PF04644; motilin-ghrelin; 1.

DR PRINTS; PR01624; GHRELIN.

DR ProDom; PD332162; Preproghrelin; 1.

DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;

KW Alternative splicing.

KW SIGNAL 1 23

FT PEPTIDE 24 51 GHRELIN.

FT PROPEP 52 117 REMOVED IN MATURE FORM.

FT LIPID 26 26 N-OCTANOATE.

FT VARSPIC 37 37 Missing (in isoform 2).

FT /FTID=VSP_003248.

SO SEQUENCE 117 AA; 13176 MW; 8857546FE51A7691 CRC64;

Query Match 15.4%; Score 18; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.3e-11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 QQRKESKPPAKLPQPRAL 53

Db 36 QQRKESKPPAKLPQPRAL 53

|||||

RESULT 5

GHRL_BOVIN

ID GHRL_BOVIN STANDARD; PRT; 116 AA.

AC Q9RDJ6; Q9GKY6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ghrelin precursor (growth hormone secretagogue) (Growth hormone

DE releasing peptide).

GN GHRL.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RA Kita K., Harada K., Yokota H.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 24-99 FROM N.A.

RA Kojima M.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue

CC receptor type 1 (GHSR) inducing the release of growth hormone from

CC the pituitary. Has an appetite-stimulating effect, induces

CC adiposity and stimulates gastric acid secretion. Involved in

CC growth regulation (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).

CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.

CC -----

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DR EMBL; AF350329; AAK18612.1; -.
DR EMBL; AF350370; BAB19047.1; -.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc.1.
DR Pfam; PF04644; motilin_ghrelin.1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 50 GHRELIN (BY SIMILARITY).
FT PROPEP 51 116 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT CONFLICT 34 34 K -> E (IN REF. 2).
SQ SEQUENCE 116 AA; 12792 MW; F55336DAC5FA59B6 CRC64;

Query Match 12.8%; Score 15; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 6.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 DLAMAGSSFLSPSEQ 33
DB 19 DLAMAGSSFLSPSEQ 33
|||||

RESULT 6
GHR_L_PIG STANDARD; PRT; 118 AA.
AC Q9GKY5; Q9BDG8; Q9GKY4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
releasing peptide).
GN GHR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP TISSUE=Stomach;
RC Rousselet J., Lacroix D., Dubreuil P.;
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Specific ligand for the growth hormone secretagogue
receptor type 1 (GHR) inducing the release of growth hormone from
the pituitary. Has an appetite-stimulating effect, induces
adiposity and stimulates gastric acid secretion. Involved in
growth regulation (By similarity).
-1- SUBCELLULAR LOCATION: Secreted (By similarity).
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Ghrelin;
IsoId=Q9GKY5-1; Sequences=Displayed;
Name=2; Synonyms=del-Gln14-ghrelin;
IsoId=Q9GKY5-2; Sequences=VSP_003247;
-1- PTM: O-n-octanoylation is essential for activity (By similarity).
-1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
-----
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DR EMBL; AB035703; BAB19048.1; -.

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DR EMBL; AB035704; BAB19049.1; -.
DR EMBL; AF308930; AAK19243.1; -.
DR EMBL; AY028942; AAK30002.1; -.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc.1.
DR Pfam; PF04644; motilin_ghrelin.1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
Alternative splicing.
FT SIGNAL 1 24 BY SIMILARITY.
FT PEPTIDE 25 52 GHRELIN.
FT PROPEP 53 118 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 27 27 N-OCTANOATE (BY SIMILARITY).
FT VARSPLIC 38 38 Missing (in isoform 2).
FT CONFLICT 17 17 L -> P (IN REF. 2; AAK30002).
FT CONFLICT 72 72 K -> E (IN REF. 2; AAK30002).
SQ SEQUENCE 118 AA; 12785 MW; 856D3E1D6DAB1A76 CRC64;

Query Match 12.8%; Score 15; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 6.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 DLAMAGSSFLSPSEQ 33
DB 20 DLAMAGSSFLSPSEQ 34
|||||

RESULT 7
MPR2_STRCO STANDARD; PRT; 328 AA.
AC Q9L127;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Small neutral protease regulatory protein.
GN MPRR OR MPRR2 OR SCO7433 OR SC6D11.29.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147 (2002).
-1- FUNCTION: TRANSCRIPTIONAL TRANS-ACTIVATOR OF THE GENE (MPRA) FOR
THE SMALL NEUTRAL PROTEASE.
-1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
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DR EMBL; AL939131; CAB76352.1; -.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; Protease; Transcription regulation; Complete proteome.
FT DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL)
SQ SEQUENCE 328 AA; 35885 MW; 2BA97730AE4FA16B CRC64;

Query Match 6.8%; Score 8; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 51 RALAGWLR 58
Db 103 RALAGWLR 110
|||||

RESULT 8
MPRR_STRLI STANDARD; PRT; 344 AA.
ID P43163;
AC P43163;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Small neutral protease regulatory protein.
GN MPRR OR SNPR.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=66 / 1326;
RX MEDLINE=93099553; PubMed=1464066;
RA Butler M.J., Davey C.C., Krygsman P., Walczyk E., Malek L.T.;
RT "Cloning of genetic loci involved in endoprotease activity in
RT Streptomyces lividans 66: a novel neutral protease gene with an
RT adjacent divergent putative regulatory gene.";
RL Can. J. Microbiol. 38:912-920(1992).
RN [2]
RP SEQUENCE OF 1-305 FROM N.A.
RC STRAIN=TK24;
RX MEDLINE=92192468; PubMed=1547948;
RA Lichenstein H.S., Busse L.A., Smith G.A., Narhi L.O.,
RA McGinley M.O., Rohde M.F., Katowitz J.L., Zukowski M.M.;
RT "Cloning and characterization of a gene encoding extracellular
RT metalloprotease from Streptomyces lividans.";
RL Gene 111:125-130(1992).
CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE GENE (SNPA) FOR THE
CC SMALL NEUTRAL PROTEASE.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
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CC -----
DR EMBL; M81703; AAA26739.1; -.
DR EMBL; M89476; AAA26804.1; ALT_INIT.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW Transcription regulation; DNA-binding; Activator.
FT DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
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```
FT CONFLICT 270 270 G -> AR (IN REF. 2).
SQ SEQUENCE 344 AA; 37415 MW; 485C82C813B52312 CRC64;

Query Match 6.8%; Score 8; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 51 RALAGWLR 58
Db 103 RALAGWLR 110
|||||

RESULT 9
DP3E_PASMU STANDARD; PRT; 253 AA.
ID AC Q9CPE0;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE DNA polymerase III, epsilon chain (EC 2.7.7.7).
GN DNAO OR PM0106.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC THE EPSILON SUBUNIT CONTAIN THE EDITING FUNCTION AND IS A
CC PROOFREADING 3'-5' EXONUCLEASE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
CC + [DNA](N).
CC -!- SUBUNIT: DNA polymerase III contains a core (composed of alpha,
CC epsilon and theta chains) that associates with a tau subunit. This
CC core dimerizes to form the POLIII' complex. POLIII' associates
CC with the gamma complex (composed of gamma, delta, delta', psi and
CC chi chains) and with the beta chain to form the complete DNA
CC polymerase III complex (By similarity).
CC -----
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CC -----
DR EMBL; AE006046; AAK02190.1; -.
DR InterPro; IPR006054; DnaQ.
DR InterPro; IPR006309; DnaQ_proteo.
DR Pfam; PF00929; Exonuclease.
DR SMART; SM00479; EXOIII; 1.
DR TIGRFAMs; TIGR00573; dnaq; 1.
DR TIGRFAMs; TIGR01406; DnaQ_proteo; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
KW Exonuclease; Complete proteome.
SQ SEQUENCE 253 AA; 28559 MW; AEF3C48030D4B64C CRC64;

Query Match 6.0%; Score 7; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 77 NAPFDVG 83
Db 101 NAPFDVG 107
|||||
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RESULT 10
DP3E_HAEIN          STANDARD;          PRT;      256 AA.
AC  P43745;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  DNA polymerase III, epsilon chain (EC 2.7.7.7).
GN  DNA OR HI0137
OS  Haemophilus influenzae.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC  Pasteurellaceae; Haemophilus.
OX  NCBI_TaxID=727;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Rd / KW20 / ATCC 51907;
RX  MEDLINE=95350630; PubMed=7542800;
RA  Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA  Klerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA  McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA  Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA  Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA  Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA  Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA  Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA  Venter J.C.;
RT  "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT  Rd.";
RL  Science 269:496-512(1995).
CC  -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC  RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC  THE EPSILON SUBUNIT CONTAIN THE EDITING FUNCTION AND IS A
CC  PROOFREADING 3'-5' EXONUCLEASE (BY SIMILARITY).
CC  -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
CC  + [DNA](n).
CC  -1- FUNCTION: DNA polymerase III contains a core (composed of alpha,
CC  epsilon and theta chains) that associates with a tau subunit. This
CC  core dimerizes to form the POLIII' complex. POLIII' associates
CC  with the gamma complex (composed of gamma, delta, delta', psi and
CC  chi chains) and with the beta chain to form the complete DNA
CC  polymerase III complex (by similarity).
-----
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EMBL; U32699; AAC21808.1;
DR  PIR; B64050; B64050.
DR  TIGR; HT0137;
DR  InterPro; IPR006054; DnaQ.
DR  InterPro; IPR006309; DnaQ_proteo.
DR  Pfam; PF00929; Exonuclease.
DR  SMART; SM00479; EXOIII; 1.
DR  TIGRFAMS; TIGR00573; dnaQ; 1.
DR  TIGRFAMS; TIGR01406; dnaQ_proteo; 1.
KW  Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
KW  Exonuclease; Complete proteome.
SQ  SEQUENCE 256 AA; 29131 MW; 694C9273AD4438D1 CRC64;

Query Match          6.0%; Score 7; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  77 NAPFDVG 83
DB  98 NAPFDVG 104

```

```

RESULT 11
CHM1_BRARE          STANDARD;          PRT;      286 AA.
ID  CHM1_BRARE
AC  P58239;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Chondromodulin-I precursor (Chm-I) (Leukocyte cell-derived chemotaxin
DE  1) [Contains: Chondrosurfactant protein (CH-SP)].
GN  LECT1 OR CHM1 OR CHM1.
OS  Brachydanio rerio (zebrafish) (Danio rerio).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC  Cyprinidae; Danio.
OX  NCBI_TaxID=7955;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21322690; PubMed=11429291;
RA  Sachdev S.W., Dietz U.H., Oshima Y., Lang M.R., Knapik E.W.,
RA  Hiraki Y., Shukunami C.;
RT  "Sequence analysis of zebrafish chondromodulin-1 and expression
RT  profile in the notochord and chondrogenic regions during cartilage
RT  morphogenesis.";
RL  Mech. Dev. 105:157-162(2001).
CC  -1- FUNCTION: Bifunctional growth regulator. May contribute to the
CC  rapid growth of cartilage and vascular invasion prior to the
CC  replacement of cartilage by bone during endochondral bone
CC  development (By similarity).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
CC  inter-territorial matrix of cartilage (By similarity).
CC  -1- PTM: After cleavage, the post-translationally modified Chm-I is
CC  secreted as a glycoprotein (By similarity).
CC  -1- SIMILARITY: BELONGS TO THE CHONDROMODULIN-I FAMILY.
-----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC  or send an email to license@isb-sib.ch).
-----
EMBL; AF322374; AAK77023.1;
DR  ZFIN; ZDB-GENE-010713-1; lect1.
DR  Pfam; PF04089; BRICHOS; 1.
KW  Cartilage; Glycoprotein; Transmembrane;
KW  Cleavage on pair of basic residues.
FT  CHAIN 1 165
FT      CHONDROSURFACTANT PROTEIN
FT      (BY SIMILARITY).
FT  PROPEP 166 169
FT      POTENTIAL.
FT  CHAIN 170 286
FT      CHONDROMODULIN-I.
FT  TRANSMEM 29 49
FT      POTENTIAL.
FT  CARBOHYD 191 191
FT      N-LINKED (GLCNAC...) (POTENTIAL).
SQ  SEQUENCE 286 AA; 32235 MW; 21B377E0348EDDB3 CRC64;

Query Match          6.0%; Score 7; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  25 SSFLSPE 31
DB  138 SSFLSPE 144

RESULT 12
NAS1_HORVU          STANDARD;          PRT;      327 AA.
ID  NAS1_HORVU
AC  Q9ZOV9;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Nicotianamine synthase 1 (EC 2.5.1.43) (S-adenosyl-L-methionine:S-

```

DE adenosyl-L-methionine:S-adenosyl-methionine 3-amino-3-
 GN carboxypropyltransferase 1) (HvNAS1).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 [1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-19; 63-69; 181-243 AND 247-266.
 RP STRAIN=cv. Ehimehata No.1; TISSUE=Root;
 RC MEDLINE=99137899; PubMed=9952442;
 RX Higuchi K., Suzuki K., Nakanishi H., Yamaguchi H., Nishizawa N.-K.,
 RA Mori S.;
 RA "Cloning of nicotianamine synthase genes, novel genes involved in the
 RT biosynthesis of phytosiderophores.";
 RL Plant Physiol. 119:471-480(1999).
 CC -1- FUNCTION: Synthesizes nicotianamine, a polyamine that is the first
 CC intermediate in the synthesis of the phytosiderophores of the
 CC mugineic acid type found in gramineae which serves as a sensor for
 CC the physiological iron status within the plant, and/or might be
 CC involved in the transport of iron (By similarity).
 CC -1- CATALYTIC ACTIVITY: 3 S-adenosyl-L-methionine + 3 5'-S-methyl-5'-
 CC thioadenosine + nicotianamine.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- TISSUE SPECIFICITY: In roots but not in leaves.
 CC -1- INDUCTION: By iron deficiency.
 CC -1- SIMILARITY: Contains 1 NAS domain.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB010086; BAA74580.1; -;
 DR InterPro; IPR004298; Nicotian_synth.
 DR Pfam; PF03059; NAS; 1.
 KW Transferase; Pyridoxal phosphate; Multigene family.
 FT INIT_MET 0 281 NAS.
 FT DOMAIN 0 281 NAS.
 SQ SEQUENCE 327 AA; 35015 MW; C476B9622E76816 CRC64;
 Query Match 6.0%; Score 7; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 28 LSPHQH 34
 Db 55 LSPHQH 61
 RESULT 13
 S3A2_HUMAN
 ID S3A2_HUMAN STANDARD; PRT; 464 AA.
 AC Q15428; 075245;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Splicing factor 3A subunit 2 (Spliceosome associated protein 62) (SAP
 DE 62) (SF3a66).
 DE SF3A2 OR SAP62.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RP BENNETT M., REED R.;
 RX MEDLINE=94023929; PubMed=8211113;
 RT "Correspondence between a mammalian spliceosome component and an
 essential yeast splicing factor.";
 Science 262:105-108(1993).
 [2]
 RP SEQUENCE FROM N.A.
 RA Lanerding J.E., McCready P.M., Skowronski E., Adamson A.W.,
 RA Burkhardt-Schultz K.J., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Garges J.,
 RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
 RA Liu S., Attix C., Andreise T., Trankhelm M., Amico-Keller G.,
 RA Cosfield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
 RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
 RA Kobayashi A., Olsen A.S., Carrano A.V.;
 RA "Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a
 RT serine protease gene cluster.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Lung, and Lymph;
 RC MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Groumouz J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RN CHARACTERIZATION OF THE SPICEOSOME.
 RX MEDLINE=20337962; PubMed=10882114;
 RA Das R., Zhou Z., Reed R.;
 RT "Functional association of U2 snRNP with the ATP-independent
 RT spliceosomal complex E.";
 RL Mol. Cell 5:779-787(2000).
 CC -1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
 CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE
 CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT
 CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS
 CC ESSENTIAL, IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE
 CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.
 CC -1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF
 CC THREE SUBUNITS: SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP114. SF3A
 CC ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO
 CC FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SF3A2 FAMILY.
 CC -1- SIMILARITY: Contains 1 matrix-type zinc finger.
 CC -----
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 CC -----
 DR EMBL; L21990; AAA60301.1; -;
 DR EMBL; AC005263; AAC25613.1; -;
 DR EMBL; BC004434; AAH04434.1; -;
 DR EMBL; BC009903; AAH09903.1; -;
 DR PIR; A47655; A47655.

DR MEROPS: C44.001; --
DR InterPro: IPR005854; Amd_phospho_trans.
DR InterPro: IPR00583; Gatase_2.
DR InterPro: IPR002375; Pr/py_ip.transf.
DR InterPro: IPR000836; PRtransferase.
DR Pfam: PF00310; Gatase_2; 1.
DR Pfam: PF00156; Ribosyltran; 1.
DR TIGRFAMs: TIGR01134; purF; 1.
DR PROSITE: PS00103; PUR_PVR_PR_TRANSFER; FALSE_NEG.
DR PROSITE: PS00443; GATASE_TYPE_II; FALSE_NEG.
KW Purine biosynthesis; Transferase; Glycosyltransferase;
KW Glutamine amidotransferase.
FT PROPEP 1 26 BY SIMILARITY.
FT CHAIN 27 493 AMIDOPHOSPHORIBOSYLTRANSFERASE.
FT ACT_SITE 27 27 GATASE (BY SIMILARITY).
SQ SEQUENCE 493 AA; 53809 MW; E03508F8A922910C CRC64;

Query Match 6.0%; Score 7; DB 1; Length 493;
Best Local Similarity 100.0%; pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 110 AKEAPAD 116
| | | | |
Db 299 AKEAPAD 305

Search completed: September 11, 2003, 17:52:38
Job time : 24.5241 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:02 : Search time 111.995 Seconds
(without alignments)
269.586 Million cell updates/sec

Title: US-09-853-253-2
Perfect score: 117
Sequence: 1 MPSPGTVCVSLLLGLMLDL.....LGKFLQDILWEAKEAPADK 117

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 71 | 60.7 | 117 | 4 | Q8TAT9 |
| 2 | 18 | 15.4 | 117 | 11 | Q8CH53 |
| 3 | 8 | 6.8 | 23 | 2 | Q9R5D1 |
| 4 | 8 | 6.8 | 111 | 13 | Q8JFY4 |
| 5 | 8 | 6.8 | 116 | 13 | Q8AV73 |
| 6 | 8 | 6.8 | 313 | 2 | Q8VP52 |
| 7 | 8 | 6.8 | 433 | 10 | Q93ZV7 |
| 8 | 8 | 6.8 | 433 | 10 | Q8L7E4 |
| 9 | 8 | 6.8 | 483 | 10 | Q65529 |
| 10 | 7 | 6.0 | 103 | 16 | Q9L063 |
| 11 | 7 | 6.0 | 114 | 16 | Q8FF03 |
| 12 | 7 | 6.0 | 138 | 16 | Q9KCN5 |
| 13 | 7 | 6.0 | 140 | 6 | Q8HXR4 |
| 14 | 7 | 6.0 | 143 | 5 | Q9VDP0 |
| 15 | 7 | 6.0 | 152 | 5 | Q9XZC4 |
| 16 | 7 | 6.0 | 207 | 16 | Q9I4Y8 |

| | | | | | | |
|----|---|-----|-----|----|--------|--------------------|
| 17 | 7 | 6.0 | 216 | 16 | Q9RW31 | Q9RW31 deinococcus |
| 18 | 7 | 6.0 | 235 | 5 | Q9U2L3 | Q9U2L3 caenorhabdi |
| 19 | 7 | 6.0 | 243 | 16 | Q8DBD4 | Q8DBD4 vibrio vuln |
| 20 | 7 | 6.0 | 247 | 16 | Q9KPY9 | Q9KPY9 vibrio chol |
| 21 | 7 | 6.0 | 253 | 16 | Q9CPE0 | Q9CPE0 pasteurie |
| 22 | 7 | 6.0 | 267 | 16 | Q9L1R0 | Q9L1R0 streptomyce |
| 23 | 7 | 6.0 | 280 | 6 | Q95JM5 | Q95JM5 macaca fasc |
| 24 | 7 | 6.0 | 289 | 16 | Q8EVS8 | Q8EVS8 mycoplasma |
| 25 | 7 | 6.0 | 365 | 11 | Q8BW62 | Q8BW62 mus musculu |
| 26 | 7 | 6.0 | 371 | 6 | Q8SPU3 | Q8SPU3 sus scrofa |
| 27 | 7 | 6.0 | 405 | 13 | Q8AVV0 | Q8AVV0 xenopus lae |
| 28 | 7 | 6.0 | 406 | 16 | Q8Z8Z8 | Q8Z8Z8 salmonella |
| 29 | 7 | 6.0 | 428 | 10 | Q94IQ8 | Q94IQ8 zea mays (m |
| 30 | 7 | 6.0 | 428 | 11 | Q8C1F2 | Q8C1F2 mus musculu |
| 31 | 7 | 6.0 | 433 | 16 | Q8CNV4 | Q8CNV4 staphylococ |
| 32 | 7 | 6.0 | 435 | 10 | Q8LGD9 | Q8LGD9 arabidopsis |
| 33 | 7 | 6.0 | 435 | 10 | Q9LNE6 | Q9LNE6 arabidopsis |
| 34 | 7 | 6.0 | 438 | 11 | Q8BL56 | Q8BL56 mus musculu |
| 35 | 7 | 6.0 | 443 | 16 | Q9A6Z5 | Q9A6Z5 caulobacter |
| 36 | 7 | 6.0 | 444 | 16 | Q9AB53 | Q9AB53 caulobacter |
| 37 | 7 | 6.0 | 452 | 2 | Q9XCK2 | Q9XCK2 streptococ |
| 38 | 7 | 6.0 | 495 | 11 | Q8K124 | Q8K124 mus musculu |
| 39 | 7 | 6.0 | 497 | 16 | Q9A0P2 | Q9A0P2 streptococ |
| 40 | 7 | 6.0 | 497 | 16 | Q8NZR7 | Q8NZR7 streptococ |
| 41 | 7 | 6.0 | 502 | 6 | Q9BDI4 | Q9BDI4 ovis aries |
| 42 | 7 | 6.0 | 502 | 6 | Q95L23 | Q95L23 sus scrofa |
| 43 | 7 | 6.0 | 502 | 11 | Q9QV77 | Q9QV77 rattus sp. |
| 44 | 7 | 6.0 | 562 | 11 | Q9CZT0 | Q9CZT0 mus musculu |
| 45 | 7 | 6.0 | 562 | 11 | Q8C3S5 | Q8C3S5 mus musculu |

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY: PRT; 117 AA.
AC Q8TAT9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Ghrelin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025791; AAH25791.1; -;
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
SQ SEQUENCE 117 AA; 12939 MW; 2580572EBECB7610 CRC64;

Query Match 60.7%; Score 71; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.5e-65;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPGTVCVSLLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPQPRALAGWLRLPE 60
DB 1 MPSPGTVCVSLLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPQPRALAGWLRLPE 60
QY 61 DGGQAEAGAEDE 71
DB 61 DGGQAEAGAEDE 71

RESULT 2

Q8CH53

```
ID Q8CH53 PRELIMINARY; PRT; 117 AA.
AC Q8CH53;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Eukaryotes unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AAO06965.1; -.
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 15.4%; Score 18; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 QQRKSKPPAKLPQPRAL 53
Db 36 QQRKSKPPAKLPQPRAL 53
|||||
|||||

RESULT 3
ID Q9R5D1 PRELIMINARY; PRT; 23 AA.
AC Q9R5D1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 14 kDa aggregative adherence fimbriae I protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE.
RA MEDLINE=93162805; PubMed=8094379;
RA Nataro J.P., Yikang D., Giron J.A., Savarino S.J., Kothary M.H.,
RA Hall R.;
RT "Aggregative adherence fimbria I expression in enteroaggregative
RT Escherichia coli requires two unlinked plasmid regions.";
RL Infect. Immun. 61:1126-1131(1993).
SQ SEQUENCE 23 AA; 2403 MW; 688113EAC484CE1E CRC64;

Query Match 6.8%; Score 8; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 IKLSGVQY 91
Db 16 IKLSGVQY 23
|||||
|||||

RESULT 4
ID Q8JFY4 PRELIMINARY; PRT; 111 AA.
AC Q8JFY4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Prepro-ghrelin precursor.
GN GHRELIN.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
```

```
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Kalya H., Kojima M., Hosoda H., Riley L.G., Hirano T., Grau G.E.,
RA Kangawa K.;
RT "Identification of eel ghrelin.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062427; BAB96565.1; -.
KW Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 111 PROGHRELIN.
FT CHAIN 27 48 GHRELIN-21.
SQ SEQUENCE 111 AA; 12831 MW; 7AF95E04DD22DE7B CRC64;

Query Match 6.8%; Score 8; DB 13; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AGSSFSLSP 30
Db 26 AGSSFSLSP 33
|||||
|||||

RESULT 5
ID Q8AV73 PRELIMINARY; PRT; 116 AA.
AC Q8AV73;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin precursor.
GN GHR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=22181232; PubMed=12193558;
RA Kalya H., Van der Geyten S., Kojima M., Hosoda H., Kitajima Y.,
RA Matsumoto M., Geelissen S., Darras V.M., Kangawa K.;
RT "Chicken ghrelin: purification, cDNA cloning, and biological
RT activity";
RL Endocrinology 143:3454-3463(2002).
DR EMBL; AB075215; BAC24980.1; -.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 49 GHRELIN-26.
SQ SEQUENCE 116 AA; 13227 MW; F5C5FA038F187DE9 CRC64;

Query Match 6.8%; Score 8; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AGSSFSLSP 30
Db 23 AGSSFSLSP 30
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|||||

RESULT 6
ID Q8VP52 PRELIMINARY; PRT; 313 AA.
AC Q8VP52;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE LysR-like transcriptional activator SnpR.
OS Streptomyces sp. C5.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Streptomycineae; Streptomyces.
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OX NCBI_TaxID=45212;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C5;
RA DeSanti C.L., Strohl W.R.;
RT "Characterization of the Streptomyces sp. strain C5 snp locus and
   development of an snp-derived expression vector family.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
   REGULATORS.
DR EMBL: AY072041; AAL61992.1; -.
DR InterPro: IPR000847; HTH_LysR.
DR InterPro: IPR005119; LysR_subst.
DR Pfam: PF00126; HTH_1; 1.
DR DR Pfam: PF03466; LysR_substrate; 1.
DR PRINTS: PR00039; HTHLYSR.
DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; transcription; transcription regulation.
SQ SEQUENCE 313 AA; 34258 MW; C907C8AF51C3FA13 CRC64;

Query Match 6.8%; Score 8; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RALAGWLR 58
DB 102 RALAGWLR 109

RESULT 7
Q932V7 ID Q932V7 PRELIMINARY; PRT; 433 AA.
AC Q932V7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative RNA-binding protein LAH1.
GN AT4G32720.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene AT4G32720 (GI:7270219).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY056237; AAL07086.1; -.
DR InterPro: IPR002344; Lupus.La.
DR InterPro: IPR006630; Lupus.La_dom.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00076; rrm; 1.
DR PRINTS: PR00302; LUPUSLA.
DR SMART: SM00715; LA; 1.
DR PROSITE: PS50102; RRM; 1.
SQ SEQUENCE 433 AA; 48095 MW; E58EBAF51C35A8F7 CRC64;

Query Match 6.8%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 QAEGAED 71
DB 287 QAEGAED 294

RESULT 8
Q932V7 ID Q932V7 PRELIMINARY; PRT; 433 AA.
AC Q932V7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative RNA-binding protein LAH1.
GN AT4G32720.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY136302; AAM96968.1; -.
DR EMBL: BT000396; AAN15715.1; -.
DR InterPro: IPR002344; Lupus.La.
DR InterPro: IPR006630; Lupus.La_dom.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00076; rrm; 1.
DR PRINTS: PR00302; LUPUSLA.
DR SMART: SM00715; LA; 1.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS50102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 433 AA; 48126 MW; CFF6F611A29AA0318 CRC64;

Query Match 6.8%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 QAEGAED 71
DB 287 QAEGAED 294

RESULT 9
O65529 ID O65529 PRELIMINARY; PRT; 483 AA.
AC O65529;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 54.1 kDa protein.
GN F4D11.80 OR AT4G32720.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

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RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoerge W., Hoheisel J.,
RA Meves H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoerge W., Meves H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022537; CAAL18589.1; -.
DR EMBL; AL161582; CAB79989.1; -.
DR InterPro; IPR002344; Lupus.La.
DR InterPro; IPR006630; Lupus.La.dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 483 AA; 54125 MW; 20840B34A0BC94E2 CRC64;

Query Match 6.8%; Score 8; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 QAEGAED 71
| | | | | | |
Db 302 QAEGAED 309

RESULT 10
Q9L063 PRELIMINARY; PRT; 103 AA.
AC Q9L063;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SC02791.
GN SC02791 OR SC0105.22C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Gobie A., Hidaigo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939114; CAB87228.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 103 AA; 10639 MW; 9316F1F38C1BD492 CRC64;

Query Match 6.0%; Score 7; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 DGGQAG 67
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Db 48 DGGQAG 54

RESULT 11
Q8FF03 PRELIMINARY; PRT; 114 AA.
AC Q8FF03;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein yfim.
GN YFIM OR C3111.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=2238234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Maynew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016764; AAN81560.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 114 AA; 12611 MW; 8FEC5A91285FA0A8 CRC64;

Query Match 6.0%; Score 7; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VCSLLLL 13
| | | | |
Db 13 VCSLLLL 19

RESULT 12
Q9KCN5 PRELIMINARY; PRT; 138 AA.
AC Q9KCN5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BHI534.
GN BHI534.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001512; BAB05253.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 138 AA; 15918 MW; C75E1FDFE5F972FF CRC64;

Query Match 6.0%; Score 7; DB 16; Length 138;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 EVRENAP 79
| | | | |
Db 10 EVRENAP 16

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RESULT 13
Q8HXR4
ID Q8HXR4 PRELIMINARY; PRT; 140 AA.
AC Q8HXR4
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Bone morphogenetic protein receptor 1B (Fragment).
GN BMP1B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Cumulus oocyte complex;
RA Einspanier R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Cumulus oocyte complex;
RA Schoenfelder M.;
RL "Expression of ovarian growth factors.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ534389; CAD59880.1; -.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 16076 MW; 0DC51D1517C1A4A6 CRC64;

Query Match 6.0%; Score 7; DB 6; Length 140;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVCSLLL 12
DB 47 TVCSLLL 53

RESULT 14
Q9VDP0
ID Q9VDP0 PRELIMINARY; PRT; 143 AA.
AC Q9VDP0
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE CG10883 protein.
GN CG10883.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananthan S.P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Gaig N.S., Gelbart W.M., Glaser K.,
RA Glodek A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003729; AAF55750.1; -.
DR FlyBase: FBgn0038781; CG10883.
SQ SEQUENCE 143 AA; 14645 MW; 09FE17B83214692B CRC64;

Query Match 6.0%; Score 7; DB 5; Length 143;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLLLL 16
DB 98 LLLLLL 104

RESULT 15
Q9XZC4
ID Q9XZC4 PRELIMINARY; PRT; 152 AA.
AC Q9XZC4
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Serine proteinase (Fragment).
GN T684.
OS Helicoverpa armigera (Cotton bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=29058;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IARI;
RA Mazumdar-Leighton S., Babu C.R., Bennett J.;
RT "Identification of novel serine proteinase gene transcripts in the
RT midguts of two tropical agricultural pests, Scirpophaga incertulas
RT (Wk.) and Helicoverpa armigera (Hb.).";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF134490; RAD31713.1; -.
DR HSSP: P00761; IAKS.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR SMART: SM00020; tryp_Spc; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1 1
FT NON_TER 152 152
SQ SEQUENCE 152 AA; 16933 MW; 1AB9F5115392A319 CRC64;

Query Match 6.0%; Score 7; DB 5; Length 152;

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Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PSPGTV 8
Db 89 PSPGTV 95

Search completed: September 11, 2003, 17:55:45
Job time : 114.995 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 122.005 Seconds
(without alignments)
152.215 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 611

Sequence: 1 MSPGTCVCSLLGLGLDL.....LCKFLQDILWEAKEAPADK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 611 | 100.0 | 117 | 20 | AAW87991 |
| 2 | 611 | 100.0 | 117 | 21 | AA1987236 |
| 3 | 611 | 100.0 | 117 | 22 | AA1988990 |
| 4 | 611 | 100.0 | 117 | 22 | AA1982649 |
| 5 | 611 | 100.0 | 117 | 22 | AA19820101 |
| 6 | 611 | 100.0 | 117 | 22 | AA1980511 |
| 7 | 611 | 100.0 | 117 | 23 | AA19878319 |
| 8 | 611 | 100.0 | 117 | 23 | AA19823838 |
| 9 | 611 | 100.0 | 117 | 23 | AA19815883 |

| | | | | | | |
|----|-------|-------|-----|----|-----------|--------------------|
| 10 | 611 | 100.0 | 117 | 24 | ABU66790 | Human PRO polypept |
| 11 | 611 | 100.0 | 117 | 24 | ABU67066 | Human secreted/tra |
| 12 | 611 | 100.0 | 117 | 24 | ABU59871 | Novel secreted and |
| 13 | 611 | 100.0 | 117 | 24 | ABU59124 | Novel human secret |
| 14 | 611 | 100.0 | 117 | 24 | ABU59271 | Human secreted/tra |
| 15 | 611 | 100.0 | 117 | 24 | ABU59420 | Novel human secret |
| 16 | 611 | 100.0 | 117 | 24 | ABU60555 | Human secreted/tra |
| 17 | 611 | 100.0 | 117 | 24 | ABU58046 | Human PRO polypept |
| 18 | 611 | 100.0 | 117 | 24 | ABU58977 | Human secreted/tra |
| 19 | 611 | 100.0 | 117 | 24 | AAE33409 | Human preproghrell |
| 20 | 611 | 100.0 | 117 | 24 | ABU13937 | Human PRO1066 poly |
| 21 | 611 | 100.0 | 117 | 24 | ABU10892 | Human PRO polypept |
| 22 | 611 | 100.0 | 118 | 21 | AA198708 | Membrane-bound pro |
| 23 | 611 | 100.0 | 118 | 22 | AAU12392 | Human PRO1066 poly |
| 24 | 611 | 100.0 | 118 | 22 | AA1985231 | Human PRO1066 (UNQ |
| 25 | 611 | 100.0 | 126 | 22 | AA1980676 | Human polypeptide |
| 26 | 595.5 | 97.5 | 116 | 22 | AA1980517 | Human des-Gln14-gh |
| 27 | 518 | 84.8 | 117 | 22 | AA1980510 | Rat ghrelin prepro |
| 28 | 502.5 | 82.2 | 116 | 22 | AA1980516 | Rat des-Gln14-ghre |
| 29 | 472.5 | 77.3 | 118 | 22 | AA1980520 | Porcine ghrelin pr |
| 30 | 457 | 74.8 | 117 | 22 | AA1980521 | Porcine des-Gln14- |
| 31 | 392 | 64.2 | 90 | 23 | ABP08375 | Human ORFX protein |
| 32 | 392 | 64.2 | 91 | 24 | AA1983410 | Human exon 3-delet |
| 33 | 315.5 | 51.6 | 89 | 22 | AA1980523 | Bovine ghrelin pre |
| 34 | 146 | 23.9 | 108 | 22 | AA1980531 | Eel ghrelin-like G |
| 35 | 145 | 23.7 | 28 | 22 | AA1980509 | Human ghrelin, SQ |
| 36 | 145 | 23.7 | 28 | 23 | AB1980532 | Human ghrelin, Ho |
| 37 | 145 | 23.7 | 28 | 23 | AA198032 | Human ghrelin pept |
| 38 | 141 | 23.1 | 28 | 23 | AA198021 | Human ghrelin pept |
| 39 | 141 | 23.1 | 28 | 23 | AA198027 | Human ghrelin pept |
| 40 | 141 | 23.1 | 28 | 23 | AA198028 | Human ghrelin pept |
| 41 | 141 | 23.1 | 28 | 23 | AA198029 | Human ghrelin pept |
| 42 | 141 | 23.1 | 28 | 23 | AA198030 | Human ghrelin pept |
| 43 | 141 | 23.1 | 28 | 23 | AA198031 | Human ghrelin pept |
| 44 | 141 | 23.1 | 28 | 23 | AA198033 | Human ghrelin pept |
| 45 | 141 | 23.1 | 28 | 23 | AA198034 | Human ghrelin pept |

ALIGNMENTS

RESULT 1
AAW87991
ID AAW87991 standard; Protein; 117 AA.
XX
AC AAW87991;
XX
DT 07-APR-1999 (first entry)
XX
DE Protein designated zsig33.
XX
KW Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
KW nutrient absorption regulation; obesity; metabolic disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /note= "signal peptide"
FT Protein 24..117
FT /note= "mature protein"
XX
PN WO9842840-A1.
XX
PD 01-OCT-1998.
XX
PF 23-MAR-1998; 98WO-US05620.
XX
PR 24-MAR-1997; 97US-0822897.
XX
PR 24-MAR-1997; 97US-0041102.
XX
PA (ZYMO) ZYMOGENETICS INC.

PI Delsner TA, Sheppard PO;
 XX WPI; 1999-070071/06.
 DR N-PSDB; AAX04550.
 XX Human polypeptide having homology to motilin, zsi933 - useful e.g.
 PT to treat gastrointestinal motility disorders, obesity etc. and to
 PT identify antagonists to treat gastrointestinal hypermotility
 XX
 PS Claim 13; Page 55-56; 69pp; English.
 XX
 CC The present sequence represents a protein designated zsi933. The nucleic
 CC acids are strongly expressed in stomach tissue. The polypeptide (or
 CC allelic variants/orthologs) can be used to stimulate gastric motility,
 CC measured as increased transit time or gastric emptying of an ingested
 CC substance in mammals. The products are used to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes/acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
 CC absorption regulation. Zsi933 polypeptides may also be important
 CC neurologically, since the family of gut-brain peptides to which the
 CC homologous protein motilin belongs has been associated with neurological
 CC and CNS functions. They may therefore be used e.g. to regulate satiety
 CC or treat obesity and other metabolic disorders where neurological
 CC feedback modulates nutritional absorption. They are useful to identify
 CC zsi933 agonists, antagonists and ligands and to produce antibodies.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 611; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.6e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQRKSKPPAKLPQALAGWLRPE 60
 DB 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQRKSKPPAKLPQALAGWLRPE 60
 QY 61 DGGQAEAGAEDELEVRNAPFDVGKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
 DB 61 DGGQAEAGAEDELEVRNAPFDVGKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
 RESULT 2
 AAY87236
 ID AAY87236 standard; Protein: 117 AA.
 XX
 AC AAY87236;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
 XX
 KW Human: signal peptide-containing protein: HSPP; diagnosis: cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 PN WO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 XX 25-JUN-1999; 99WO-US14484.
 PF
 XX 26-JUN-1998; 98US-0090762.
 PR
 XX 31-JUL-1998; 98US-0094983.
 PR
 XX 01-OCT-1998; 98US-0102686.
 PR

PR 11-DEC-1998; 98US-0112129.
 XX (INCY-) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone CA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX WPI; 2000-160673/14.
 DR N-PSDB; AAZ98121.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease
 XX
 PS Claim 1; Page 168-169; 327pp; English.
 XX
 CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
 CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can
 CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPP. Antagonists of
 CC HSPP are used to treat or prevent disorders associated with increased
 CC activity or function of HSPP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
 CC nucleic acids can be used for the recombinant production of HSPP, for
 CC detecting HSPP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPP
 CC from natural sources.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 611; DB 21; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.6e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQRKSKPPAKLPQALAGWLRPE 60
 DB 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQRKSKPPAKLPQALAGWLRPE 60
 QY 61 DGGQAEAGAEDELEVRNAPFDVGKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
 DB 61 DGGQAEAGAEDELEVRNAPFDVGKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
 RESULT 3
 AAM38890
 ID AAM38890 standard; Protein: 117 AA.
 XX
 AC AAM38890;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2035.
 XX
 KW Human: neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

```

XX OS Homo sapiens.
XX KW WO200153312-A1.
XX PN 26-JUL-2001.
XX PD 26-DEC-2000; 2000WO-US3263.
XX PF 21-JAN-2000; 2000US-0488725.
XX PR 25-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.
XX PR 29-NOV-2000; 2000US-0727344.
XX PA (HYSE-) HYSEQ INC.
XX XX
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX XX
XX DR WPI; 2001-442253/47.
XX DR N-PSDB; AAI58046.
XX XX
XX PT Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries -
XX XX
XX PS Example 3; SEQ ID NO 2035; 10078pp; English.
XX XX
XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
XX CC the encoded polypeptides (AAI38642-AAI42213) with nootropic,
XX CC immunosuppressant and cytostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression,
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX CC C.N.S disorders.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification.
XX XX
XX SQ Sequence 117 AA;
XX XX
XX Query Match 100.0%; Score 611; DB 22; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 4.6e-59;
XX Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1 MPSPGTVCSSLLGLMLWLDLAMAGSSFLSPFHQRVQQRKESKPPAKLPALAGWLRLPE 60
XX DB 1 MPSPGTVCSSLLGLMLWLDLAMAGSSFLSPFHQRVQQRKESKPPAKLPALAGWLRLPE 60
XX XX
XX QY 61 DGGQAGAGDELEVRNAPFDVGIKLSGVQYQHQSOALGKFLQDILWEEAKEAPADK 117
XX DB 61 DGGQAGAGDELEVRNAPFDVGIKLSGVQYQHQSOALGKFLQDILWEEAKEAPADK 117
XX XX
XX RESULT 4
XX AAB62649
XX ID AAB62649 standard; Protein; 117 AA.
XX XX
XX AC AAB62649;
XX XX
XX DT 23-JUL-2001 (first entry)
XX XX
XX DE Human zsig33 polypeptide.

```

```

XX XX zsig33; signal transduction; hormone; enzyme; neural development;
XX KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
XX KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
XX KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
XX KW G-protein coupled receptor.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT Peptide 24..37
XX FT /note= "specifically claimed fragment that binds to
XX FT the GHS-R"
XX XX
XX PN WO200138355-A2.
XX XX
XX PD 31-MAY-2001.
XX XX
XX PF 22-NOV-2000; 2000WO-US32074.
XX XX
XX PR 22-NOV-1999; 99US-0166765.
XX XX
XX PA (ZYMO ) ZYMOGENETICS INC.
XX XX
XX PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX XX
XX DR WPI; 2001-355879/37.
XX DR N-PSDB; AAF83678.
XX XX
XX PT Forming reversible peptide receptor complex for purifying cell and
XX PT peptides, stimulating signal transduction and modulating hormone
XX PT secretion, involves contacting a receptor with zsig33 polypeptide -
XX XX
XX XX Claim 1; Page 93-94; 111pp; English.
XX XX
XX CC The invention relates to a method of forming a reversible peptide-
XX CC receptor complex that involves providing an immobilized receptor, and
XX CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
XX CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
XX CC is useful for purifying cells, purifying a peptide, stimulating signal
XX CC transduction in a cell expressing a receptor. It is also useful for
XX CC modulating secretion of hormones, neural development and/or utilization,
XX CC gastric contractility, nutrient uptake, secretion of digestive and
XX CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
XX CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
XX CC hormone secretion in a mammal having a disease associated with abnormal
XX CC levels of growth hormone, such as osteoporosis, bone repair, bone
XX CC remodeling, low osteoblast levels, cartilage repair and remodeling,
XX CC skeletal dysplasia, immune suppression, obesity, growth retardation,
XX CC protein catabolic responses after surgery, cachexia, protein loss,
XX CC dwarfism, wound healing and ovulation induction, treating a mammal having
XX CC a metabolic disorder requiring neurological feedback, such as satiety
XX CC regulation, glucose absorption and metabolism and neuropathy-associated
XX CC gastrointestinal disorders, and stimulating glucose-induced insulin
XX CC release in a mammal. The present sequence represents the human zsig33
XX CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
XX XX
XX SQ Sequence 117 AA;
XX XX
XX Query Match 100.0%; Score 611; DB 22; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 4.6e-59;
XX Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1 MPSPGTVCSSLLGLMLWLDLAMAGSSFLSPFHQRVQQRKESKPPAKLPALAGWLRLPE 60
XX DB 1 MPSPGTVCSSLLGLMLWLDLAMAGSSFLSPFHQRVQQRKESKPPAKLPALAGWLRLPE 60
XX XX
XX QY 61 DGGQAGAGDELEVRNAPFDVGIKLSGVQYQHQSOALGKFLQDILWEEAKEAPADK 117
XX DB 61 DGGQAGAGDELEVRNAPFDVGIKLSGVQYQHQSOALGKFLQDILWEEAKEAPADK 117
XX XX
XX RESULT 5

```

AAB20101
 ID AAB20101 standard; Protein; 117 AA.
 XX AAB20101;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE zsig33 protein.
 XX
 KW SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
 KW nutritional absorption modulator; growth hormone secretagogue;
 KW therapy; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Signal_peptide
 FT Protein 24..117
 FT /label= Mature_protein
 FT Peptide 24..34
 FT /label= SGIP_peptide
 FT /note= "this peptide is claimed in Claim 1"
 XX
 PN WO200100830-A1.
 XX PD 04-JAN-2001.
 XX
 PF 30-JUN-2000; 2000WO-US18306.
 XX
 PR 30-JUN-1999; 99US-0345157.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sheppard PO, Jaspers SR, Delsher TA, Bishop PD;
 XX
 DR WPI; 2001-123010/13.
 DR N-PSDB; AAF30033.
 XX
 XX Novel variants of SGIP peptides for modulating contractility in
 PT duodenum or jejunum tissue, pancreatic secretion of hormones and
 PT digestive enzymes, inducing growth hormone secretion or modulating
 PT gastric emptying -
 XX
 PS Disclosure; 54; 61pp; English.
 XX
 CC The present sequence is that of zsig33, a secreted protein with
 CC homology to motilin (see AAB20102). zsig33 is expressed at high
 CC levels in the stomach, and at lower levels in the small intestine
 CC and pancreas. A novel peptide fragment of zsig33, termed SGIP (see
 CC AAB20100), is claimed. SGIP is a ligand for growth hormone
 CC secretagogue receptor, and is therefore useful for modulating
 CC secretion of growth hormone and insulin like growth factor 1.
 CC SGIP, and variant SGIP peptides, are used in claimed methods for
 CC stimulating contractility in duodenum or jejunum tissue,
 CC modulating pancreatic secretion of hormones and digestive enzymes,
 CC inducing growth hormone secretion, and modulating gastric emptying.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.6e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWL RPE 60
 |||||
 DB 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWL RPE 60
 |||||
 OY 61 DGGQAEAGAEDELEVRNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117
 |||||
 DB 61 DGGQAEAGAEDELEVRNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117
 |||||

RESULT 6
 AAB60511
 ID AAB60511 standard; Protein; 117 AA.
 XX
 AC AAB60511;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human ghrelin preproprotein, SEQ ID NO:5.
 XX
 KW Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX
 PN WO200107475-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-JP04907.
 XX
 PR 23-JUL-1999; 99JP-0210002.
 PR 29-NOV-1999; 99JP-0338841.
 PR 26-APR-2000; 2000JP-0126623.
 XX
 PA (KANG/) KANGAWA K.
 XX
 PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 XX
 DR WPI; 2001-159704/16.
 DR N-PSDB; AAF59645.
 XX
 PT New peptide compounds which induce growth hormone secretion and
 FT elevate cell calcium concentrations, useful in treatment and diagnosis
 FT of infant growth disorders -
 XX
 PS Claim 3; Page 182; 210pp; Japanese.
 XX
 CC The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.6e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWL RPE 60
 |||||
 DB 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWL RPE 60
 |||||
 OY 61 DGGQAEAGAEDELEVRNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117
 |||||
 DB 61 DGGQAEAGAEDELEVRNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117
 |||||

RESULT 7

ABB78319
ID ABB78319 standard; Protein: 117 AA.

XX ABB78319;

05-DEC-2002 (first entry)

XX Amino acid sequence of a human zslq

| | |
|----|-------------------------------------|
| XX | Short gastrointestinal peptide; SGI |
| KW | Short gastrointestinal peptide; SGI |

XX
OS Homo sapiens.

| XX | Key | Location/Qualifiers |
|----|-----|---------------------|
| FH | | |

| FT | peptide | 1..23 | /note= "signal pept |
|----|---------|-------|---------------------|
| FT | | | |

| FT | Protein | 24..119 | /note= "mature prot |
|----|---------|---------|---------------------|
| FT | Protein | 24..119 | /note= "mature prot |

XX
PN
US6420521-B1.

XX
PD 16-JUL-2002.

XX
PF 30-JUN-2000; 2000US-0608810.

XX AAE23838: AC

| | |
|----|---------------------------|
| AC | ANZ5050, |
| XX | |
| DT | 10-SEP-2002 (first entry) |

DE Human zslg33 protein.
XX
XX 10 SEP 2002 (first entry)
DI

XX human zsig33 protein.
KW Human: zsig33-like peptide: gastric contractility; nutrient uptake;

KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.

XX Protein (heparin) glycosylated; endocrine, androgenic.
 QS Homo sapiens.

US2002055156-A1.

082002050130 HZ;
XX
PD 09-MAY-2002.

0.5 mm 2002.
XX
PF 10-MAY-2001: 2001US-0853253.

| | |
|----------|---|
| RESULT 9 | |
| AAEI5883 | |
| ID | AAEI5883 standard; Protein; 117 AA. |
| XX | |
| XX | AAEI5883; |
| XX | |
| DT | 26-MAR-2002 (first entry) |
| XX | |
| DE | Human zsig33 protein. |
| XX | |
| KW | Human; zsig33-like peptide; ZS3LP; immunity; developmental process; |
| KW | infection; human immunodeficiency virus; vaccine; antihypoglycaemic; |
| KW | adsorption enhancer; gastrointestinal disease; growth related disease; |
| KW | inflammation; gene therapy; growth regulation; blood vessel formation; |
| KW | HIV; zsig33 protein. |
| XX | |
| XX | Homo sapiens. |
| XX | |
| XX | |
| PH | Key |
| FT | Peptide |
| FT | 1..23 |
| FT | /label= Signal_peptide |
| FT | Protein |
| FT | 24..117 |
| FT | /note= "Human mature zsig33 protein" |
| XX | |
| PN | WO200187933-A2. |
| XX | |
| PD | 22-NOV-2001. |
| XX | |
| PF | 10-MAY-2001; 2001WO-US15091. |
| XX | |
| PR | 11-MAY-2000; 2000US-0569271. |
| XX | |
| PA | (ZYMO) ZYMOGENETICS INC. |
| XX | |
| PI | Jaspers SR, Sheppard PO, Deisher TA, Bishop PD; |
| XX | |
| DR | WPI; 2002-082982/11. |
| DR | N-PSDB; AAD25759. |
| XX | |
| PT | New polypeptides, useful for modulating gastric contractility, nutrient |
| PT | uptake, pancreatic secretion of hormones, digestive enzymes and |
| PT | treating gastrointestinal and growth related diseases, comprises |
| PT | zsig33-like peptides - |
| XX | |
| PS | Disclosure: Page 80-81: 89pp; English. |
| XX | |
| CC | The invention relates to zsig33-like peptides (ZS3LP) including |
| CC | zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and |
| CC | zsig33-epsilon peptides and nucleic acid molecules encoding such |
| CC | zsig33-like peptides. ZS3LP peptides activate the immune system |
| CC | in boosting immunity to infectious diseases, treating immunocompromised |
| CC | patients such as human immunodeficiency virus (HIV) patients, in |
| CC | improving vaccines and in treatment of bacterial, viral, protozoal and |
| CC | fungal infections. Peptides of the invention are used to identify and |
| CC | isolate receptors involved in growth regulation in the liver, blood |
| CC | vessel formation and other developmental processes. They are useful for |
| CC | evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate |
| CC | growth and/or differentiation of tumour cells, as additives to anti- |
| CC | hypoglycaemic preparations containing glucose and as adsorption |
| CC | enhancers for oral drugs which require fast nutrient action and to |
| CC | stimulate glucose-induced insulin release. They are also useful as |
| CC | research reagents for the expansion, differentiation, growth factor and |
| CC | hormone secretion and/or cell-cell interactions of tissues associated |
| CC | with gastrointestinal system, brain and central nervous system. These |
| CC | molecules are useful for treating dysfunction associated with contractile |
| CC | tissues or to suppress or enhance contractility in vivo and to treat |
| CC | gastrointestinal and growth related diseases. ZS3LP peptides, nucleic |
| CC | acids and/or antibodies are useful for treating disorders associated |
| CC | with gastrointestinal contractility, secretion of digestive enzymes, |
| CC | hormone and acids, secretion of hormones in the pancreas and/or brain, |
| CC | gastrointestinal motility, recruitment of digestive enzymes, inflammation |
| CC | and regulation of nutrient absorption. Sequences of the invention are |
| CC | useful in gene therapy. The present sequence is human zsig33 protein. |

[illegible]

PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 21-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-332040/31.
 DR

DR N-PSDB; ACA03823.
 XX New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification
 XX
 PS Claim 12; Fig 442; 660pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating the
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. ABU66570-ABU66844 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsideEntry.html.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 611; DB 24; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4, 6e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPTGVCSSLLLLGLMLDLAMAGSFLSPHEHQVQQRKESKPPAKLQPRALAGWL RPE 60
 Db 1 MPSPTGVCSSLLLLGLMLDLAMAGSFLSPHEHQVQQRKESKPPAKLQPRALAGWL RPE 60
 QY 61 DGGQAEAGDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
 Db 61 DGGQAEAGDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
 RESULT 11
 ABU67066
 ID ABU67066 standard; Protein; 117 AA.
 XX
 AC ABU67066;
 DT 27-MAY-2003 (first entry)
 XX
 DE Human secreted/transmembrane, PRO, protein SEQ ID 442.
 XX
 KW Human; secreted protein; transmembrane protein; PRO;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioreactor; tumour.
 XX
 OS Homo sapiens.
 XX
 XX US2003032155-A1.
 PN
 XX
 PD 13-FEB-2003.
 XX
 XX 03-MAY-2002; 2002US-0137865.
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.

PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 98WO-US00106.
 PR 08-MAR-1999; 98WO-US05028.
 PR 10-MAR-1999; 98WO-US05190.
 PR 20-APR-1999; 98WO-US08615.
 PR 14-MAY-1999; 98WO-US10733.
 PR 02-JUN-1999; 98WO-US12252.
 PR 01-SEP-1999; 98WO-US20111.
 PR 08-SEP-1999; 98WO-US20594.
 PR 13-SEP-1999; 98WO-US20944.
 PR 15-SEP-1999; 98WO-US21090.
 PR 15-SEP-1999; 98WO-US21547.
 PR 05-OCT-1999; 98WO-US23089.
 PR 29-NOV-1999; 98WO-US28214.
 PR 30-NOV-1999; 98WO-US28313.
 PR 30-NOV-1999; 98WO-US28409.
 PR 01-DEC-1999; 98WO-US28301.
 PR 01-DEC-1999; 98WO-US28634.
 PR 02-DEC-1999; 98WO-US28551.
 PR 02-DEC-1999; 98WO-US28564.
 PR 02-DEC-1999; 98WO-US28585.
 PR 16-DEC-1999; 98WO-US30095.
 PR 20-DEC-1999; 98WO-US30911.
 PR 20-DEC-1999; 98WO-US30999.
 PR 22-DEC-1999; 98WO-US30720.
 PR 30-DEC-1999; 98WO-US31243.
 PR 30-DEC-1999; 98WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 28-JUL-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06320.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.

PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-331925/31.

DR N-PSDB; ACA04244.

XX New secreted and transmembrane nucleic acids and polypeptides,
 designated as PRO, useful for treating inflammation, organ failure,
 atherosclerosis, cardiac injury, infertility, birth defects, premature
 aging, AIDS, or cancer

XX Claim 12; Fig 442; 659pp; English.

PS The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 611; DB 24; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.6e-59;

Matches 117: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSGTVCSLLLGLMWLDLAWAGSSFLSPHQVQQRKESKPKAKLPQPRALAGWLPE 60
|||||
Db 1 MPSGTVCSLLLGLMWLDLAWAGSSFLSPHQVQQRKESKPKAKLPQPRALAGWLPE 60
|||||

QY 61 DGGQAGAEDELEVRFNAPFDVGKLSGVYQHQHSGALGKFLQDLILWEAKEAPADK 117
|||||
Db 61 DGGQAGAEDELEVRFNAPFDVGKLSGVYQHQHSGALGKFLQDLILWEAKEAPADK 117
|||||

RESULT 12
ABU59871
ID ABU59871 standard; Protein: 117 AA.
AC ABU59871;
XX
DT 13-MAY-2003 (first entry)
XX
DE Novel secreted and transmembrane protein PRO1066.
XX
KW Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
QN
PN
PD US2003017563-A1.
XX
XX 23-JAN-2003.
XX
XX 07-MAY-2002; 2002US-0140808.
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12450.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24853.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.
PR 16-DEC-1999; 99WO-US28565.
PR 20-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 22-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 05-JAN-2000; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX

DR WPI; 2003-148238/14.
 DR N-PSDB; ABX89361.
 XX
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments -
 XX
 XX
 PS Claim 12; Fig 442; 659pp; English.
 PS
 XX
 CC The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of
 CC retinal neurons cells (PRO132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO130, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and
 CC are thus useful for treating sports injuries, and arthritis. This
 CC is the amino acid sequence of a novel human PRO protein.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 611; DB 24; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.6e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MPSPTVCSLLGLGLDLAMAGSSFLSPSEHORVQQRKESKPPAKLQPRALAGWLRLPE 60
 Db 1 MPSPTVCSLLGLGLDLAMAGSSFLSPSEHORVQQRKESKPPAKLQPRALAGWLRLPE 60
 Qy 61 DGGQGAEGAEDELEVRFPDVGIKLSGVYQVQHSQALGRFLQDILWEAKEAPADK 117
 Db 61 DGGQGAEGAEDELEVRFPDVGIKLSGVYQVQHSQALGRFLQDILWEAKEAPADK 117
 RESULT 13
 ABUS9124
 ID ABUS9124 standard; Protein; 117 AA.
 AC ABUS9124;
 XX
 XX 28-APR-2003 (first entry)
 XX
 XX Novel human secreted or transmembrane protein PRO1066.
 XX
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosum; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;

KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.
 XX Homo sapiens.
 XX US2002132252-A1.
 XX 19-SEP-2002.
 XX
 XX 14-NOV-2001; 2001US-0990442.
 XX
 PR 05-NOV-1997; 97WO-US20069.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US12252.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 30-NOV-1999; 99WO-US28313.
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 PR 16-DEC-1999; 99WO-US28634.
 PR 20-DEC-1999; 99WO-US30095.
 PR 06-JAN-2000; 99WO-US30911.
 PR 06-JAN-2000; 2000WO-US00219.
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 PR 28-AUG-2001: 2001US-0941992.

(GETH) GENENTECH INC.

XX
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber AL, Herritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;

XX WPI: 2003-247083/24.
 DR N-PSDB: ABX80294.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments

XX Claim 12; Fig 186; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with

CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and
 CC are thus useful for treating sports injuries, and arthritis. This
 CC is the amino acid sequence of a novel human PRO protein.
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 KW diagnostic; biosensor; bioreactor; tumour; therapeutic;
 KW gene therapy; tumour-associated antigenic target; FAT; ADEPT;
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 OS Homo sapiens.
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XX DT 22-APR-2003 (first entry)
XX DE Novel human secreted or transmembrane protein PRO1184.
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KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX OS Homo sapiens.
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XX PD 06-FEB-2003.
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 31.2834 Seconds
(without alignments)
158.243 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 611

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Post-processing: Minimum Match 0%

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- 5: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 611 | 100.0 | 117 | 3 | US-09-046-479-2 |
| 2 | 611 | 100.0 | 117 | 4 | US-08-822-897C-2 |
| 3 | 611 | 100.0 | 117 | 4 | US-09-608-810A-4 |
| 4 | 611 | 100.0 | 117 | 4 | US-09-996-243-268 |
| 5 | 86 | 14.1 | 119 | 3 | US-09-046-479-4 |
| 6 | 86 | 14.1 | 119 | 4 | US-08-822-897C-4 |
| 7 | 86 | 14.1 | 119 | 4 | US-09-608-810A-5 |
| 8 | 73 | 11.9 | 323 | 3 | US-09-029-213B-25 |
| 9 | 72.5 | 11.9 | 244 | 1 | US-08-696-827-1 |
| 10 | 72.5 | 11.9 | 773 | 4 | US-09-252-991A-23192 |
| 11 | 70 | 11.5 | 220 | 2 | US-08-761-248B-4 |
| 12 | 69.5 | 11.4 | 247 | 4 | US-09-252-991A-27419 |
| 13 | 69.5 | 11.4 | 341 | 4 | US-09-252-991A-27327 |
| 14 | 69 | 11.3 | 406 | 4 | US-09-252-991A-28102 |
| 15 | 69 | 11.3 | 1088 | 3 | US-09-130-242-2 |
| 16 | 68.5 | 11.2 | 360 | 4 | US-09-252-991A-17420 |
| 17 | 68.5 | 11.2 | 676 | 4 | US-09-252-991A-24713 |
| 18 | 67.5 | 11.0 | 901 | 4 | US-09-252-991A-25653 |
| 19 | 67 | 11.0 | 699 | 4 | US-09-252-991A-17073 |
| 20 | 66.5 | 10.9 | 443 | 4 | US-09-252-991A-29446 |
| 21 | 66 | 10.8 | 174 | 4 | US-09-252-991A-18600 |
| 22 | 66 | 10.8 | 247 | 5 | PCIT-US94-10257A-2 |
| 23 | 66 | 10.8 | 770 | 1 | US-08-416-581B-1 |
| 24 | 66 | 10.8 | 770 | 1 | US-08-416-581B-5 |
| 25 | 66 | 10.8 | 770 | 1 | US-08-416-581B-9 |
| 26 | 66 | 10.8 | 770 | 3 | US-09-087-465-6 |
| 27 | 66 | 10.8 | 770 | 4 | US-09-526-542-2 |

28 66 10.8 770 4 US-09-972-800A-6 Sequence 6, Appli
29 66 10.8 771 1 US-08-276-099A-14 Sequence 14, Appl
30 66 10.8 771 1 US-08-781-890-14 Sequence 14, Appl
31 66 10.8 843 4 US-09-252-991A-29483 Sequence 29483, A
32 66 10.8 1034 4 US-09-252-991A-20969 Sequence 20969, A
33 65 10.6 154 4 US-09-387-418A-8 Sequence 8, Appli
34 65 10.6 231 4 US-09-265-540E-4 Sequence 4, Appli
35 65 10.6 405 4 US-09-252-991A-20326 Sequence 20326, A
36 65 10.6 423 4 US-09-252-991A-20162 Sequence 20162, A
37 65 10.6 770 1 US-08-369-796-12 Sequence 12, Appl
38 65 10.6 770 2 US-08-852-091-12 Sequence 12, Appl
39 65 10.6 770 2 US-08-820-754-12 Sequence 12, Appl
40 65 10.6 770 3 US-08-956-652-12 Sequence 12, Appl
41 65 10.6 770 3 US-08-956-869-12 Sequence 12, Appl
42 65 10.6 770 3 US-09-012-710-8 Sequence 8, Appli
43 65 10.6 770 3 US-08-948-547-12 Sequence 12, Appl
44 65 10.6 770 3 US-09-364-970-3 Sequence 3, Appli
45 65 10.6 770 3 US-09-364-970-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc. East
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 100.0%; Score 611; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.le-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 1 | MPSPGTVCSLLILGLMWLQALWAGSSFLSPHQHVQQRKESKKPAKIQPRALAGWL | RPE | 60 |
| Db | 1 | MPSPGTVCSLLILGLMWLQALWAGSSFLSPHQHVQQRKESKKPAKIQPRALAGWL | RPE | 60 |
| Qy | 61 | DGQQAEGADELEVRNAPFDVGIKLSGVQYQOQSOALGKFLQDILWEAKEAPADK | | 117 |
| Db | 61 | DGQQAEGADELEVRNAPFDVGIKLSGVQYQOQSOALGKFLQDILWEAKEAPADK | | 117 |

RESULT 2

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US-08-822-897C-2
: Sequence 2, Application US/08822897C
: Patent No. 6380158
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Deisher, Theresa A.
: TITLE OF INVENTION: MOTILIN HOMOLOGS
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Zymogenetics, Inc.
: STREET: 1201 Eastlake Avenue East
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98102
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/822,897C
: FILING DATE:
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Sawislak, Deborah A
: REGISTRATION NUMBER: 37,438
: REFERENCE/DOCKET NUMBER: 97-04
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-442-6672
: TELEFAX: 206-442-6678
: TELEX:
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 117 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal
US-08-822-897C-2

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RESULT 3

US-09-608-810A-4
; Sequence 4, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:

;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

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Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 DGGQAGAEDELEVRNAPFDVGIKLSGVYQOQHSQALGKFLQDILWEEAKEAPADK 117
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RESULT 5
US-09-046-479-4
; Sequence 4, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
US-09-046-479-4

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Best Local Similarity 26.0%; Pred. No. 0.0067;
Matches 20; Conservative 19; Mismatches 38; Indels 0; Gaps 0;

Qy 26 SFLSPSHQVQQRKESKPPAKLPALAGWLRPEDGGQAGAEDELEVRNAPFDVGIK 85
Db 29 SFTYGELQRMQEKERNKGOKKSLSVQQAASELGLDPSEPTKEERVVIKLLAPVDIGIR 88

Qy 86 LSGVYQOQHSQALGKFL 102
Db 89 MDSRQLEKYRATLERLL 105

RESULT 6
US-08-822-897C-4
; Sequence 4, Application US/08822897C
; Patent No. 6380158
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,897C
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-822-897C-4

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Qy 115 ADK 117
Db 107 VDK 109

RESULT 10
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; Sequence 23192, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23192
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23192

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Best Local Similarity 28.7%; Pred. No. 3.7;
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Qy 62 -----GGQAGAEDEVRENAF 79
Db 466 ASALRARLLGSPREGASEVPELRENL 492

RESULT 11
US-08-761-248B-4
; Sequence 4, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761.248B
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/008,348
; FILING DATE: 07-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723
; REFERENCE/DOCKET NUMBER: 34012.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)9513310
; TELEFAX: (713)9513314
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-761-248B-4
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Best Local Similarity 32.7%; Pred. No. 1.4;
Matches 37; Conservative 10; Mismatches 36; Indels 30; Gaps 7;
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Db 90 PHRRCCYNGCAYACLEAVPPVLDLWLPKPRWLGGWLDGPPEVLQAEACSTTED 149
Qy 67 GADEL-----EVRFNAPFDV--GIKLSGVYQOHSQALGKFLQDILWEEAKE 112
Db 150 GAEPLLCPSGYECHILSPGDVAEGIPNRGOCVKORROADGRILRHLYKEYPE 202

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US-09-252-991A-27419
; Sequence 27419, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27419
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27419

Query Match 11.4%; Score 69.5; DB 4; Length 247;
Best Local Similarity 24.1%; Pred. No. 1.8;
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Db 43 GGOSQGAEDQPGRTGDRDRDTCQRRHPRRLDHRHRRROQPPHPLNIRGRRVRRTF 102
Qy 77 NAFPDVGIKLSGVYQOHSQALG 99
Db 103 NRPARAGLFVCGVRHGHSQPF 125

RESULT 13
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; Sequence 27327, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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(without alignments)
239.348 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 611

Sequence: 1 MPSPTVCGLLLGLMLDL.....LGKFLQILWEEAKEAPADK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 611 | 100.0 | 117 | 9 | US-09-794-987-2 |
| 2 | 611 | 100.0 | 117 | 9 | US-09-853-253-2 |
| 3 | 611 | 100.0 | 117 | 9 | US-09-989-722-268 |
| 4 | 611 | 100.0 | 117 | 9 | US-09-989-723-268 |
| 5 | 611 | 100.0 | 117 | 9 | US-09-989-279-268 |
| 6 | 611 | 100.0 | 117 | 9 | US-09-989-727-268 |
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| 8 | 611 | 100.0 | 117 | 10 | US-09-989-732-268 |
| 9 | 611 | 100.0 | 117 | 10 | US-09-991-073-268 |
| 10 | 611 | 100.0 | 117 | 10 | US-09-990-442-268 |
| 11 | 611 | 100.0 | 117 | 10 | US-09-991-163-268 |
| 12 | 611 | 100.0 | 117 | 10 | US-09-993-604-268 |
| 13 | 611 | 100.0 | 117 | 10 | US-09-990-456-268 |
| 14 | 611 | 100.0 | 117 | 10 | US-09-989-721-268 |
| 15 | 611 | 100.0 | 117 | 10 | US-09-992-598-268 |

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| 16 | 611 | 100.0 | 117 | 10 | US-09-989-293A-268 | Sequence 268, App |
| 17 | 611 | 100.0 | 117 | 10 | US-09-989-735-268 | Sequence 268, App |
| 18 | 611 | 100.0 | 117 | 10 | US-09-990-444-268 | Sequence 268, App |
| 19 | 611 | 100.0 | 117 | 10 | US-09-991-181-268 | Sequence 268, App |
| 20 | 611 | 100.0 | 117 | 10 | US-09-989-730-268 | Sequence 268, App |
| 21 | 611 | 100.0 | 117 | 10 | US-09-990-436-268 | Sequence 268, App |
| 22 | 611 | 100.0 | 117 | 10 | US-09-993-687-268 | Sequence 268, App |
| 23 | 611 | 100.0 | 117 | 11 | US-09-989-734-268 | Sequence 268, App |
| 24 | 611 | 100.0 | 117 | 11 | US-09-997-653-268 | Sequence 268, App |
| 25 | 611 | 100.0 | 117 | 11 | US-09-993-667-268 | Sequence 268, App |
| 26 | 611 | 100.0 | 117 | 11 | US-09-997-428-268 | Sequence 268, App |
| 27 | 611 | 100.0 | 117 | 11 | US-09-997-666-268 | Sequence 268, App |
| 28 | 611 | 100.0 | 117 | 11 | US-09-990-438-268 | Sequence 268, App |
| 29 | 611 | 100.0 | 117 | 11 | US-09-990-562-268 | Sequence 268, App |
| 30 | 611 | 100.0 | 117 | 11 | US-09-990-711-268 | Sequence 268, App |
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| 32 | 611 | 100.0 | 117 | 11 | US-09-998-156-268 | Sequence 268, App |
| 33 | 611 | 100.0 | 117 | 11 | US-09-990-437-268 | Sequence 268, App |
| 34 | 611 | 100.0 | 117 | 11 | US-09-991-157-268 | Sequence 268, App |
| 35 | 611 | 100.0 | 117 | 11 | US-09-997-514-268 | Sequence 268, App |
| 36 | 611 | 100.0 | 117 | 11 | US-09-997-573-268 | Sequence 268, App |
| 37 | 611 | 100.0 | 117 | 11 | US-09-991-172-268 | Sequence 268, App |
| 38 | 611 | 100.0 | 117 | 11 | US-09-990-726-268 | Sequence 268, App |
| 39 | 611 | 100.0 | 117 | 11 | US-09-997-559-268 | Sequence 268, App |
| 40 | 611 | 100.0 | 117 | 11 | US-09-997-601-268 | Sequence 268, App |
| 41 | 611 | 100.0 | 117 | 11 | US-09-990-443-268 | Sequence 268, App |
| 42 | 611 | 100.0 | 117 | 11 | US-09-991-854-268 | Sequence 268, App |
| 43 | 611 | 100.0 | 117 | 11 | US-09-997-628-268 | Sequence 268, App |
| 44 | 611 | 100.0 | 117 | 11 | US-09-997-683-268 | Sequence 268, App |
| 45 | 611 | 100.0 | 117 | 11 | US-09-989-729A-268 | Sequence 268, App |

ALIGNMENTS

RESULT 1
US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. US20010041791A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

Query Match          100.0%; Score 611; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRPE 60
Db 1 MPSPGTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRPE 60

Qy 61 DGGQAEAGDELEVRFNAPFDVGIKLSGVQYQHQSHQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAEAGDELEVRFNAPFDVGIKLSGVQYQHQSHQALGKFLQDILWEEAKEAPADK 117

RESULT 2
US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPEERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-2

Query Match          100.0%; Score 611; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRPE 60
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Qy 61 DGGQAEAGDELEVRFNAPFDVGIKLSGVQYQHQSHQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAEAGDELEVRFNAPFDVGIKLSGVQYQHQSHQALGKFLQDILWEEAKEAPADK 117

RESULT 3
US-09-989-722-268
; Sequence 268, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730FIC83
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-11-24
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; PRIOR FILING DATE: 1998-06-09
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; PRIOR APPLICATION NUMBER: 60/090542
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 611; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.7e-60; Mismatches 0; Indels 0; Gaps 0;

Matches 117; Conservative 0;

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Db 1 MPSPGTVCVCLLLGLMLDLAMAGSSFLSPHQVQQRKESKPPAKLPRLAGWLKPE 60

QY 61 DGGQEGABDELEVRNAPFDVGIKLSGVQYQOHSQALGKFTQDILWEEAKEPADK 117

Db 61 DGGQEGABDELEVRNAPFDVGIKLSGVQYQOHSQALGKFTQDILWEEAKEPADK 117

RESULT 5

US-09-989-279-268

; Sequence 268, Application US/09989279

; Patent No. US20020072496A1

GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James

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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-01
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; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 611; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.7e-60; Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPSEHORVQQRKSKPPAKLQPRALAGWLRPE 60
Db 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPSEHORVQQRKSKPPAKLQPRALAGWLRPE 60
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Db 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQHQSHQALGKFLQDILWEEAKEAPADK 117

RESULT 6

US-09-989-727-268
; Sequence 268, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC65
CURRENT FILING DATE: 2001-11-19
PRIORITY APPLICATION NUMBER: US/09/989,727
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| : | PRIOR FILING DATE: | 1998-07-09 |

Query Match 100.0%; Score 611; DB 9; Length 117;

QY 1 MPSPGTVCSLLLLLGMWLWDLAMAGSSFLSPEHQRVQQRKESKPPAKLQPRALAGWLRPE 60

Db 1 MPSPGTVCSSLGLMLWLDLAMAGSSFLSPEHQRVQQRKESKPPAKLQPRALAGWLRPE 60

Qy 61 DGGQAEGADELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117

db 61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117

RESULT 7

US-09-989-731-268

; Sequence 268, Application US/099898731

; Patent No. US20020103125A1

; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: FONG, SUEI MAI
 GERBER HANSEN
 APPLICANT: GERBER HANSEN

APPLICANT: GERBER, Hanspeter
: APPLICANT: Gerriksen, Mrs. E

APPLICANT: GEFITSEN, MARY E.
APPLICANT: GEDDARD, ANNE

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christ

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: ROY, Margaret Ann

APPLICANT: Stewart, Timothy

APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; PRIOR APPLICATION NUMBER: 60/088858
 ; PRIOR FILING DATE: 1998-06-11
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 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 611; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. No. 6.7e-60;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPGTVCSSLLGLMLWLDLAMAGSSFLSPHQRVQORRESKPPAKLQPRALAGWL RPE 60
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 Db 1 MPSPGTVCSSLLGLMLWLDLAMAGSSFLSPHQRVQORRESKPPAKLQPRALAGWL RPE 60
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QY 61 DGGQAGAEDELEVRNAPFDVGKILSGVYQOHSQALGKFLQDILWEEAKEAPADK 117
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 Db 61 DGGQAGAEDELEVRNAPFDVGKILSGVYQOHSQALGKFLQDILWEEAKEAPADK 117
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RESULT 8
 US-09-989-732-268
 ; Sequence 268, Application US/09989732
 ; Patent No. US20020123463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 611; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPGTVCSSLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPRLAGWLRE 60
Db 1 MSPGTVCSSLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPRLAGWLRE 60

QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSOALGKFTQDILWEAKAPADK 117
Db 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSOALGKFTQDILWEAKAPADK 117

RESULT 9

US-09-991-073-268
; Sequence 268, Application US/09991073
; Patent No. US2002012756A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnovers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC15
;; CURRENT APPLICATION NUMBER: US/09/991,073

;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 611; DB 10; Length 117;
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RESULT 10
 US-09-990-442-268
 ; Sequence 268, Application US/09990442
 ; Patent No. US20020132252A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Geritsen, Mary E.
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 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
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 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C8
 ; CURRENT APPLICATION NUMBER: US/09/990.442
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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RESULT 12
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; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
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; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 611; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.7e-60;
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RESULT 13

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GENERAL INFORMATION:

? APPLICANT: Ashkenazi, Avi J.
 ? APPLICANT: Baker, Kevin P.
 ? APPLICANT: Botstein, David
 ? APPLICANT: Desnoyers, Luc
 ? APPLICANT: Eaton, Dan L.
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 Qy 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQQHSHQALGKFLQDILWEEAKEAPADK 117
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 Db 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQQHSHQALGKFLQDILWEEAKEAPADK 117

 RESULT 14
 US-09-989-721-268
 ; Sequence 268, Application US/09989721
 ; Patent No. US20020142961A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C55
 ; CURRENT APPLICATION NUMBER: US/09/989,721
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 611; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPGTVCSSLLLLGMLWLDLDMAGSSFLSPHQRVQORKESSKPPAKLQPRALAGWLRPE 60
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Db 1 MPSPGTVCSSLLLLGMLWLDLDMAGSSFLSPHQRVQORKESSKPPAKLQPRALAGWLRPE 60
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QY 61 DGGQAGGADELEVRFNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
|||||
Db 61 DGGQAGGADELEVRFNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
|||||

Search completed: September 11, 2003, 17:48:31
Job time : 74.3262 secs

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| Result No. | Query | Score | Match | | Length | DB | ID | Description |
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| | | | Match | Score | | | | |
| 1 | 609 | 99.7 | 117 | 4 | Q8TA19 | | Q8TA19 homo sapien | |
| 2 | 515 | 84.3 | 117 | 11 | Q8CH53 | | Q8CH53 meriones un | |
| 3 | 229.5 | 37.6 | 116 | 13 | Q8AV73 | | Q8AV73 gallus gall | |
| 4 | 146 | 23.9 | 111 | 13 | Q8JFY4 | | Q8JFY4 anguilla ja | |
| 5 | 97.5 | 16.0 | 103 | 13 | Q8AUU1 | | Q8AUU1 carassius a | |
| 6 | 87 | 14.2 | 114 | 13 | Q9UW22 | | Q9UW22 rana catesb | |
| 7 | 79 | 12.9 | 1239 | 5 | O01505 | | O01505 caenorhabdi | |
| 8 | 78.5 | 12.8 | 119 | 16 | Q8PF9 | | Q8PF9 xanthomonas | |
| 9 | 75.5 | 12.4 | 410 | 17 | Q9HS01 | | Q9HS01 halobacteri | |
| 10 | 75 | 12.3 | 158 | 16 | Q8XW90 | | Q8XW90 ralstonia s | |
| 11 | 73.5 | 12.0 | 709 | 16 | Q9PCM1 | | Q9PCM1 xylella fas | |
| 12 | 73 | 11.9 | 359 | 5 | Q9VQX3 | | Q9VQX3 drosophila | |
| 13 | 73 | 11.9 | 534 | 2 | Q9RPV9 | | Q9RPV9 bacillus me | |
| 14 | 73 | 11.9 | 961 | 10 | Q9SXN6 | | Q9SXN6 nicotiana t | |
| 15 | 73 | 11.9 | 1035 | 10 | Q9M7J0 | | Q9M7J0 populus tre | |
| 16 | 72.5 | 11.9 | 482 | 4 | Q8WBV7 | | Q8WBV7 homo sapien | |

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ID Q8CH53 PRELIMINARY; PRT; 117 AA.
AC Q8CH53;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AAC06965.1; -
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 84.3%; Score 515; DB 11; Length 117;
Best Local Similarity 82.1%; Pred. No. 4.8e-48;
Matches 96; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 MPSPGVCSLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPQALAGLWLRPE 60
DB 1 MMSSGTCISLLGLVMDVAMAGSFLSPHQVQQRKESKPPAKLPQALAGLWLRPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQHSQALGKFLQDILWEAKEAPADK 117
DB 61 GRCQAGAEDELEVRNAPFDVGIKLSGVQYQHSQALGKFLQDILWEAKEATDK 117

RESULT 3
Q8AV73 PRELIMINARY; PRT; 116 AA.
ID Q8AV73;
AC Q8AV73;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Ghrelin precursor.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=22181232; PubMed=12193558;
RA Kaiya H., Van der Gevelen S., Kojima M., Hosoda H., Kitajima Y.,
RA Matsumoto M., Geelissen S., Darras V.M., Kangawa K.;
RT "Chicken ghrelin: purification, cDNA cloning, and biological
RT activity.";
RL Endocrinology 143:3454-3463(2002).
DR EMBL; AB075215; BAC24980.1; -
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 49 GHRELIN-26.
SQ SEQUENCE 116 AA; 13227 MW; F5C3FA038F187DE9 CRC64;

Query Match 37.6%; Score 229.5; DB 13; Length 116;
Best Local Similarity 43.4%; Pred. No. 4.1e-17;
Matches 46; Conservative 27; Mismatches 26; Indels 7; Gaps 3;

QY 10 LLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPQALAGLWLRPE 68
DB 10 ILLSLGTETALAGSFLSPYKNIQQQDKTRKPTARLHRRGTSF---DTDETEGE 65

QY 69 ED--ELEVNRNAPFDVGIKLSGVQYQHSQALGKFLQDILWEAKE 112
DB 66 DDNNVDIKFNPVFEIGVITEREYQYGOALEKMLQDILAENAE 111

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RESULT 4

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Q8JFY4 PRELIMINARY; PRT; 111 AA.
ID Q8JFY4;
AC Q8JFY4;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Prepro-ghrelin precursor.
GN GHRELIN.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Kaiya H., Kojima M., Hosoda H., Riley L.G., Hirano T., Grau G.E.,
RA Kangawa K.;
RT "Identification of eel ghrelin.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062427; BAB96565.1; -
KW Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 111 PROGHRELIN.
FT CHAIN 27 48 GHRELIN-21.
SQ SEQUENCE 111 AA; 12831 MW; 7AF95E04DD22DE7B CRC64;

Query Match 23.9%; Score 146; DB 13; Length 111;
Best Local Similarity 38.1%; Pred. No. 4.4e-08;
Matches 43; Conservative 19; Mismatches 29; Indels 22; Gaps 8;

QY 7 VCSLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPQALAGLWLRPE 60
DB 14 VCVL----ALMDSVQAGSFLSPS-QRPQK--DKKPP-RVGRDSDGLDLFMRPLQ 65
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQHSQALGKFLQDILWEAKE 112
DB 66 D-----EDIRHITNTPEIGITWTEELFQQYGEVMQKIMQDLMDDTPAKE 111

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RESULT 5

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Q8AUU1 PRELIMINARY; PRT; 103 AA.
ID Q8AUU1;
AC Q8AUU1;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Preproghrelin.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22224486; PubMed=12239128;
RA Unniappan S., Lin X., Cervini L., Rivier J., Kaiya H., Kangawa K.,
RA Peter R.E.;
RT "Goldfish ghrelin: molecular characterization of the complementary
RT deoxyribonucleic acid, partial gene structure and evidence for its
RT stimulatory role in food intake.";
RL Endocrinology 143:4143-4146(2002).
DR EMBL; AF454389; AAN16215.1; -
DR EMBL; AF454390; AAN16216.1; -
SQ SEQUENCE 103 AA; 11520 MW; 0881343BCDC0C012 CRC64;

Query Match 16.0%; Score 97.5; DB 13; Length 103;
Best Local Similarity 25.7%; Pred. No. 0.0072;
Matches 29; Conservative 22; Mismatches 31; Indels 31; Gaps 4;

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66
QY 7 VCSLLGLMLWLDLAMAGSSFLSPHQRVQQRKSKKPPAKLPQALAGWLRPEDGGQAE 66
Db 14 LCAI-----SLCVESVKGSTFSLSP-----AQKPGGRPPRR-----GRD 49
QY 67 GABDELEV-----RFNAPFDVGIKSLGVQYQQHSQALGKFLDILWEEAKE 112
Db 50 VAEPEPTVKEDQFMASAPFELSVLSBAEYKGPVLKLVNLVNGDSPLE 102

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| Q90W22 | |
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| AC | Q90W22; |
| DT | 01-DEC-2001 (TREMBlrel. 19, Created) |
| DT | 01-DEC-2001 (TREMBlrel. 19, Last sequence update) |
| DT | 01-DEC-2001 (TREMBlrel. 19, Last annotation update) |
| DE | Preproghrelin precursor. |
| OS | Rana catesbeiana (Bull frog). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OX | Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana. |
| OX | NCBI_Taxid=8400; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | TISSUE-Stomach; |
| RX | MEDLINE=21538897; PubMed=11546772; |
| RA | Kaiya H., Kojima M., Hosoda H., Koda A., Yamamoto K., Kitajima Y., Matsumoto M., Minamitake Y., Kikuyama S., Kangawa K.; |
| RT | "Bullfrog Ghrelin Is Modified by n-Octanoic Acid at Its Third Threonine Residue." ; |
| RL | J. Biol. Chem. 276:40441-40448(2001) . |
| DR | EMBL; AB058510; BAB71718.1; -. |
| KW | Signal. |
| FT | SIGNAL. 1 24 POTENTIAL. |
| FT | CHAIN 25 52 BULLFROG GHRELIN-28. |
| FT | CHAIN 25 51 BULLFROG GHRELIN-27. |
| SQ | SEQUENCE 114 AA; 12756 MW; lFE4I9ACB30AA141 CRC64; |

```

Query Match      14.2%  Score 87;  DB 13;  Length 114;
Best Local Similarity 27.9%  Pred. No. 0.11;
Matches 2%  Conservative 19;  Mismatches 36;  Indels 20;  Gaps 5;

Qy  7  VCSLLGLMLWDLAMAGSSFLSP-EHQRVQQRKESKPPAKLQPRALAGWLRPDGGQA 65
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  8  IFGVFCLLWTGGAQAGLFTFLSPADNMQIAERQSQNK-----LR-HGNMNR 53

Qy  66  EGAEDEL---EVRFNAPFDVGIKLSGVQYQOQSQAALGKFLQDIL 106
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  54  RGVEDDLDAIEIGVTFPLD--MKWTQFOFQKRAAAYODEFLYSLL 95
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

| | |
|----------|--|
| RESULT 7 | |
| 001505 | |
| ID | 001505 PRELIMINARY; PRT; 1239 AA. |
| AC | 001505; |
| DT | 01-JUL-1997 (TREMBLrel. 04, Created) |
| DT | 01-OCT-2001 (TREMBLrel. 18, Last sequence update) |
| DT | 01-MAR-2003 (TREMBLrel. 23, Last annotation update) |
| DE | Hypothetical 135.4 kDa protein. |
| DE | C37A2.2. |
| GN | Caenorhabditis elegans. |
| GN | Caenorhabditis elegans. |
| OC | Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; |
| OC | Rhabditidae; Peloderinae; Caenorhabditis. |
| OX | NCBI_TaxID=6239; |
| RP | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN-Bristol N2; |
| RA | MDLline=99069613; PubMed=9851916; |
| RA | None; |
| RT | "Genome sequence of the nematode C. elegans: a platform for |
| RT | investigating biology. The C. elegans Sequencing Consortium."; |
| RL | Science 282:2012-2018(1998). |
| RP | [2] |
| RP | SEQUENCE FROM N.A. |

[illegible]

| | |
|-----------|--|
| | SA lanoubat M., Gedin S., Artiguenave F., Guzy J., Mangenot S., |
| | Arlat M., Billault A., Brotier P., Camus J.C., Cattolico L., |
| | Chandler M., Cholsine N., Claudel-Renard C., Cunnean S., Demange N., |
| | Gaspin C., Lavie M., Molisan A., Robert C., Saurin W., Schlex T., |
| | Sigulier P., Thiebaut P., Whalen M., Wincker P., Levy M., |
| | Weissenbach J., Boucher C.A.; |
| RA | "Genome sequence of the plant pathogen Ralstonia solanacearum."; |
| RL | Nature 415:497-502(2002). |
| RN | ENBL; AL646070; CAD16292.1; -. |
| DR | InterPro: IPR002145; HTH_CopG. |
| DR | Pfam; PF01402; HTH_4; 1. |
| DW | Hypothetical protein; Complete proteome. |
| KQ | SEQUENCE 158 AA; 17814 MW; C9BAM2BF9C10E1BC CRC64; |
| | Query Match 12.3%; Score 75; DB 16; Length 158; |
| | Best Local Similarity 38.6%; Pred No. 3.3; |
| | Matches 17; Conservative 7; Mismatches 18; Indels 2; Gaps |
| QY | 27 FLSPHQRVQRKESKKPPAK--LQPALAGWLRPEDGGQAEGA 68 I : : : : : : |
| DB | 9 FIQPEHAKRLEEAARKGVSKSSIAAALASMLSPDAGDQREMA 52 |
| RESULT 11 | |
| Q9PGM1 | ID Q9PGM1 PRELIMINARY; PRT: 709 AA. |
| AC | COPGM1 |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Created) |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) |
| DT | 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) |
| DE | Hypothetical protein Xf0277. |
| GN | Xf0277. |
| OS | Xylella fastidiosa. |
| OC | Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; |
| OC | Xanthomonadaceae; Xylella. |
| ON | NCBI_TaxID=2371; |
| OX | [1] |
| RC | SEQUENCE FROM N.A. |
| RP | STRAIN=9a5c; |
| RX | MEDLINE=20365717; PubMed=10910347; |
| RA | Simpson A.J.G., Alves F.C., Arruda P., Abreu F.A., Acencio M., |
| RA | Alvarenga R., Alves L.M.C., Araya J.B., Baia G.S., Baptista C.S., |
| RA | Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., |
| RA | Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H., |
| RA | Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Netto C.M., |
| RA | Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., |
| RA | Facincini A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., |
| RA | Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R., |
| RA | Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., |
| RA | Ho P.L., Hohenseil J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., |
| RA | Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., |
| RA | Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., |
| RA | Machado M.A., Madeira A.M.N., Madeira H.M.F., Marino C.L., |
| RA | Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., |
| RA | Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteirol-Vitorello C.B., |
| RA | Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., |
| RA | Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., |
| RA | de Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A., |
| RA | Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., |
| RA | Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., |
| RA | de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., |
| RA | da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., |
| RA | da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., |
| RA | de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchida M.H., |
| RA | Vallada H., Van Sluys M.A., Varjosviki-Almeida S., Vettore A.L., |
| RA | Zago M.A., Zatz M., Meidanis J., Setubal J.C. |
| RT | "The genome sequence of the plant pathogen Xylella fastidiosa."; |
| RL | Nature 406:151-159(2000). |
| DR | ENBL; AE003881; RAJF83090.1; -. |
| DR | InterPro: IPR000352; PDA. |
| DR | InterPro: IPR000326; PPA_PTPase. |
| DR | Pfam; PF00597; DedA; 1. |
| DR | Pfam; PF01569; PAP2; 1. |


```
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 709 AA; 79163 MW; 0EAA922E4B463318 CRC64;

Query Match 12.0%; Score 73.5; DB 16; Length 709;
Best Local Similarity 23.5%; Pred. No. 28;
Matches 36; Conservative 14; Mismatches 52; Indels 51; Gaps 6;

Oy 5 GTVCSL-----LLGLMLWLDLMAAGSSF----- 27
Db 422 GALASLGFARLYLGAHWLSDVGLGMLFGIFWLVLGYAIRRRLTHELOVNPLSWLYGT 481
Oy 28 -----LSPHORVQQRKESKPPAKLQPRALA--GWLRPEDGGQAGDELEVRFA 78
Db 482 FSIAIVMAPRHLBOKLTKEPPPPS---PRAIAEGWVK-NDWRQLPARNEFDDAERW 537
Oy 79 PFDVGILSGVQVQHQSHQALGKFLQ-DILWEEA 110
Db 538 PLNVQVAGSLVPLQOHLETOGWRROPQTGMKEA 570

RESULT 12
Q9VQX3 SEQUENCE FROM N.A.
ID Q9VQX3 PRELIMINARY; PRT; 359 AA.
AC Q9VQX3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG2958 protein (HL05328P) (LP02926P).
GN LECTIN-24DB OR CG2958.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]

Query Match 11.9%; Score 73; DB 5; Length 359;
Best Local Similarity 28.1%; Pred. No. 14;
Matches 27; Conservative 16; Mismatches 33; Indels 20; Gaps 4;

Oy 31 EHQRVQQRKESKPPAKL-----QPRALAGLRPDGQAGDELEVRFA-PF 80
Db 111 EHLQTLQESLKKMPAELDARLKMENQOKTKLDQLENQINLTRESQDQLEALKNPMPI 170
Oy 81 DVGKILSGVQVQHQSHQALGKFLQDILWEEAKEAPAD 116
Db 171 NFEMRLAQIEQQ-----KLLQETL-----RKIPED 196

RESULT 13
Q9RPV9 SEQUENCE FROM N.A.
ID Q9RPV9 PRELIMINARY; PRT; 534 AA.
AC Q9RPV9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 60.1 kDa protein.
OS Bacillus megaterium.
OX Plasmid pBM400.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=1404;
RN [1]

Query Match 11.9%; Score 73; DB 2; Length 534;
Best Local Similarity 22.3%; Pred. No. 22;
Matches 33; Conservative 19; Mismatches 46; Indels 50; Gaps 5;

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuncio J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003577; AAF51038.1; -.
DR EMBL; AY061025; AAL28573.1; -.
DR EMBL; AY119000; AAM50860.1; -.
DR HSSP; P22897; 1EGG.
DR FlyBase; FBgn0040102; lectin-24Db.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PROSITE; PS0041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 359 AA; 41546 MW; 1895E525594584C4 CRC64;

Query Match 11.9%; Score 73; DB 5; Length 359;
Best Local Similarity 28.1%; Pred. No. 14;
Matches 27; Conservative 16; Mismatches 33; Indels 20; Gaps 4;

Oy 31 EHQRVQQRKESKPPAKL-----QPRALAGLRPDGQAGDELEVRFA-PF 80
Db 111 EHLQTLQESLKKMPAELDARLKMENQOKTKLDQLENQINLTRESQDQLEALKNPMPI 170
Oy 81 DVGKILSGVQVQHQSHQALGKFLQDILWEEAKEAPAD 116
Db 171 NFEMRLAQIEQQ-----KLLQETL-----RKIPED 196

RESULT 13
Q9RPV9 SEQUENCE FROM N.A.
ID Q9RPV9 PRELIMINARY; PRT; 534 AA.
AC Q9RPV9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 60.1 kDa protein.
OS Bacillus megaterium.
OX Plasmid pBM400.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=1404;
RN [1]

Query Match 11.9%; Score 73; DB 2; Length 534;
Best Local Similarity 22.3%; Pred. No. 22;
Matches 33; Conservative 19; Mismatches 46; Indels 50; Gaps 5;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA Sutton G.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fodor B.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy L., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
```

QY 6 TVCSLLGLMLDLAMAGSFLSPHQH----- 34
| | | | : : : | | | | |
Db 349 TTWGLLAKLIFIMLVAGVIGILIREHLKRNDSPLTKFLMSDVSEMLIIVLIVGTIAHL 408
| | | | : : : | | | | |
QY 35 --VQOR-----KESKK-----PPAKLPALAGWLR---PEDGGQAGAEDELEVRFN- 77
| | | | : : : | | | | |
Db 409 NPVPQNEPLVKNKODIEFLVKTSTUSPKASLWLKASLPQDGSISQSTIEIALSPKNKG 468
| | | | : : : | | | | |
QY 78 --APFDVGIKLSGVQVQOQHQAQKFLQ 103
| | | | : : : | | | | |
Db 469 ELAPIDVPLAVNKDESOEQVQVKNYE 496

RESULT 14

Q9SXN6 PRELIMINARY; PRT; 961 AA.
ID Q9SXN6
AC Q9SXN6
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE NTRB1 protein.
GN NTRB1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA Sekine M.;
RT "Tumor suppressor gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB015221; BAA76477.1; -
DR HSSP; P06400; IGUX.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR002720; RB_A.
DR InterPro; IPR002719; RB_B.
DR Pfam; PF01858; RB_A; 1.
DR Pfam; PF01857; RB_B; 1.
DR SMART; SM00385; CYCLIN; 1.
SQ SEQUENCE 961 AA; 106602 MW; 0138DE06FC89ED2C CRC64;

Query Match 11.9%; Score 73; DB 10; Length 961;
Best Local Similarity 33.3%; Pred. No. 45;
Matches 30; Conservative 8; Mismatches 40; Indels 12; Gaps 4;

QY 3 SPCTVCSLLGLMLDLAMAGSFLSPHQH--VQORRESKPPAKLPALAGWLRPE 60
| | | | : : : | | | | |
Db 666 SPKKVCS-----EYRSVLVERNSFTSPVKDRFLALNNTIKSFPPALQ-SAFASPTRPN 718
| | | | : : : | | | | |
QY 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQ 90
| | | | : : : | | | | |
Db 719 PGG--GGETCAETAINVFGKIVKLA VR 745

RESULT 15

Q9M7J0 PRELIMINARY; PRT; 1035 AA.
ID Q9M7J0
AC Q9M7J0
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Retinoblastoma-related protein 1.
GN RB1.
OS Populus tremula x Populus tremuloides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Salicaceae; Populus.
OX NCBI_TaxID=47664;
RN [1]
RP SEQUENCE FROM N.A.
RA Bhalarao R.P., Sivertson M., Sterky F., Lundeborg J., Sandberg G.;
RT "The role of Rb-related protein from hybrid aspen in wood formation.";

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF133675; AAF61377.1; -
DR HSSP; P06400; IGUX.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR002720; RB_A.
DR InterPro; IPR002719; RB_B.
DR Pfam; PF01858; RB_A; 1.
DR Pfam; PF01857; RB_B; 1.
DR SMART; SM00385; CYCLIN; 1.
SQ SEQUENCE 1035 AA; 114608 MW; F66191BF50BAAAA5 CRC64;

Query Match 11.9%; Score 73; DB 10; Length 1035;
Best Local Similarity 35.0%; Pred. No. 49;
Matches 28; Conservative 5; Mismatches 33; Indels 14; Gaps 3;

QY 25 SSFLSPHQHVRVQQRKESKPPAKLPALAGWLRPEGGQAGAEDELEVRFNAPFDVGI 84
| | | | : : : | | | | |
Db 709 NSFTSPVKDRLLGLNLKSLPPPLQ-SAFASPTRPNPG--GGETCAETGINVFFTKIN 764
| | | | : : : | | | | |
QY 85 KLSGVQY-----QQH 94
| | | | : : : | | | | |
Db 765 KLAAYRINGMIEKLPQSQQH 784

Search completed: September 11, 2003, 17:30:24
Job time : 115.369 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:48:42 ; Search time 8.2139 seconds
(without alignments)
123.627 Million cell updates/sec

Title: US-09-853-253-4

Perfect score: 24

Sequence: 1 ALAGWLRPEDGQAEGBAELEVR 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------------------|-------------------|
| 1 | 24 | 100.0 | 117 | 3 US-09-046-479-2 | Sequence 2, Appl |
| 2 | 24 | 100.0 | 117 | 4 US-08-822-897C-2 | Sequence 2, Appl |
| 3 | 24 | 100.0 | 117 | 4 US-09-608-810A-4 | Sequence 4, Appl |
| 4 | 24 | 100.0 | 117 | 4 US-09-996-243-268 | Sequence 268, App |
| 5 | 7 | 29.2 | 442 | 4 US-09-134-001C-3033 | Sequence 3033, Ap |
| 6 | 7 | 29.2 | 552 | 4 US-09-252-991A-27032 | Sequence 27032, A |
| 7 | 7 | 29.2 | 599 | 4 US-09-252-991A-20368 | Sequence 20368, A |
| 8 | 7 | 29.2 | 981 | 4 US-09-252-991A-16798 | Sequence 16798, A |
| 9 | 6 | 25.0 | 39 | 1 US-08-428-488-13 | Sequence 13, Appl |
| 10 | 6 | 25.0 | 97 | 2 US-08-403-852D-31 | Sequence 31, Appl |
| 11 | 6 | 25.0 | 97 | 3 US-08-510-646B-32 | Sequence 32, Appl |
| 12 | 6 | 25.0 | 97 | 3 US-09-231-818-31 | Sequence 31, Appl |
| 13 | 6 | 25.0 | 129 | 3 US-09-135-994-12 | Sequence 12, Appl |
| 14 | 6 | 25.0 | 129 | 4 US-09-684-843A-12 | Sequence 12, Appl |
| 15 | 6 | 25.0 | 183 | 4 US-09-198-452A-612 | Sequence 612, App |
| 16 | 6 | 25.0 | 199 | 4 US-09-252-991A-32089 | Sequence 32089, A |
| 17 | 6 | 25.0 | 202 | 4 US-09-252-991A-26333 | Sequence 26333, A |
| 18 | 6 | 25.0 | 259 | 4 US-09-252-991A-17300 | Sequence 17300, A |
| 19 | 6 | 25.0 | 288 | 1 US-08-396-650-1 | Sequence 1, Appl |
| 20 | 6 | 25.0 | 288 | 1 US-08-768-626-1 | Sequence 1, Appl |
| 21 | 6 | 25.0 | 292 | 4 US-09-252-991A-18951 | Sequence 18951, A |
| 22 | 6 | 25.0 | 292 | 4 US-09-252-991A-30162 | Sequence 30162, A |
| 23 | 6 | 25.0 | 305 | 4 US-09-328-352-6794 | Sequence 6794, Ap |
| 24 | 6 | 25.0 | 326 | 4 US-09-252-991A-33000 | Sequence 33000, A |
| 25 | 6 | 25.0 | 329 | 4 US-09-843-297-2 | Sequence 2, Appl |
| 26 | 6 | 25.0 | 359 | 4 US-09-266-965-120 | Sequence 120, App |
| 27 | 6 | 25.0 | 366 | 4 US-09-252-991A-29569 | Sequence 29569, A |

28 6 25.0 378 4 US-09-325-932A-158 Sequence 158, App
29 6 25.0 399 4 US-09-252-991A-25687 Sequence 25687, A
30 6 25.0 402 3 US-09-464-483-4 Sequence 4, Appl
31 6 25.0 402 3 US-09-414-664-4 Sequence 4, Appl
32 6 25.0 461 4 US-09-252-991A-32421 Sequence 32421, A
33 6 25.0 489 4 US-09-252-991A-22896 Sequence 22896, A
34 6 25.0 502 4 US-09-207-388-19 Sequence 19, Appl
35 6 25.0 510 4 US-09-252-991A-17695 Sequence 17695, A
36 6 25.0 529 3 US-09-464-483-2 Sequence 2, Appl
37 6 25.0 529 3 US-09-414-664-2 Sequence 2, Appl
38 6 25.0 531 1 US-08-531-601-1 Sequence 1, Appl
39 6 25.0 531 2 US-08-859-032-1 Sequence 1, Appl
40 6 25.0 535 1 US-08-737-597-10 Sequence 10, Appl
41 6 25.0 548 4 US-09-207-388-23 Sequence 23, Appl
42 6 25.0 550 4 US-09-207-388-20 Sequence 20, Appl
43 6 25.0 568 4 US-09-207-388-22 Sequence 22, Appl
44 6 25.0 568 4 US-09-207-388-24 Sequence 24, Appl
45 6 25.0 570 4 US-09-207-388-21 Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 100.0%; Score 24; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 2

US-08-822-897C-2
; Sequence 2, Application US/08822897C
; Patent No. 6380158
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,897C
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-822-897C-2

Query Match 100.0%; Score 24; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.le-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 3

US-09-608-810A-4
; Sequence 4, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608,810A
; CURRENT FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4

Query Match 100.0%; Score 24; DB 4; Length 117;

Best Local Similarity 100.0%; Pred. No. 2.le-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 4

US-09-996-243-268
; Sequence 268, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2;le-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQGAEGAEDELEVR 24
Db 52 ALAGWLRPDGGQGAEGAEDELEVR 75

RESULT 5

US-09-134-001C-3033
; Sequence 3033, Application US/09134001C
; Patent No. 6380370

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3033
; LENGTH: 442
; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3033

Query Match 29.2%; Score 7; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAG 16
Db 189 DGGQAG 195

RESULT 6

US-09-252-991A-27032
; Sequence 27032, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27032
; LENGTH: 552
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27032

Query Match 29.2%; Score 7; DB 4; Length 552;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAG 16

Db 22 DGGQAG 28

RESULT 7

US-09-252-991A-20368
; Sequence 20368, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20368
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20368

Query Match 29.2%; Score 7; DB 4; Length 599;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGOAEGA 17
Db 383 GGOAEGA 389

RESULT 8

US-09-252-991A-16798
; Sequence 16798, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16798
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16798

Query Match 29.2%; Score 7; DB 4; Length 981;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
Db 136 ALAGWLR 142

RESULT 9

US-08-428-488-13
; Sequence 13, Application US/08428488
; Patent No. 5624894

GENERAL INFORMATION:

; APPLICANT: BOBOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE

;; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
;; NUMBER OF SEQUENCES: 107
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/428,488
;; FILING DATE: 27-APR-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Baumeister, Mary Katherine
;; REGISTRATION NUMBER: 26,254
;; REFERENCE/DOCKET NUMBER: 028724-087
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 39 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1
;; OTHER INFORMATION: /note= "Position 1 - H-Ser."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 39
;; OTHER INFORMATION: /note= "Position 39 - Phe-OH."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 30
;; OTHER INFORMATION: /note= "Position 30 - Glu-NH2."
US-08-428-488-13

Query Match 25.0%; Score 6; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GAEDEL 21
| | | | |
Db 26 GAEDEL 31

RESULT 10
US-08-403-852D-31
; Sequence 31, Application US/08403852D
; Patent No. 5891695

;; GENERAL INFORMATION:
;; APPLICANT: Blanc, Veronique
;; APPLICANT: Blanche, Francis
;; APPLICANT: Crouzet, Joel
;; APPLICANT: Jacques, Nathalie
;; APPLICANT: Lacroix, Patricia
;; APPLICANT: Thibaut, Denis
;; APPLICANT: Zagorec, Monique
;; APPLICANT: Debussche, Laurent
;; APPLICANT: De Crecy Lagard, Valerie
;; TITLE OF INVENTION: Polypeptides Involved In The
;; Biosynthesis Of Streptogramins, Nucleotide Sequences
;; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
;; NUMBER OF SEQUENCES: 43

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/403,852D
;; FILING DATE: 10-MAY-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR 93/00923
;; FILING DATE: 25-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 92/11441
;; FILING DATE: 25-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03806.0054-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 97 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-403-852D-31

Query Match 25.0%; Score 6; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAE 18
| | | | |
Db 2 QAEGAE 7

RESULT 11

US-08-510-646B-32
; Sequence 32, Application US/08510646B
; Patent No. 6077699

;; GENERAL INFORMATION:
;; APPLICANT: Blanc, Veronique
;; APPLICANT: Blanche, Francis
;; APPLICANT: Crouzet, Joel
;; APPLICANT: Jacques, Nathalie
;; APPLICANT: Lacroix, Patricia
;; APPLICANT: Thibaut, Denis
;; APPLICANT: Zagorec, Monique
;; APPLICANT: Debussche, Laurent
;; APPLICANT: De Crecy Lagard, Valerie
;; TITLE OF INVENTION: Polypeptides Involved In The
;; Biosynthesis Of Streptogramins, Nucleotide Sequences
;; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,646B
; FILING DATE: 03-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-510-646B-32

Query Match 25.0%; Score 6; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAE 18
Db 2 QAEGAE 7

RESULT 12
US-09-231-818-31
; Sequence 31, Application US/09231818
; Patent No. 6171846
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,818
; FILING DATE:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/403,852
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-231-818-31

Query Match 25.0%; Score 6; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAE 18
Db 2 QAEGAE 7

RESULT 13
US-09-135-994-12
; Sequence 12, Application US/09135994A
; Patent No. 6280938
; GENERAL INFORMATION:
; APPLICANT: Ranum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/135,994A
; CURRENT FILING DATE: 1998-08-18
; EARLIER APPLICATION NUMBER: 60/056,170
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-135-994-12

Query Match 25.0%; Score 6; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RPEDGG 12
Db 57 RPEDGG 62

RESULT 14
US-09-684-843A-12
; Sequence 12, Application US/09684843A
; Patent No. 6514755
; GENERAL INFORMATION:
; APPLICANT: Ranum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: Regents of the University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/684,843A
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/056,170
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 09/135,994

; PRIOR FILING DATE: 1998-08-18
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 129
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-684-843A-12

Query Match 25.0%; Score 6; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RPEDGG 12
 |||||
 Db 57 RPEDGG 62

RESULT 15
 US-09-198-452A-612
 ; Sequence 612, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Grifffais, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 612
 ; LENGTH: 183
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 US-09-198-452A-612

Query Match 25.0%; Score 6; DB 4; Length 183;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AEGAEED 19
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 Db 155 AEGAEED 160

Search completed: September 11, 2003, 17:58:13
 Job time : 9.2139 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:27:22 ; Search time 25.2834 Seconds
(without alignments)
150.669 Million cell updates/sec

Title: US-09-853-253-4
Perfect score: 24
Sequence: 1 ALAGWLRPEDGGGAEGAELEVR 24

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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| 12: | /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:* |
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| 18: | /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:* |
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| 22: | /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:* |
| 23: | /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:* |
| 24: | /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 24 | 100.0 | 24 | AAE23839 | Human zsig33-linker |
| 2 | 24 | 100.0 | 24 | AAE15884 | Human zsig33-linker |
| 3 | 24 | 100.0 | 91 | AAE33410 | Human exon 3-delet |
| 4 | 24 | 100.0 | 116 | AAE60517 | Human des-Gln14-gh |
| 5 | 24 | 100.0 | 117 | AAW87991 | Protein designated |
| 6 | 24 | 100.0 | 117 | AAW87236 | Human signal pepti |
| 7 | 24 | 100.0 | 117 | AAW38890 | Human polypeptide |
| 8 | 24 | 100.0 | 117 | AAE62649 | Human zsig33 polyp |
| 9 | 24 | 100.0 | 117 | AAE20101 | Zsig33 protein. H |

| | | | | | | |
|----|----|-------|------|----|----------|---------------------|
| 10 | 24 | 100.0 | 117 | 22 | AAE60511 | Human ghrelin prep |
| 11 | 24 | 100.0 | 117 | 23 | ABW78319 | Amino acid sequenc |
| 12 | 24 | 100.0 | 117 | 23 | AAE23838 | Human zsig33 prote |
| 13 | 24 | 100.0 | 117 | 23 | AAE15883 | Human zsig33 prote |
| 14 | 24 | 100.0 | 117 | 24 | ABU66790 | Human PRO polypept |
| 15 | 24 | 100.0 | 117 | 24 | ABU67066 | Human secreted/tr |
| 16 | 24 | 100.0 | 117 | 24 | ABU59871 | Novel secreted and |
| 17 | 24 | 100.0 | 117 | 24 | ABU59124 | Novel human secret |
| 18 | 24 | 100.0 | 117 | 24 | ABU59271 | Human secreted/tr |
| 19 | 24 | 100.0 | 117 | 24 | ABU59420 | Novel human secret |
| 20 | 24 | 100.0 | 117 | 24 | ABU60555 | Human secreted/tr |
| 21 | 24 | 100.0 | 117 | 24 | ABU58046 | Human PRO polypept |
| 22 | 24 | 100.0 | 117 | 24 | ABU58977 | Human secreted/tr |
| 23 | 24 | 100.0 | 117 | 24 | AAE33409 | Human preproghreli |
| 24 | 24 | 100.0 | 117 | 24 | ABU13937 | Human PRO1066 poly |
| 25 | 24 | 100.0 | 117 | 24 | ABU10892 | Human PRO polypept |
| 26 | 24 | 100.0 | 118 | 21 | AAW66708 | Membrane-bound pro |
| 27 | 24 | 100.0 | 118 | 22 | AAU12392 | Human PRO1066 poly |
| 28 | 24 | 100.0 | 118 | 22 | AAE65231 | Human PRO1066 (UNQ |
| 29 | 24 | 100.0 | 126 | 22 | AAW40676 | Human polypeptide |
| 30 | 23 | 95.8 | 23 | 23 | AAE23840 | Human zsig33-linker |
| 31 | 23 | 95.8 | 23 | 23 | AAE23841 | Human zsig33-linker |
| 32 | 23 | 95.8 | 23 | 23 | AAE15885 | Human zsig33-linker |
| 33 | 23 | 95.8 | 23 | 23 | AAE15886 | Human zsig33-linker |
| 34 | 10 | 41.7 | 89 | 22 | AAE60523 | Bovine ghrelin pre |
| 35 | 8 | 33.3 | 334 | 21 | AAG29677 | Arabidopsis thalia |
| 36 | 8 | 33.3 | 428 | 21 | AAG29676 | Arabidopsis thalia |
| 37 | 8 | 33.3 | 483 | 21 | AAG29675 | Arabidopsis thalia |
| 38 | 7 | 29.2 | 311 | 19 | AAW36129 | Snpr activator pro |
| 39 | 7 | 29.2 | 311 | 21 | AAE30494 | Amino acid sequenc |
| 40 | 7 | 29.2 | 442 | 23 | ABP38188 | Staphylococcus epi |
| 41 | 7 | 29.2 | 1931 | 22 | ABE66948 | Drosophila melanog |
| 42 | 6 | 25.0 | 14 | 22 | AAW96893 | Human peptide #168 |
| 43 | 6 | 25.0 | 26 | 24 | AAE33406 | PD-1-related peptid |
| 44 | 6 | 25.0 | 26 | 24 | ABJ18534 | Neutrophil-activat |
| 45 | 6 | 25.0 | 39 | 20 | AAW50239 | |

ALIGNMENTS

RESULT 1
AAE23839
ID AAE23839 standard; peptide; 24 AA.

XX AAE23839;

AC AAE23839;

XX 10-SEP-2002 (first entry)

DT Human zsig33-linker peptide #1.

DE Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 7..18

FT /note= "Hydrophilic region"

XX US2002055156-A1.

XX 09-MAY-2002.

XX 10-MAY-2001; 2001US-0853253.

XX 11-MAY-2000; 2000US-203300P.

XX (JASP/) JASPERS S R.

XX (SHEP/) SHEPPARD P O.

XX (DEIS/) DEISHER T A.

XX (BISH/) BISHOP P D.

```

XX Jaspers SR, Sheppard PO, Delsher TA, Bishop PD;
PI WPI: 2002-443750/47.
XX N-PSDB: AAD38239.
XX
XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones -
XX
XX Claim 1: Page 28; 34pp; English.
XX
XX The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.
XX
XX Sequence 24 AA;
SQ
Query Match 100.0%; Score 24; DB 23; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
DB 1 ALAGWLRPEDGGQAGAEDELEVR 24
|||||
RESULT 2
AAE15884
ID AAE15884 standard; peptide; 24 AA.
XX
XX AAE15884;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Human zsig33-linker peptide #1.
DE
XX
XX Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
KW adsorption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33-linker peptide.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Region 6..22
FT /note= "Hydrophilic antigenic site"
FT Region 7..18
FT /note= "Hydrophilic region"
XX
XX W0200187933-A2.
PN
XX
XX 22-NOV-2001.
PD
XX
XX 10-MAY-2001; 2001WO-US15091.
PF

```

```

XX 11-MAY-2000; 2000US-0569271.
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Jaspers SR, Sheppard PO, Delsher TA, Bishop PD;
PI WPI: 2002-082982/11.
XX N-PSDB: AAD25760.
XX
XX New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and
PT treating gastrointestinal and growth related diseases, comprises
PT zsig33-like peptides -
XX
XX Claim 1a; Page 81; 89pp; English.
XX
XX The invention relates to zsig33-like peptides (ZS33LP) including
CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and
CC zsig33-epsilon peptides and nucleic acid molecules encoding such
CC zsig33-like peptides. ZS33LP peptides activate the immune system
CC in boosting immunity to infectious diseases, treating immunocompromised
CC patients such as human immunodeficiency virus (HIV) patients, in
CC improving vaccines and in treatment of bacterial, viral, protozoal and
CC fungal infections. Peptides of the invention are used to identify and
CC isolate receptors involved in growth regulation in the liver, blood
CC vessel formation and other developmental processes. They are useful for
CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
CC growth and/or differentiation of tumour cells, as additives to anti-
CC hypoglycaemic preparations containing glucose and as adsorption
CC enhancers for oral drugs which require fast nutrient action and to
CC stimulate glucose-induced insulin release. They are also useful as
CC research reagents for the expansion, differentiation, growth factor and
CC hormone secretion and/or cell-cell interactions of tissues associated
CC with gastrointestinal system, brain and central nervous system. These
CC molecules are useful for treating dysfunction associated with contractile
CC tissues or to suppress or enhance contractility in vivo and to treat
CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
CC acids and/or antibodies are useful for treating disorders associated
CC with gastrointestinal contractility, secretion of digestive enzymes,
CC hormone and acids, secretion of hormones in the pancreas and/or brain,
CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
CC and regulation of nutrient absorption. Sequences of the invention are
CC useful in gene therapy. The present sequence is human zsig33-linker
CC peptide.
XX
XX SQ Sequence 24 AA;
Query Match 100.0%; Score 24; DB 23; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
DB 1 ALAGWLRPEDGGQAGAEDELEVR 24
|||||
RESULT 3
AAE33410
ID AAE33410 standard; Protein; 91 AA.
XX
XX AAE33410;
AC
XX
XX 02-APR-2003 (first entry)
DT
XX
XX Human exon 3-deleted ghrelin protein.
DE
XX
XX Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
KW cancer; human.
XX
XX Homo sapiens.
OS
XX

```

PN WO200290387-A1.
 XX 14-NOV-2002.
 PD
 XX 10-MAY-2002; 2002WO-AU00582.
 XX
 PF 10-MAY-2001; 2001AU-0004919.
 PR 17-DEC-2001; 2001AU-0009567.
 PR
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 PA
 XX Chopin LK, Jeffery PL, Herington AC;
 PI
 XX WPI: 2003-111957/10.
 DR N-PSDB; AAD50726.
 DR
 XX Identifying a cancer cell or tissue for treating prostate, ovarian,
 PT breast cancer, or benign prostatic hyperplasia, by detecting the
 PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
 PT 1b proteins or nucleic acids -
 XX
 PS Claim 14; Page 34; 50pp; English.
 XX
 CC The invention relates to a method for identifying a cancer cell or
 CC tissue of the reproductive system by detecting expression of a ghrelin,
 CC an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic
 CC acids. The antibodies, exon 3-deleted form of preproghrelin and
 CC antagonists are useful for treating cancer of the reproductive system
 CC such as prostate, ovarian, breast, cervical or uterine cancer,
 CC choriocarcinoma or benign prostatic hyperplasia. The present sequence
 CC is human exon 3-deleted ghrelin protein.
 XX
 XX Sequence 91 AA;
 SQ
 Query Match 100.0%; Score 24; DB 24; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.1e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRLPEDGGQAGGADELEVR 24
 Db 52 ALAGWLRLPEDGGQAGGADELEVR 75
 RESULT 4
 AAB60517
 ID AAB60517 standard; Protein; 116 AA.
 XX
 AC AAB60517;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
 XX
 KW Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX
 PN WO200107475-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-JP04907.
 XX
 PR 23-JUL-1999; 99JP-0210002.
 PR 29-NOV-1999; 99JP-0338841.
 PR 26-APR-2000; 2000JP-0126623.
 XX
 XX (KANG/) KANGAWA K.
 PA
 XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 PI
 XX WPI: 1999-070071/06.
 DR

DR WPI: 2001-159704/16.
 DR N-PSDB; AAF59647.
 XX
 PT New peptide compounds which induce growth hormone secretion and
 PT elevate cell calcium concentrations, useful in treatment and diagnosis
 PT of infant growth disorders -
 XX
 PS Claim 3; Page 186-187; 210pp; Japanese.
 XX
 CC The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX
 XX Sequence 116 AA;
 SQ
 Query Match 100.0%; Score 24; DB 22; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRLPEDGGQAGGADELEVR 24
 Db 51 ALAGWLRLPEDGGQAGGADELEVR 74
 RESULT 5
 AAW87991
 ID AAW87991 standard; Protein; 117 AA.
 XX
 AC AAW87991;
 XX
 DT 07-APR-1999 (first entry)
 DT
 XX Protein designated zsig33.
 DE
 XX Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
 KW nutrient absorption regulation; obesity; metabolic disorder.
 KW
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /note= "signal peptide"
 FT Protein 24..117
 FT /note= "mature protein"
 XX
 XX WO9842840-A1.
 PN
 XX 01-OCT-1998.
 PD
 XX 23-MAR-1998; 98WO-US05620.
 XX
 PR 24-MAR-1997; 97US-0822897.
 PR 24-MAR-1997; 97US-0041102.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Deisher TA, Sheppard PO;
 PI
 XX WPI: 1999-070071/06.
 DR

DR N-PSDB; AAX04550.

XX Human polypeptide having homology to motilin, zsig33 - useful e.g.

PT to treat gastrointestinal motility disorders, obesity etc. and to

PT identify antagonists to treat gastrointestinal hypermotility

XX

PS Claim 13; Page 55-56; 69pp; English.

XX

CC The present sequence represents a protein designated Zsig33. The nucleic

CC acids are strongly expressed in stomach tissue. The polypeptide (or

CC allelic variants/orthologs) can be used to stimulate gastric motility,

CC measured as increased transit time or gastric emptying of an ingested

CC substance in mammals. The products are used to treat disorders associated

CC with gastrointestinal cell contractility, secretion of digestive

CC enzymes/acids, gastrointestinal motility, recruitment of digestive

CC enzymes, gastrointestinal inflammation, reflux disease and nutrient

CC absorption regulation. Zsig33 polypeptides may also be important

CC neurologically, since the family of gut-brain peptides to which the

CC homologous protein motilin belongs has been associated with neurological

CC and CNS functions. They may therefore be used e.g. to regulate satiety

CC or treat obesity and other metabolic disorders where neurological

CC feedback modulates nutritional absorption. They are useful to identify

CC zsig33 agonists, antagonists and ligands and to produce antibodies.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 24; DB 20; Length 117;

Best Local Similarity 100.0%; Pred. No. 2.6e-15;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24

DB 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 6

AAY87236

ID AAY87236 standard; Protein; 117 AA.

XX

AC AAY87236;

XX

DT 11-MAY-2000 (first entry)

XX

DE Human signal peptide containing protein HSP-13 SEQ ID NO:13.

XX

KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;

KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;

KW antimicrobial; nontropic; neuroprotective; cardiovascular; hepatotropic;

KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;

KW reproductive disorder; developmental disorder; arteriosclerosis;

KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;

KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;

KW Parkinson's disease; Huntington's diseases; ovulatory defect;

KW muscular dystrophy.

XX

OS Homo sapiens.

XX

PN WO200000610-A2.

XX

PD 06-JAN-2000.

XX

PF 25-JUN-1999; 99WO-US14484.

XX

XX 26-JUN-1998; 98US-0090762.

PR 31-JUL-1998; 98US-0094983.

PR 01-OCT-1998; 98US-0102886.

PR 11-DEC-1998; 98US-0112129.

XX

PA (INCY-) INCYTE PHARM INC.

XX

XX Lai P, Tang YT, Gorgone GA, Corley NC, Guegler KT, Baughn MR;

PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;

PI Bandman O;

XX WPI; 2000-160673/14.

DR N-PSDB; AAZ98121.

XX

PT New human signal peptide-containing proteins useful in treatment,

PT prevention and diagnosis of e.g. cancer, inflammation and

PT cardiovascular disease

XX

PS Claim 1; Page 168-169; 327pp; English.

XX

CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the

CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPPs have

CC anticancer, anti-inflammatory, antimicrobial, nontropic, hepatotropic,

CC neuroprotective, cardiovascular and antiasthmatic activities, and can

CC be used in gene therapy. HSPPs can be used to treat or prevent disorders

CC associated with decreased activity or function of HSP. Antagonists of

CC HSPP are used to treat or prevent disorders associated with increased

CC activity or function of HSPP. Such diseases include cell proliferation

CC (including cancer), inflammation, cardiovascular, neurological,

CC reproductive or developmental disorders, (e.g. arteriosclerosis,

CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,

CC asthma, Crohn's disease, microbial or other infections, congestive or

CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's

CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP

CC nucleic acids can be used for the recombinant production of HSP, for

CC detecting HSP in standard hybridisation and amplification assays (for

CC diagnosis and monitoring), in gene therapy, as antisense,

CC triplex-forming or ribozyme therapeutics, for detecting related sequences

CC or genetic variations, and for chromosomal mapping. HSPP are also used to

CC raise specific antibodies (Ab) and to screen for agonists and

CC antagonists (potential therapeutic agents). Ab are used to diagnose, or

CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic

CC antagonists, in competitive drug screens, and for purification of HSPP

CC from natural sources.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 24; DB 21; Length 117;

Best Local Similarity 100.0%; Pred. No. 2.6e-15;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24

DB 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 7

AAM38890

ID AAM38890 standard; Protein; 117 AA.

XX

AC AAM38890;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 2035.

XX

DE Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

PD 26-JUL-2001.

XX

XX 26-DEC-2000; 2000WO-US34263.

PF 21-JAN-2000; 2000US-0488725.

XX 23-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB: AAI58046.
 XX
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 3: SEQ ID NO 2035; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAW38642-AAW42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 117 AA;
 SQ
 Query Match 100.0%; Score 24; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRLPEDGGQGAEGAEDELEVR 24
 DB 52 ALAGWLRLPEDGGQGAEGAEDELEVR 75
 RESULT 8
 AAB62649
 ID AAB62649 standard; Protein; 117 AA.
 AC AAB62649;
 XX
 XX 23-JUL-2001 (first entry)
 DT
 DE Human zsig33 polypeptide.
 XX
 KW zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R;
 KW G-protein coupled receptor.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Peptide 24..37
 FT /note= "specifically claimed fragment that binds to
 FT the GHS-R"
 XX
 PN WO200138355-A2.

XX 31-MAY-2001.
 PD
 XX 22-NOV-2000; 2000WO-US32074.
 PF
 XX 22-NOV-1999; 99US-0166765.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 PI WPI: 2001-355879/37.
 DR N-PSDB: AAF83678.
 DR
 XX Forming reversible peptide receptor complex for purifying cell and
 PT peptides, stimulating signal transduction and modulating hormone
 PT secretion, involves contacting a receptor with zsig33 polypeptide -
 XX
 PS Claim 1; Page 93-94; 111pp; English.
 XX
 CC The invention relates to a method of forming a reversible peptide-
 CC receptor complex that involves providing an immobilized receptor, and
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
 CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
 CC is useful for purifying cells, purifying a peptide, stimulating signal
 CC transduction in a cell expressing a receptor. It is also useful for
 CC modulating secretion of hormones, neural development and/or utilization,
 CC gastric contractility, nutrient uptake, secretion of digestive and
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
 CC hormone secretion in a mammal having a disease associated with abnormal
 CC levels of growth hormone, such as osteoporosis, bone repair, bone
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,
 CC protein catabolic responses after surgery, cachexia, protein loss,
 CC dwarfism, wound healing and ovulation induction, treating a mammal having
 CC a metabolic disorder requiring neurological feedback, such as satiety
 CC regulation, glucose absorption and metabolism and neuropathy-associated
 CC gastrointestinal disorders, and stimulating glucose-induced insulin
 CC release in a mammal. The present sequence represents the human zsig33
 CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
 XX
 SQ Sequence 117 AA;
 SQ
 Query Match 100.0%; Score 24; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRLPEDGGQGAEGAEDELEVR 24
 DB 52 ALAGWLRLPEDGGQGAEGAEDELEVR 75
 RESULT 9
 AAB20101
 ID AAB20101 standard; Protein; 117 AA.
 AC AAB20101;
 XX
 XX 23-APR-2001 (first entry)
 DT
 DE Zsig33 protein.
 XX
 KW SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
 KW nutritional absorption modulator; growth hormone secretagogue;
 KW therapy; human.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= signal_peptide
 FT Protein 24..117

| | | |
|--|-----------|--|
| | FT | /label= Mature_protein 24..34 |
| | FT | /label= SGIP_peptide |
| | FT | /note= "this peptide is claimed in Claim 1" |
| | XX | |
| | PN | WO200100830-A1. |
| | XX | |
| | PD | 04-JAN-2001. |
| | XX | |
| | PP | 30-JUN-2000; 2000WO-US18306. |
| | XX | |
| | PR | 30-JUN-1999; 99US-0345157. |
| | XX | |
| | PA | (Zymo) ZYMOGENETICS INC. |
| | XX | |
| | PI | Sheppard PO, Jaspers SR, Deisher TA, Bishop PD; |
| | DR | WFI; 2001-123010/13. |
| | DR | N-PSDB; AAF30033. |
| | XX | |
| | PT | Novel variants of SGIP peptides for modulating contractility in duodenum or jejunum tissue, pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion or modulating gastric emptying - |
| | PT | |
| | XX | |
| | PS | Disclosure; 54; 6lpp; English. |
| | XX | |
| | CC | The present sequence is that of zsig33, a secreted protein with homology to motilin (see AAB20102). zsig33 is expressed at high levels in the stomach, and at lower levels in the small intestine and pancreas. A novel peptide fragment of zsig33, termed SGIP (see AAB20100), is claimed. SGIP is a ligand for growth hormone secretagogue receptor, and is therefore useful for modulating secretion of growth hormone and insulin like growth factor 1. SGIP, and variant SGIP peptides, are used in claimed methods for stimulating contractility in duodenum or jejunum tissue, modulating pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion, and modulating gastric emptying. |
| | XX | |
| | SQ | Sequence 117 AA; |
| | | |
| | | Query Match 100.0%; Score 24; DB 22; Length 117; |
| | | Best Local Similarity 100.0%; Pred. No. 2.6e-15; |
| | | Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| | | |
| | QY | 1 ALAGWLRPDGGGAEGAEDELEVR 24 |
| | | |
| | Dd | 52 ALAGWLRPDGGGAEGAEDELRV 75 |
| | | |
| | RESULT 10 | |
| | AAB60511 | |
| | ID | AAB60511 standard; Protein; 117 AA. |
| | XX | |
| | AC | AAB60511; |
| | XX | |
| | DT | 24-APR-2001 (first entry) |
| | XX | |
| | DE | Human ghrelin preproprotein, SEQ ID NO:5. |
| | XX | |
| | KW | Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; |
| | KW | calcium concentration elevation; infant growth disorder; |
| | KX | growth hormone deficiency. |
| | XX | |
| | OS | Homo sapiens. |
| | XX | |
| | PN | WO200107475-A1. |
| | XX | |
| | PD | 01-FEB-2001. |
| | XX | |
| | PF | 24-JUL-2000; 2000WO-JP04907. |
| | XX | |
| | PR | 23-JUL-1999; 99JP-0210002. |
| | XX | |

PA (ZYMO) ZYMOGENETICS INC.
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 PI
 DR WPI: 2002-634794/68.
 DR N-PSDB; ABV72214.
 XX
 XX New Short Gastrointestinal Peptide, which has homology to motilin,
 PT useful for preventing, diagnosing and treating gastrointestinal
 PT disorders -
 XX
 XX Disclosure: Columns 39-40; 23pp; English.
 XX
 XX The present sequence represents human zsig33. The specification describes
 CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.
 CC SGIP has homology to motilin. The SGIP peptide may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate SGIP expression. For example, SGIP may be used to treat
 CC disorders associated with decreased expression by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of SGIP by
 CC expressing inactive proteins or to supplement the patients own production
 CC of SGIP. SGIP may also be used as an antigen in the production of
 CC antibodies against SGIP and in assays to identify modulators of SGIP
 CC expression and activity. The anti-SGIP antibodies, agonists and
 CC antagonists may also be used to regulate expression and activity. The
 CC anti-SGIP antibodies may also be used as diagnostic agents for detecting
 CC the presence of SGIP in samples.
 XX
 XX Sequence 117 AA;
 SQ
 Query Match 100.0%; Score 24; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGGAEGADELEVR 24
 DB 52 ALAGWLRPEDGGGAEGADELEVR 75
 |||||||||||||||||||
 RESULT 12
 AAE23838
 ID AAE23838 standard; Protein; 117 AA.
 XX
 AC AAE23838;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human zsig33 protein.
 XX
 KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
 KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
 KW protein therapy; gastrointestinal; endocrine; anabolic.
 XX
 OS Homo sapiens.
 XX
 PN US2002055156-A1.
 XX
 PD 09-MAY-2002.
 XX
 PF 10-MAY-2001; 2001US-0853253.
 XX
 PR 11-MAY-2000; 2000US-203300P.
 XX
 XX (JASP/) JASPERS S R.
 PA (SHEP/) SHEPPARD P O.
 PA (DEIS/) DEISHER T A.
 PA (BISH/) BISHOP P D.
 XX
 PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 XX
 DR WPI: 2002-443750/47.
 DR N-PSDB; AAD38238.
 XX

PT zsig33-Like peptides and polynucleotides, useful for modulating gastric
 PT contractility, nutrient uptake, and growth hormones and/or secretion of
 PT digestive/pancreatic enzymes and hormones -
 XX
 PS Disclosure: Page 27; 34pp; English.
 XX
 XX The invention relates to zsig33-like peptides and their corresponding
 CC nucleic acids and methods for modulating gastric contractility, nutrient
 CC uptake, growth hormones, secretion of digestive enzymes and hormones.
 CC The sequences of the invention are used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate zsig33 expression.
 CC The nucleic acids of the invention and their complements are used as
 CC DNA probes in diagnostic assays to detect and quantitate the presence
 CC of similar nucleic acids in samples, and therefore which patients may be
 CC in need of restorative therapy. The zsig33 peptides are used as antigens
 CC in the production of antibodies against zsig33 and in assays to identify
 CC modulators of zsig33 expression and activity. The anti-zsig33 antibodies
 CC and antagonists are used to down regulate expression and activity. The
 CC anti-zsig33 antibodies are also used as diagnostic agents for detecting
 CC the presence of zsig33 in samples (e.g. by enzyme linked immunosorbent
 CC assay (ELISA)). The peptides and nucleic acids of the invention are used
 CC to modulate gastric contractility, nutrient uptake, growth hormones, the
 CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
 CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
 CC and zsig33-like peptide is used in protein therapy. The present sequence
 CC is human zsig33 protein.
 XX
 XX Sequence 117 AA;
 SQ
 Query Match 100.0%; Score 24; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGGAEGADELEVR 24
 DB 52 ALAGWLRPEDGGGAEGADELEVR 75
 |||||||||||||||||||
 RESULT 13
 AAE15883
 ID AAE15883 standard; Protein; 117 AA.
 XX
 AC AAE15883;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human zsig33 protein.
 XX
 KW Human; zsig33-like peptide; zsig33LP; immunity; developmental process;
 KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
 KW adsorption enhancer; gastrointestinal disease; growth related disease;
 KW inflammation; gene therapy; growth regulation; blood vessel formation;
 KW HIV; zsig33 protein.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide 1..23
 FT /label= Signal_peptide
 FT Protein 24..117
 FT /note= "Human mature zsig33 protein"
 XX
 PN WO200187933-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-US15091.
 XX
 PR 11-MAY-2000; 2000US-0569271.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 XX
 PI

XX WPI; 2002-082982/11.
 DR N-PSDB; AAD25759.
 XX
 PT New polypeptides, useful for modulating gastric contractility, nutrient
 PT uptake, pancreatic secretion of hormones, digestive enzymes and
 PT treating gastrointestinal and growth related diseases, comprises
 PT zsig33-like peptides -
 XX
 PS Disclosure; Page 80-81; 89pp; English.
 XX
 CC The invention relates to zsig33-like peptides (ZS33LP) including
 CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and
 CC zsig33-epsilon peptides and nucleic acid molecules encoding such
 CC zsig33-like peptides. ZS33LP peptides activate the immune system
 CC in boosting immunity to infectious diseases, treating immunocompromised
 CC patients such as human immunodeficiency virus (HIV) patients, in
 CC improving vaccines and in treatment of bacterial, viral, protozoal and
 CC fungal infections. Peptides of the invention are used to identify and
 CC isolate receptors involved in growth regulation in the liver, blood
 CC vessel formation and other developmental processes. They are useful for
 CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
 CC growth and/or differentiation of tumour cells, as additives to anti-
 CC hypoglycaemic preparations containing glucose and as adsorption
 CC enhancers for oral drugs which require fast nutrient action and to
 CC stimulate glucose-induced insulin release. They are also useful as
 CC research reagents for the expansion, differentiation, growth factor and
 CC hormone secretion and/or cell-cell interactions of tissues associated
 CC with gastrointestinal system, brain and central nervous system. These
 CC molecules are useful for treating dysfunction associated with contractile
 CC tissues or to suppress or enhance contractility in vivo and to treat
 CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
 CC acids and/or antibodies are useful for treating disorders associated
 CC with gastrointestinal contractility, secretion of digestive enzymes,
 CC hormone and acids, secretion of hormones in the pancreas and/or brain,
 CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
 CC and regulation of nutrient absorption. Sequences of the invention are
 CC useful in gene therapy. The present sequence is human zsig33 protein.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 24; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQGADELEVR 24
 Db |||||
 52 ALAGWLRPEDGGQGADELEVR 75
 RESULT 14
 ABU66790
 ID ABU66790 standard; Protein; 117 AA.
 XX
 AC ABU66790;
 XX
 XX 23-MAY-2003 (first entry)
 DT
 XX
 DE Human PRO polypeptide #221.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
 KW differentiation; chondrocyte; tumour; genetic disorder;
 KW cytostatic.
 XX
 XX Homo sapiens.
 OS
 XX US2003036180-A1.
 FN
 XX 20-FEB-2003.
 PD
 XX 09-MAY-2002; 2002US-0143114.
 PF
 XX

PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 98WO-US00106.
 PR 08-MAR-1999; 98WO-US05028.
 PR 10-MAR-1999; 98WO-US05190.
 PR 20-APR-1999; 98WO-US08615.
 PR 14-MAY-1999; 98WO-US10733.
 PR 02-JUN-1999; 98WO-US12252.
 PR 01-SEP-1999; 98WO-US20111.
 PR 08-SEP-1999; 98WO-US20594.
 PR 13-SEP-1999; 98WO-US20944.
 PR 15-SEP-1999; 98WO-US21090.
 PR 15-SEP-1999; 98WO-US21547.
 PR 05-OCT-1999; 98WO-US23089.
 PR 29-NOV-1999; 98WO-US28214.
 PR 30-NOV-1999; 98WO-US28313.
 PR 30-NOV-1999; 98WO-US28409.
 PR 01-DEC-1999; 98WO-US28301.
 PR 01-DEC-1999; 98WO-US28634.
 PR 02-DEC-1999; 98WO-US28551.
 PR 02-DEC-1999; 98WO-US28584.
 PR 02-DEC-1999; 98WO-US28585.
 PR 16-DEC-1999; 98WO-US30095.
 PR 20-DEC-1999; 98WO-US30911.
 PR 20-DEC-1999; 98WO-US30999.
 PR 22-DEC-1999; 98WO-US30720.
 PR 30-DEC-1999; 98WO-US31243.
 PR 30-DEC-1999; 98WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 01-MAR-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.

PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 03-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX (GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI: 2003-332040/31.
DR N-PSDB; ACA03823.

XX
PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in
PT tissue typing, and in chromosome identification -
XX
PS Claim 12; Fig 442; 660pp; English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists.
CC The PRO polypeptides are useful for stimulating the release of
CC the tumour necrosis factor (TNF)-alpha from human blood, for stimulating
CC the proliferation or differentiation of chondrocytes, and detecting the
CC presence of tumours. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and
CC gene mapping, in the generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptides, for generating transgenic animals or
CC knockout animals, for the genetic analysis of individuals with genetic
CC disorders, and in gene therapy. AB066570-AB066844 represent the human
CC PRO polypeptides of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdsIDentry.html.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 24; DB 24; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.6e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGGAEGAEDELEVR 24
|||||
DB 52 ALAGWLRPDGGGAEGAEDELEVR 75

RESULT 15
ABU67066
ID ABU67066 standard; Protein; 117 AA.
XX
AC ABU67066;
XX
DT 27-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane, PRO, protein SEQ ID 442.
XX
KW Human; secreted protein; transmembrane protein; PRO;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bioreactor; tumour.
XX
OS Homo sapiens.
XX
PN US2003032155-A1.
XX
PD 13-FEB-2003.
XX
PF 03-MAY-2002; 2002US-0137865.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17886.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28309.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
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 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
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 PR 28-FEB-2001; 2001WO-US06540.
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 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21086.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
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 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
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(GETH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI: 2003-331925/31.
 N-PSDB; ACA04244.

New secreted and transmembrane nucleic acids and polypeptides,
 designated as PRO, useful for treating inflammation, organ failure,
 atherosclerosis, cardiac injury, infertility, birth defects, premature
 aging, AIDS, or cancer

Claim 12: Fig 442: 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is
 at least 80% identical to, or the full-length coding sequence of, any of
 the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 (one of 275 secreted or transmembrane proteins). The nucleic acid
 further comprises the full-length coding sequence of the DNA deposited

* * *

CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins. PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 24; DB 24; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAGAEDELEVR 24

Db 52 ALAGWLRPEDGGGAGAEDELEVR 75

Search completed: September 11, 2003, 17:51:54
 Job time : 26.2834 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:55:57 ; Search time 14.7594 Seconds
(without alignments)
237.266 Million cell updates/sec

Title: US-09-853-253-4

Perfect score: 24

Sequence: 1 ALAGWLPRPDGGGAEGAEDELEVR 24

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 541936 seqs, 145912426 residues

Word size : 0

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*

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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 24 | 100.0 | 24 | 9 | US-09-853-253-4 |
| 2 | 24 | 100.0 | 117 | 9 | US-09-794-987-2 |
| 3 | 24 | 100.0 | 117 | 9 | US-09-853-253-2 |
| 4 | 24 | 100.0 | 117 | 9 | US-09-989-723-268 |
| 5 | 24 | 100.0 | 117 | 9 | US-09-989-723-268 |
| 6 | 24 | 100.0 | 117 | 9 | US-09-989-723-268 |
| 7 | 24 | 100.0 | 117 | 9 | US-09-989-723-268 |
| 8 | 24 | 100.0 | 117 | 10 | US-09-989-731-268 |
| 9 | 24 | 100.0 | 117 | 10 | US-09-989-732-268 |
| 10 | 24 | 100.0 | 117 | 10 | US-09-991-073-268 |
| 11 | 24 | 100.0 | 117 | 10 | US-09-990-442-268 |
| 12 | 24 | 100.0 | 117 | 10 | US-09-991-163-268 |
| 13 | 24 | 100.0 | 117 | 10 | US-09-993-604-268 |
| 14 | 24 | 100.0 | 117 | 10 | US-09-990-456-268 |
| 15 | 24 | 100.0 | 117 | 10 | US-09-989-721-268 |

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| 16 | 24 | 100.0 | 117 | 10 | US-09-992-598-268 | Sequence 268, App |
| 17 | 24 | 100.0 | 117 | 10 | US-09-989-293A-268 | Sequence 268, App |
| 18 | 24 | 100.0 | 117 | 10 | US-09-989-735-268 | Sequence 268, App |
| 19 | 24 | 100.0 | 117 | 10 | US-09-990-444-268 | Sequence 268, App |
| 20 | 24 | 100.0 | 117 | 10 | US-09-991-181-268 | Sequence 268, App |
| 21 | 24 | 100.0 | 117 | 10 | US-09-989-730-268 | Sequence 268, App |
| 22 | 24 | 100.0 | 117 | 10 | US-09-990-436-268 | Sequence 268, App |
| 23 | 24 | 100.0 | 117 | 10 | US-09-993-687-268 | Sequence 268, App |
| 24 | 24 | 100.0 | 117 | 11 | US-09-989-734-268 | Sequence 268, App |
| 25 | 24 | 100.0 | 117 | 11 | US-09-997-653-268 | Sequence 268, App |
| 26 | 24 | 100.0 | 117 | 11 | US-09-993-667-268 | Sequence 268, App |
| 27 | 24 | 100.0 | 117 | 11 | US-09-997-428-268 | Sequence 268, App |
| 28 | 24 | 100.0 | 117 | 11 | US-09-997-666-268 | Sequence 268, App |
| 29 | 24 | 100.0 | 117 | 11 | US-09-990-438-268 | Sequence 268, App |
| 30 | 24 | 100.0 | 117 | 11 | US-09-990-562-268 | Sequence 268, App |
| 31 | 24 | 100.0 | 117 | 11 | US-09-990-711-268 | Sequence 268, App |
| 32 | 24 | 100.0 | 117 | 11 | US-09-989-726-268 | Sequence 268, App |
| 33 | 24 | 100.0 | 117 | 11 | US-09-998-156-268 | Sequence 268, App |
| 34 | 24 | 100.0 | 117 | 11 | US-09-990-437-268 | Sequence 268, App |
| 35 | 24 | 100.0 | 117 | 11 | US-09-991-157-268 | Sequence 268, App |
| 36 | 24 | 100.0 | 117 | 11 | US-09-997-514-268 | Sequence 268, App |
| 37 | 24 | 100.0 | 117 | 11 | US-09-997-573-268 | Sequence 268, App |
| 38 | 24 | 100.0 | 117 | 11 | US-09-991-172-268 | Sequence 268, App |
| 39 | 24 | 100.0 | 117 | 11 | US-09-990-726-268 | Sequence 268, App |
| 40 | 24 | 100.0 | 117 | 11 | US-09-997-559-268 | Sequence 268, App |
| 41 | 24 | 100.0 | 117 | 11 | US-09-997-601-268 | Sequence 268, App |
| 42 | 24 | 100.0 | 117 | 11 | US-09-990-443-268 | Sequence 268, App |
| 43 | 24 | 100.0 | 117 | 11 | US-09-991-854-268 | Sequence 268, App |
| 44 | 24 | 100.0 | 117 | 11 | US-09-997-628-268 | Sequence 268, App |
| 45 | 24 | 100.0 | 117 | 11 | US-09-997-683-268 | Sequence 268, App |

ALIGNMENTS

RESULT 1
US-09-853-253-4
; Sequence 4, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-4

Query Match 100.0%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLPRPDGGGAEGAEDELEVR 24
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Db 1 ALAGWLPRPDGGGAEGAEDELEVR 24

RESULT 2
US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. US20010041791A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.

Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/046,479
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

Query Match 100.0%; Score 24; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEVR 24
Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 3
US-09-853-253-2
Sequence 2, Application US/09853253
Patent No. US20020055156A1
GENERAL INFORMATION:
APPLICANT: JASPERS, STEPHEN
APPLICANT: SHEPPARD, PAUL
APPLICANT: DEISHER, THERESA
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: zsig33-like Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-853-253-2

Query Match 100.0%; Score 24; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ALAGWLRPEDGGGAEGAEDELEVR 24
Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 4
US-09-989-722-268
Sequence 268, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Garber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04

RESULT 5

US-09-989-723-268 Application US/09898723
; Sequence 268
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grøttsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049878
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; PRIOR APPLICATION NUMBER: 60/090676
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; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-26
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24
|||||
Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 6
US-09-989-279-268
; Sequence 268, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/090431

; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
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; PRIOR APPLICATION NUMBER: 60/091626
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.9e-16;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24

Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 7

US-09-989-727-268
; Sequence 268, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

; PRIOR APPLICATION NUMBER: 60/090472
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090535
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090540
 ; PRIOR FILING DATE: 1998-06-24
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 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.9e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEVR 24
 Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 8
 US-09-989-731-268
 ; Sequence 268, Application US/09989731
 ; Patent No. US20020103125A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PLC70
 ; CURRENT APPLICATION NUMBER: US/09/989,731
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.9e-16;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAEDELEVR 24
Db 52 ALAGWLRPEDGGQAEDELEVR 75
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RESULT 9

US-09-989-732-268
; Sequence 268, Application US/09989732
; Patent No US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.

; PRIOR APPLICATION NUMBER: 60/090690
 ; PRIOR FILING DATE: 1998-06-25
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 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.9e-16;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAELEVR 24
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 Db 52 ALAGWLRPEDGGGAEGAELEVR 75

RESULT 10

US-09-991-073-268

; Sequence 268, Application US/09991073

; Patent No. US20020127576A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC15
 ; CURRENT APPLICATION NUMBER: US/09/991,073

; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR FILING DATE: 1998-07-02
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 ; PRIOR FILING DATE: 1998-07-07
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.9e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAEAELEVR 24
 |||||
 Db 52 ALAGWLRPEDGGQAEAELEVR 75

RESULT 11

US-09-990-442-268
 ; Sequence 268, Application US/09990442
 ; Patent No. US20020132252A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tamas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730P1C8
 ; CURRENT APPLICATION NUMBER: US/09/990,442
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/091478
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.9e-16;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEVR 24

Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 12

US-09-991-163-268

; Sequence 268, Application US/09991163

; Patent No. US20020132253A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

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; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavlin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanebe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C17

; CURRENT APPLICATION NUMBER: US/09/991,163

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

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; PRIOR FILING DATE: 1997-11-24

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 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09
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 Query Match 100.0%; Score 24; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.9e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24
 DB 52 ALAGWLRPEDGGGAEGAEDELEVR 75
 RESULT 13
 US-09-993-604-268
 ; Sequence 268, Application US/09993604
 ; Patent No. US20020137075A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
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 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730PIC25
 ; CURRENT APPLICATION NUMBER: US/09/993,604
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
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| 60/088655 | PRIOR FILING DATE: 1998-06-05 |
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| 60/088203 | PRIOR FILING DATE: 1998-06-05 |
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| 60/088217 | PRIOR FILING DATE: 1998-06-05 |
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| 60/088738 | PRIOR APPLICATION NUMBER: 60/088738 |
| 60/088742 | PRIOR FILING DATE: 1998-06-10 |
| 60/088810 | PRIOR APPLICATION NUMBER: 60/088810 |
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| 60/088858 | PRIOR APPLICATION NUMBER: 60/088858 |
| 60/088861 | PRIOR FILING DATE: 1998-06-11 |
| 60/088876 | PRIOR APPLICATION NUMBER: 60/088876 |
| 60/089105 | PRIOR FILING DATE: 1998-06-11 |
| 60/089440 | PRIOR APPLICATION NUMBER: 60/089440 |
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| 60/089599 | PRIOR APPLICATION NUMBER: 60/089599 |
| 60/089600 | PRIOR FILING DATE: 1998-06-17 |
| 60/089653 | PRIOR APPLICATION NUMBER: 60/089653 |
| 60/089801 | PRIOR FILING DATE: 1998-06-17 |

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| 1 | PRIOR FILING DATE: 1998-06-18 | 60/089907 | |
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| 3 | PRIOR FILING DATE: 1998-06-18 | 60/089908 | |
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| 5 | PRIOR FILING DATE: 1998-06-18 | 60/089947 | |
| 6 | PRIOR APPLICATION NUMBER: 60/089947 | | |
| 7 | PRIOR FILING DATE: 1998-06-19 | 60/089948 | |
| 8 | PRIOR APPLICATION NUMBER: 60/089948 | | |
| 9 | PRIOR FILING DATE: 1998-06-19 | 60/089952 | |
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| 11 | PRIOR FILING DATE: 1998-06-19 | 60/090246 | |
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| 19 | PRIOR FILING DATE: 1998-06-23 | 60/090355 | |
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| 21 | PRIOR FILING DATE: 1998-06-23 | 60/090429 | |
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| 29 | PRIOR FILING DATE: 1998-06-24 | 60/090445 | |
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| 31 | PRIOR FILING DATE: 1998-06-24 | 60/090472 | |
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| 59 | PRIOR FILING DATE: 1998-07-01 | 60/091478 | |
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| 65 | PRIOR FILING DATE: 1998-07-02 | 60/091626 | |
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| 67 | PRIOR FILING DATE: 1998-07-02 | 60/091633 | |
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| 70 | PRIOR APPLICATION NUMBER: 60/091778 | | |
| 71 | PRIOR FILING DATE: 1998-07-07 | 60/091982 | |
| 72 | PRIOR APPLICATION NUMBER: 60/091982 | | |
| 73 | PRIOR FILING DATE: 1998-07-07 | | |

; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALAGWLRPEDGGQAGAEDELEVR 24
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Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 14

US-09-990-456-268

; Sequence 268, Application US/09990456

; Patent No. US20020137890A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC22
; CURRENT APPLICATION NUMBER: US/09/990,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR FILING DATE: 1998-06-19

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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.9e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAEDELEVR 24
 Db 52 ALAGWLRPEDGGQAEDELEVR 75
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 US-09-989-721-268
 ; Sequence 268, Application US/09989721
 ; Patent No. US20020142961A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C55
 ; CURRENT APPLICATION NUMBER: US/09/989,721
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
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 ; PRIOR FILING DATE: 1998-06-04

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:37 ; Search time 9.1123 seconds
(without alignments)
253.289 Million cell updates/sec

Title: US-09-853-253-4

Perfect score: 24

Sequence: 1 ALAGWLRPDGGQAGAEDELEVR 24

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|-------|-------|--------|----------|---------------------|
| 1 | 24 | 100.0 | 117 | 1 A59316 | ghrelin precursor |
| 2 | 8 | 33.3 | 483 | 2 T04453 | hypothetical prote |
| 3 | 7 | 29.2 | 302 | 2 JH0572 | hypothetical prote |
| 4 | 7 | 29.2 | 344 | 2 A48990 | transcription regu |
| 5 | 7 | 29.2 | 910 | 2 B83451 | aconitate hydratase |
| 6 | 7 | 29.2 | 1239 | 1 Q08E10 | BOLFI protein - hu |
| 7 | 6 | 25.0 | 69 | 2 C87574 | cold-shock domain |
| 8 | 6 | 25.0 | 103 | 2 F82266 | conserved hypothet |
| 9 | 6 | 25.0 | 142 | 2 AB0401 | probable membrane |
| 10 | 6 | 25.0 | 175 | 2 E82118 | conserved hypothet |
| 11 | 6 | 25.0 | 178 | 2 A30230 | quiescence-specifi |
| 12 | 6 | 25.0 | 180 | 2 T46695 | hypothetical prote |
| 13 | 6 | 25.0 | 189 | 2 A91082 | hypothetical prote |
| 14 | 6 | 25.0 | 189 | 2 B85927 | hypothetical prote |
| 15 | 6 | 25.0 | 198 | 2 D69070 | imidazoleglycerol- |
| 16 | 6 | 25.0 | 223 | 2 A40866 | HL-60-induced diff |
| 17 | 6 | 25.0 | 237 | 2 T30002 | hypothetical prote |
| 18 | 6 | 25.0 | 265 | 2 A95298 | hypothetical prote |
| 19 | 6 | 25.0 | 267 | 1 CTPGP | corticotropin / li |
| 20 | 6 | 25.0 | 284 | 2 B25624 | tropomyosin I, tho |
| 21 | 6 | 25.0 | 284 | 2 A25624 | tropomyosin I, emb |
| 22 | 6 | 25.0 | 288 | 2 A55737 | PD-1 protein - hum |
| 23 | 6 | 25.0 | 289 | 2 T48894 | lipoprotein mtsA, |
| 24 | 6 | 25.0 | 289 | 2 H83433 | hypothetical prote |
| 25 | 6 | 25.0 | 290 | 2 H71852 | hypothetical prote |
| 26 | 6 | 25.0 | 293 | 2 H72757 | hypothetical prote |
| 27 | 6 | 25.0 | 299 | 2 T35144 | glutamate transpor |
| 28 | 6 | 25.0 | 302 | 2 T48871 | catechol 1,2-dioxy |
| 29 | 6 | 25.0 | 308 | 2 F72508 | probable hydrogena |

ALIGNMENTS

RESULT 1

A59316
ghrelin precursor - human
N:Alternate names: preproghrelin
C:Species: Homo sapiens (man)
C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C:Accession: A59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: A59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-117 <KOJ>
A:Cross-references: GB:AB029434; NID:g6691571; PIDN:BAA89371.1; PID:g6691572
A:Experimental source: tissue stomach endocrine cells
A:Note: submitted to GenBank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (gr
C:Superfamily: motilin
C:Keywords: hormone; lipoprotein; stomach
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <MAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanote (Ser) (covalent) #status experimental

Query Match 100.0%; Score 24; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAGAEDELEVR 24
DB 52 ALAGWLRPDGGQAGAEDELEVR 75
|||||

RESULT 2

T04453
hypothetical protein F4D11.80 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C:Accession: T04453
R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Hohelsel, J.; Mewes,
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15360
A:Accession: T04453
A:Molecule type: DNA
A:Residues: 1-483 <BEV>
A:Cross-references: EMBL:AL022537
A:Experimental source: cultivar Columbia; BAC clone F4D11
C:Genetics:
A:Map position: 4
A:Introns: 17/3; 44/1; 94/1; 141/3; 206/2; 247/2; 345/3; 395/1; 434/2

| | | | | | | |
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| 30 | 6 | 25.0 | 313 | 2 | E82762 | conserved hypothet |
| 31 | 6 | 25.0 | 315 | 2 | F64129 | probable phosphogl |
| 32 | 6 | 25.0 | 326 | 1 | E69690 | transcription repr |
| 33 | 6 | 25.0 | 343 | 2 | AH1823 | 30S ribosomal prot |
| 34 | 6 | 25.0 | 343 | 2 | T35063 | probable prolipopr |
| 35 | 6 | 25.0 | 345 | 2 | A83526 | hypothetical prote |
| 36 | 6 | 25.0 | 346 | 2 | AE3323 | sam-dependent meth |
| 37 | 6 | 25.0 | 350 | 2 | S71923 | cysteine proteinase |
| 38 | 6 | 25.0 | 360 | 2 | S59598 | cysteine proteinase |
| 39 | 6 | 25.0 | 368 | 2 | G96668 | protein FIN19.7 [l |
| 40 | 6 | 25.0 | 376 | 2 | AD2697 | hypothetical prote |
| 41 | 6 | 25.0 | 377 | 2 | G97314 | alcohol dehydrogen |
| 42 | 6 | 25.0 | 377 | 2 | T47471 | cysteine proteinase |
| 43 | 6 | 25.0 | 379 | 1 | DCBSPK | phosphoribosylamin |
| 44 | 6 | 25.0 | 379 | 2 | D82801 | molybdopterin bios |
| 45 | 6 | 25.0 | 383 | 2 | F83321 | hypothetical prote |

C:Superfamily: major cold shock protein; cold shock domain homology

Query Match 25.0%; Score 6; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PEDGGQ 13
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DB 20 PEDGGQ 25

RESULT 8

F82266 conserved hypothetical protein VC0887 [imported] - Vibrio cholerae (strain N16961 serogr

C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Dec-2002
C:Accession: F82266
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301

A:Accession: F82266
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-103 <HE>

A:Cross-references: GB:AE004173; GB:AE003852; NID:g9655341; PIDN:AAF94049.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0887
A:Map position: 1

C:Superfamily: uncharacterized conserved protein

Query Match 25.0%; Score 6; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 DELEVR 24
|||||
DB 12 DELEVR 17

RESULT 9

AB0401 probable membrane protein YPO3302 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0401

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Parraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AB0401
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-142 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC92534.1; PID:gl5981232; GSPDB:GN00175

C:Genetics:
A:Gene: YPO3302
A:Superfamily: hypothetical protein HI0489

Query Match 25.0%; Score 6; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAGWLR 7
|||||
DB 104 LAGWLR 109

RESULT 10

E82118 conserved hypothetical protein VC2111 [imported] - Vibrio cholerae (strain N16961 ser

C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82118

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: AB2035; MUID:20406833; PMID:10952301

A:Accession: E82118
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-175 <HE>

A:Cross-references: GB:AE004284; GB:AE003852; NID:g9656649; PIDN:AAF95256.1; GSPDB:GN

A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2111
A:Map position: 1

Query Match 25.0%; Score 6; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GOAEGA 17
|||||
DB 54 GOAEGA 59

RESULT 11

A30230 quiescence-specific protein precursor - chicken

N:Alternat names: Ch21 protein

C:Species: Gallus gallus (chicken)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 15-Nov-1996
C:Accession: A30230; A42581; A36595; A35491

R:Bedard, P.A.; Yannoni, Y.; Simmons, D.L.; Erikson, R.L.
Mol. Cell. Biol. 9, 1371-1375, 1989

A:Title: Rapid repression of quiescence-specific gene expression by epidermal growth

A:Reference number: A30230; MUID:89261749; PMID:2498647

A:Accession: A30230
A:Molecule type: mRNA

A:Residues: 1-178 <BE>

R:Dozin, B.; Descalzi, F.; Briata, L.; Hayashi, M.; Gentili, C.; Hayashi, K.; Quarto,
J. Biol. Chem. 267, 2979-2985, 1992

A:Title: Expression, regulation, and tissue distribution of the Ch21 protein during c

A:Reference number: A42581; MUID:92147639; PMID:1737754

A:Accession: A42581
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-95, 'L', 97-178 <DOZ>

A:Experimental source: tibia hypertrophic cartilage

A:Note: sequence extracted from NCBI backbone (NCBI:80796, NCBIP:80797)

R:Cancedda, F.D.; Dozin, B.; Rossi, F.; Molina, F.; Cancedda, R.; Negri, A.; Ronchi,
J. Biol. Chem. 265, 19060-19064, 1990

A:Title: The Ch21 protein, developmentally regulated in chick embryo, belongs to the

A:Reference number: A36595; MUID:91035433; PMID:2229062

A:Accession: A36595
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 21-95, 'L', 97-178 <CAN>

A:Cross-references: GB:M37611
R:Cancedda, F.D.; Asaro, D.; Molina, F.; Cancedda, R.; Caruso, C.; Camardella, L.; Ne

Biochem. Biophys. Res. Commun. 168, 933-938, 1990

A:Title: The amino terminal sequence of the developmentally regulated CH21 protein sh

A:Reference number: A35491; MUID:90267487; PMID:2346493

A:Accession: A35491
A:Status: preliminary

A:Molecule type: protein
A:Residues: 21-48 <CA2>

C:Superfamily: lipocalin; lipocalin homology

F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-178/Product: quiescence-specific protein #status predicted <MAT>
 F:25-173/Domain: lipocalin homology <LIP>

Query Match 25.0%; Score 6; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EDELEV 23
 |||||
 Db 65 EDELEV 70

RESULT 12

T46695

hypothetical protein ORF-180 [imported] - Lactobacillus helveticus plasmid pLH1

C:Species: Lactobacillus helveticus

C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 04-Mar-2000

C:Accession: T46695

R:Thompson, K.; McConville, K.J.; McReynolds, C.; Foley, S.

submitted to the EMBL Data Library, December 1997

A:Description: Complete sequence of plasmid pLH1 from Lactobacillus helveticus ATCC15009

A:Reference number: 223135

A:Accession: T46695

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-180 <THO>

A:Cross-references: EMBL:AJ222725; PIDN:CAAL0962.1

C:Genetics: ATCC 15009

A:Gene: plasmid pLH1

C:Superfamily: Lactobacillus helveticus plasmid pLH1 hypothetical protein ORF-180

Query Match 25.0%; Score 6; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
 |||||
 Db 31 ALAGWL 36

RESULT 13

A91082

hypothetical protein ECS3625 [imported] - Escherichia coli (strain O157:H7, substrain R)

C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C:Accession: A91082

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome analysis

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: A91082

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-189 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA037048.1; PID:q13363096; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: ECS3625

Query Match 25.0%; Score 6; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
 |||||
 Db 14 ALAGWL 19

RESULT 14

B85927

hypothetical protein 24080 [imported] - Escherichia coli (strain O157:H7, substrain E
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: B85927

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimailanta, E.; Potamousis, K.; Apoda
 Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: B85927

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-189 <STO>

A:Cross-references: GB:AE005174; NID:q12517231; PIDN:AAG57878.1; GSPDB:GN00145; UWGP:

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: 24080

Query Match 25.0%; Score 6; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
 |||||
 Db 14 ALAGWL 19

RESULT 15

D69070

imidazoleglycerol-phosphate synthase - Methanobacterium thermoautotrophicum (strain D
 C:Species: Methanobacterium thermoautotrophicum

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C:Accession: D69070

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T
 ; Qiu, D.; Spadafora, R.; Vicair, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, I.
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.N. J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: D69070

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-198 <MTH>

A:Cross-references: GB:AE000912; GB:AE000666; NID:g2622632; PIDN:AAB85999.1; PID:g262

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH1524

A:Start codon: TTTG

C:Superfamily: amidotransferase hish; trpG homology

Query Match 25.0%; Score 6; DB 2; Length 198;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EGAEDE 20
 |||||
 Db 130 EGAEDE 135

Search completed: September 11, 2003, 17:57:05
 Job time : 11.1123 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:30:37 ; Search time 4.62032 Seconds
(without alignments)
244.278 Million cell updates/sec

Title: US-09-853-253-4
Perfect score: 24
Sequence: 1 ALAGWLRPDGGQAEARDELEVR 24

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result NO. | Score | Query Match | ID | Description |
|------------|-------|-------------|--------------|---------------------|
| 1 | 24 | 100.0 | 1 GHRL_HUMAN | Q9ubu3 homo sapien |
| 2 | 10 | 41.7 | 1 GHRL_BOVIN | Q9bdj6 bos taurus |
| 3 | 7 | 29.2 | 1 MPR2_STRCO | Q91127 streptomyc |
| 4 | 7 | 29.2 | 1 MPR2_STRLI | P43161 streptomyc |
| 5 | 7 | 29.2 | 1 V120_EBV | P03189 epstein-bar |
| 6 | 6 | 25.0 | 1 GHRL_CANFA | Q9bef8 canis fami |
| 7 | 6 | 25.0 | 1 EFAB_CHICK | P21760 gallus gall |
| 8 | 6 | 25.0 | 1 HIS5_METHH | O27568 methanobact |
| 9 | 6 | 25.0 | 1 COLI_PIG | P01192 s corticotr |
| 10 | 6 | 25.0 | 1 TPM2_DROME | P09491 drosophila |
| 11 | 6 | 25.0 | 1 PCP1_HUMAN | Q15116 homo sapien |
| 12 | 6 | 25.0 | 1 OPSD_LIMPA | O42431 limnocottus |
| 13 | 6 | 25.0 | 1 PARB_HELPJ | Q92x75 helicobacte |
| 14 | 6 | 25.0 | 1 MTSB_STRPB | Q8p280 streptococc |
| 15 | 6 | 25.0 | 1 MTSB_STRPY | Q9af88 streptococc |
| 16 | 6 | 25.0 | 1 MRAW_XYLFA | Q15045 xyliella fas |
| 17 | 6 | 25.0 | 1 YF56_HAEIN | P45250 haemophilus |
| 18 | 6 | 25.0 | 1 RBSR_BACSU | P36944 bacillus su |
| 19 | 6 | 25.0 | 1 MRAW_BRUME | Q8y174 brucella me |
| 20 | 6 | 25.0 | 1 CYS2_MAIZE | Q10717 zea mays (m |
| 21 | 6 | 25.0 | 1 PURK_BACSU | P12045 bacillus su |
| 22 | 6 | 25.0 | 1 IF5_SCHPO | Q09689 schizosacch |
| 23 | 6 | 25.0 | 1 TIG_STAAM | Q99t16 staphylococ |
| 24 | 6 | 25.0 | 1 CUS1_YEAST | Q02554 saccharomyc |
| 25 | 6 | 25.0 | 1 RPSD_MYCGE | P47491 mycoplasma |
| 26 | 6 | 25.0 | 1 RPSD_MYCPN | P78022 mycoplasma |
| 27 | 6 | 25.0 | 1 SYS_MOUSE | P26638 mus musculu |
| 28 | 6 | 25.0 | 1 SYS_BOVIN | Q9gmb8 bos taurus |
| 29 | 6 | 25.0 | 1 SYS_HUMAN | P49591 homo sapien |
| 30 | 6 | 25.0 | 1 AMYB_HORVU | P16098 hordeum vul |
| 31 | 6 | 25.0 | 1 Z173_HUMAN | Q12899 homo sapien |
| 32 | 6 | 25.0 | 1 CH60_BUCTC | Q8k1x3 buchnera ap |
| 33 | 6 | 25.0 | 1 HS60_CANAL | O74261 candida alb |

| | | | | | | |
|----|---|------|-----|---|------------|--------------------|
| 34 | 6 | 25.0 | 572 | 1 | HS60_YEAST | P19882 saccharomyc |
| 35 | 6 | 25.0 | 590 | 1 | HS60_AJECA | P50142 ajellomyces |
| 36 | 6 | 25.0 | 620 | 1 | SMP_COTJA | Q92154 coturnix co |
| 37 | 6 | 25.0 | 641 | 1 | DXS_RHOCA | P26242 rhodobacter |
| 38 | 6 | 25.0 | 650 | 1 | APPI_HUMAN | P51693 homo sapien |
| 39 | 6 | 25.0 | 657 | 1 | HUTH_MOUSE | P33492 mus musculu |
| 40 | 6 | 25.0 | 683 | 1 | Z263_HUMAN | Q14978 homo sapien |
| 41 | 6 | 25.0 | 702 | 1 | HELS_AERPE | O9yfq8 aeropyrum p |
| 42 | 6 | 25.0 | 728 | 1 | UVRC_STRCO | Q92512 streptomyc |
| 43 | 6 | 25.0 | 886 | 1 | SM6B_MOUSE | O54951 mus musculu |
| 44 | 6 | 25.0 | 887 | 1 | SM6B_RAT | O70141 rattus norv |
| 45 | 6 | 25.0 | 890 | 1 | ACOL_ECOLI | P22516 escherichia |

ALIGNMENTS

RESULT 1
GHRL_HUMAN
ID GHRL_HUMAN STANDARD; PRT; 117 AA.
AC Q9UBU3: QBTAT9; Q9H3R3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
GN GHRL OR MTLRP
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
RX MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach."
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Stomach;
RA Tomasetto C., Karam S.M., Rio M.-C.;
RT "Identification of a novel gastric protein m46."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Wajraich M.P., Ten I.S., Gertner J.M., Leibell R.L.;
RT "Genomic organization of the human Ghrelin gene."
RL J. Endocrinol. Genet. 1:231-233(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stachenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [6]
RQ SEQUENCE OF 24-33.
RX TISSUE=Stomach;
RC MEDLINE=20389976; PubMed=10930375;
RA Tonasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RT Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RL "Identification and characterization of a novel gastric peptide
hormone: the motilin-related peptide.";
RN Gastroenterology 119:395-405(2000).
RP [7]
RQ REVIEW
RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RL hormone secretagogue receptor.";
RN Trends Endocrinol. Metab. 12:118-122(2001).
RQ -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9UBU3-1; Sequence=Displayed;
CC Name=2; Synonyms=dal-Gln14-ghrelin;
CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
CC -1- PTM: O-n-octanoylation is essential for activity.
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobogen.fr/services/chromancer/Genes/GhrelinID327.html".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
CC EMBL; AB029434; BAA89371.1; -
CC EMBL; AB035700; BAB19045.1; -
CC EMBL; AJ252278; CAB65733.1; -
CC EMBL; AF296558; AAG10300.1; -
CC EMBL; BC025791; AAH25791.1; -
CC PIR; A59316; A59316.
CC MIM; 605353; -
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0005625; C:soluble fraction; TAS.
CC GO; GO:0005331; P:cell-cell signaling; TAS.
CC GO; GO:0007267; P:growth hormone receptor ligand activity; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signaling. . . ; TAS.
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC InterPro; IPR005441; Preproghrelin.
CC Pfam; PF04643; motilin_assoc.1.
CC Pfam; PF04644; motilin_ghrelin.1.
CC PRINTS; PR01624; GHRELIN.
CC ProDom; PD332162; Preproghrelin.1.
CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing
FT SIGNAL 1 23
FT PEPTIDE 24 51 GHRELIN.
FT PROPEP 52 117 REMOVED IN MATURE FORM.
FT LIPID 26 26 N-OCTANOATE.
FT VARSPIC 37 37 Missing (in isoform 2).
FT CONFLICT 72 72 L -> M (IN REF. 5).
FT

SQ SEQUENCE 117 AA; 12911 MW; 39C0572EBECAA2755 CRC64;
Query Match 100.0%; Score 24; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
DB 52 ALAGWLRPEDGGQAGAEDELEVR 75
|||||
RESULT 2
GHRL_BOVIN STANDARD; PRT; 116 AA.
ID GHRL_BOVIN STANDARD; PRT; 116 AA.
AC Q9BDJ6; Q9GKY6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide).
GN GHRL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Kita K., Harada K., Yokota H.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 24-99 FROM N.A.
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
CC EMBL; AF350329; AAK18612.1; -
CC EMBL; AB035702; BAB19047.1; -
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC InterPro; IPR005441; Preproghrelin.
CC Pfam; PF04643; motilin_assoc.1.
CC Pfam; PF04644; motilin_ghrelin.1.
CC PRINTS; PR01624; GHRELIN.
CC ProDom; PD332162; Preproghrelin.1.
CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 50 GHRELIN (BY SIMILARITY).
FT PROPEP 51 116 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT CONFLICT 34 34 K -> E (IN REF. 2).
SQ SEQUENCE 116 AA; 12792 MW; F55536DAC5FA59B6 CRC64;
Query Match 41.7%; Score 10; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 QAQGADELE 22

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Db          63 QAEGAPELE 72
|||||||
RESULT 3
MPR2_STRCO
ID MPR2_STRCO STANDARD; PRT; 328 AA.
AC Q9L127;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Small neutral protease regulatory protein.
GN MPRR OR MPRR2 OR SCO7433 OR SC6011.29.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TK24; PubMed=1547948;
RX MEDLINE=92192468; PubMed=1547948;
RA Lichenstein H.S., Busse L.A., Smith G.A., Narhi L.O.,
RA McGinley M.O., Rohde M.F., Katowitz J.L., Zukowski M.M.;
RT "Cloning and characterization of a gene encoding extracellular
RT metalloprotease from Streptomyces lividans.";
RL Gene 111:125-130(1992).
CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE GENE (SNPA) FOR THE
CC SMALL NEUTRAL PROTEASE.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC -----
DR EMBL; M81703; AAA26739.1; -
DR EMBL; M89476; AAA26804.1; ALT INIT.
DR InterPro: IPR000847; HTH_LysR.
DR InterPro: IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; Protease; Transcription regulation; Complete proteome.
FT DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
FT CONFLICT 270 270 G -> AR (IN REF. 2).
SQ SEQUENCE 328 AA; 35885 MW; 2BA97730AB4FA16B CRC64;
Query Match 29.2%; Score 7; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLR 7
Db 104 ALAGWLR 110
|||||
RESULT 4
MPR2_STRLI
ID MPR2_STRLI STANDARD; PRT; 344 AA.
AC P43161;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Small neutral protease regulatory protein.
GN MPRR OR SNPR.
OS Streptomyces lividans.
OC Bacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=66 / 1326; PubMed=1464066;
RX MEDLINE=93099553; PubMed=1464066;
RA Butler M.J., Davey C.C., Krygman P., Walczyk E., Malek L.T.;
RT "Cloning of genetic loci involved in endoprotease activity in
RT Streptomyces lividans 66: a novel neutral protease gene with an
RT adjacent divergent putative regulatory gene.";
RL Can. J. Microbiol. 38:912-920(1992).
RN [2]
RP SEQUENCE OF 1-305 FROM N.A.
RC STRAIN=TK24; PubMed=1547948;
RX MEDLINE=92192468; PubMed=1547948;
RA Lichenstein H.S., Busse L.A., Smith G.A., Narhi L.O.,
RA McGinley M.O., Rohde M.F., Katowitz J.L., Zukowski M.M.;
RT "Cloning and characterization of a gene encoding extracellular
RT metalloprotease from Streptomyces lividans.";
RL Gene 111:125-130(1992).
CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE GENE (SNPA) FOR THE
CC SMALL NEUTRAL PROTEASE.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M81703; AAA26739.1; -
DR EMBL; M89476; AAA26804.1; ALT INIT.
DR InterPro: IPR000847; HTH_LysR.
DR InterPro: IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; Protease; Transcription regulation; Complete proteome.
FT DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
FT CONFLICT 270 270 G -> AR (IN REF. 2).
SQ SEQUENCE 344 AA; 37415 MW; 485C82C813B52312 CRC64;
Query Match 29.2%; Score 7; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLR 7
Db 104 ALAGWLR 110
|||||
RESULT 5
V120_EBV
ID V120_EBV STANDARD; PRT; 1239 AA.
AC P03189;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Capsid assembly protein BOLF1.
GN BOLF1.
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tufnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,
CC EHV-1 23, EBV BOLEF1, VZV 21, HVS-1 63, AND HCMV UL47.
CC -----
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CC -----
DR EMBL; V01555; CAA24841.1; -.
DR PIR; A43041; Q0BE10.
KW Capsid assembly.
SQ SEQUENCE 1239 AA; 132748 MW; 6C5DBFC55F2FF729 CRC64;

Query Match 29.28; Score 7; DB 1; Length 1239;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AEGAED 20
DB 696 AEGAED 702
|||||||

RESULT 6
GHRL CANFA
ID GHRL CANFA STANDARD; PRT; 117 AA.
AC Q9BEF8: Q9BEF7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide).
GN GHRL OR MTLRP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Gastric fundus;
RA Tomasetto C., Wendling C., Rio M.-C., Poltras P.;
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
RT fundus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9BEF8-1; Sequence=Displayed;
CC Name=2; Synonyms=Del-Gln14-ghrelin;
CC IsoId=Q9BEF8-2; Sequence=VSP_003244;
CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
DR EMBL; AJ298295; CAC29155.1; -.
DR EMBL; AJ298296; CAC29156.1; -.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin-ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin-ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR PRODOM; PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPLOC 37 37 Missing (in isoform 2).
FT FT /FTID=VSP_003244.
SQ SEQUENCE 117 AA; 13007 MW; 3E57ED9D1847CF7 CRC64;

Query Match 25.08; Score 6; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AEDELE 22
DB 68 AEDELE 73
|||||||

RESULT 7
EFAB CHICK
ID EFAB CHICK STANDARD; PRT; 178 AA.
AC P21760: P21928; Q9PWN9;
DT 01-MAY-1991 (Rel. 18, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Extracellular fatty acid binding protein precursor (Ex-FABP)
DE (Quiescence-specific protein) (p20K) (Ch21 protein).
GN EXFABP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89261749; PubMed=2498647;
RA Bedard P.-A., Yannoni Y., Simmons D.L., Erikson R.L.;
RT "Rapid repression of quiescence-specific gene expression by epidermal
RT growth factor, insulin, and pp60v-src.";
RL Mol. Cell. Biol. 9:1371-1375(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92147639; PubMed=1737754;
RA Dozin B., Descalzi F., Briata L., Hayashi M., Gentili C.,
RA Hayashi K., Quarto R., Cancedda R.;
RT "Expression, regulation, and tissue distribution of the Ch21 protein
RT during chicken embryogenesis.";
RL J. Biol. Chem. 267:2979-2985(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Leghorn;
RA Giannoni P., Dozin B., Zambotti A., Neri M., Cancedda R.;
RT "Differentiation-dependent activation of the extracellular fatty acid
RT binding protein (EXFABP) gene in chicken embryo chondrocytes.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 25-178 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91035433; PubMed=2229062;
RA Cancedda F.D., Dozin B., Rossi F., Molina F., Cancedda R.,
RA Negri A., Ronchi S.;
RT "The Ch21 protein, developmentally regulated in chick embryo, belongs

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to the superfamily of lipophilic molecule carrier proteins.";
 RL J. Biol. Chem. 265:19060-19064(1990).
 RN [5]
 RP SEQUENCE OF 21-48.
 RX MEDLINE-90267487; PubMed-2346493;
 RA Cancedda F.D., Asaro D., Molina F., Cancedda R., Caruso C.,
 RA Camardella L., Negri A., Ronchi S.;
 RT "The amino terminal sequence of the developmentally regulated Ch21
 RT protein shows homology with amino terminal sequences of low molecular
 RT weight proteins binding hydrophobic molecules";
 RL Biochem. Biophys. Res. Commun. 168:933-938(1990).
 RN [6]
 RP SEQUENCE OF 103-178 FROM N.A.
 RX STRAIN-White leghorn; TISSUE-Bone marrow;
 RC MEDLINE-92195690; PubMed-1549365;
 RA Nakano T., Graf T.;
 RT "Identification of genes differentially expressed in two types of
 RT v-myb-transformed avian myelomonocytic cells.";
 RN Oncogene 7:527-534(1992).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE-96355330; PubMed-8702740;
 RA Cancedda F.D., Maipelli M., Gentili C., Di Marzo V., Bet P.,
 RA Carlevaro M., Cermelli S., Cancedda R.;
 RT "The developmentally regulated avian Ch21 lipocalin is an
 RT extracellular fatty acid-binding protein.";
 RL J. Biol. Chem. 271:20163-20169(1996).
 RN [8]
 RP CHARACTERIZATION.
 RX MEDLINE-20513977; PubMed-11058755;
 RA Descalzi Cancedda F., Dozin B., Zerega B., Cermelli S., Cancedda R.;
 RT "Ex-FABP: a fatty acid binding lipocalin developmentally regulated in
 RT chicken endochondral bone formation and myogenesis.";
 RL Biochim. Biophys. Acta 1482:127-135(2000).
 CC -1- FUNCTION: Preferentially binds long-chain unsaturated fatty acids
 CC such as linoleic acid, oleic acid, arachidonic acid. Also binds
 CC with a lower affinity long chain saturated fatty acids such as
 CC stearic acid. May act as survival protein by playing a role in
 CC maintaining cell viability.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY SYNTHESIZED IN NONPROLIFERATING
 CC CELLS.
 CC -1- PTM: Does not seem to be glycosylated.
 CC -1- MISCELLANEOUS: Developmentally regulated in chick embryo.
 CC -1- SIMILARITY: Belongs to the lipocalin family.
 CC -----
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 CC -----
 CC EMBL: M25784; AAA53371.1; -;
 CC EMBL: M55644; AAA48677.1; -;
 CC EMBL: AF121346; RAD23569.1; -;
 CC EMBL: X61199; -; NOT_ANNOTATED_CDS.
 CC PIR: A30230; A30230.
 CC InterPro: IPR002345; Lipocalin.
 CC InterPro: IPR000566; Lipocalin_cytFABP.
 CC Pfam: PF00061; Lipocalin; 1.
 CC PRINTS: PR00179; LIPOCALIN.
 CC PROSITE: PS00113; LIPOCALIN; 1.
 CC Lipocalin; Transport; Signal.
 KW SIGNAL
 FT CHAIN 1 20 EXTRACELLULAR FATTY ACID BINDING PROTEIN.
 FT MOD_RES 21 178 BLOCKED.
 FT DISULFID 80 173 BY SIMILARITY.
 FT CONFLICT 4 4 L -> S (IN REF. 2).
 FT CONFLICT 27 27 R -> S (IN REF. 2 AND 4).
 FT CONFLICT 45 45 F -> S (IN REF. 2 AND 4).

FT CONFLICT 62 62 F -> S (IN REF. 1).
 FT CONFLICT 96 96 L -> V (IN REF. 1).
 SQ SEQUENCE 178 AA; 20201 MW; 0DDBDC33C1A0C6B8 CRC64;
 Query Match 25.0%; Score 6; DB 1; Length 178;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 EDELEV 23
 Db 65 EDELEV 70
 RESULT 8
 HIS5_METTH STANDARD; PRT; 198 AA.
 ID HIS5_METTH
 AC 027568;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Imidazole glycerol phosphate synthase subunit hish (EC 2.4.2.-) (IGP
 DE synthase glutamine amidotransferase subunit) (IGP synthase subunit
 DE hish) (ImGP synthase subunit hish) (IGP subunit hish).
 GN HISH OR MTH1524.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OC NCBI_Taxid=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-Delta H;
 RC MEDLINE-98037514; PubMed-9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiواني N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shiner G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -1- FUNCTION: IGPs catalyze the conversion of PRFAR and glutamine to
 CC IGP, AICAR and glutamate. The hish subunit provides the glutamine
 CC amidotransferase activity that produces the ammonia necessary to
 CC hifs for the synthesis of IGP and AICAR (By similarity).
 CC -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulo)-1-
 CC ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-
 CC carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-
 CC aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
 CC -1- PATHWAY: Histidine biosynthesis; fifth step.
 CC -1- SUBUNIT: Heterodimer of hish and hifs (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
 CC -----
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 CC -----
 CC EMBL: A5000912; AAB85999.1; -;
 CC PIR: D69070; D69070.
 CC HAMAP: MF_00278; -; 1.
 CC InterPro: IPR000991; GATase_1.
 CC Pfam: PF00117; GATase; 1.
 CC PROSITE: PS00442; GATASE_TYPE_I; 1.
 CC Histidine biosynthesis; Transferase; Glutamine amidotransferase;
 CC Complete proteome.
 FT ACT_SITE 77 77 BY SIMILARITY.
 FT ACT_SITE 177 177 BY SIMILARITY.

FT ACT_SITE 179 179 BY SIMILARITY.
SQ SEQUENCE 198 AA; 21348 MW; E8EFA43EC9163AEF CRC64;

Query Match 25.0%; Score 6; DB 1; Length 198;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15 EGADE 20
| | | | |
Db 130 EGADE 135

RESULT 9
COLI_PIG STANDARD; PRT; 267 AA.

AC P01192; O95246;
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Corticotropin-lipotropin precursor (Pro-opiomelanocortin) (POMC)
DE (Contains: NPP; Melanotropin gamma (Gamma-MSH); Corticotropin
DE (Adrenocorticotrophic hormone) (ACTH); Melanotropin alpha (Alpha-MSH);
DE Corticotropin-like intermediary peptide (CLIP); Lipotropin beta (Beta-
DE LPH); Lipotropin gamma (Gamma-LPH); Melanotropin beta (Beta-MSH);
DE Beta-endorphin; Met-enkephalin].
GN POMC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86131687; PubMed=3753882;
RA Gossard F.J., Chang A.C.Y., Cohen S.N.;
RT "Sequence of the cDNA encoding porcine pro-opiomelanocortin.";
RL Biochim. Biophys. Acta 866:68-74(1986).
RN [1]

[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84069823; PubMed=6196724;
RA Boileau G., Barbeau C., Jeannotte L., Chretien M., Drouin J.;
RT "Complete structure of the porcine pro-opiomelanocortin mRNA derived
from the nucleotide sequence of cloned cDNA.";
RL Nucleic Acids Res. 11:8063-8071(1983).
RN [2]

[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95046835; PubMed=7958386;
RA Gen K., Hirai T., Kato T., Kato Y.;
RT "Presence of the same transcript of pro-opiomelanocortin (POMC) genes
in the porcine anterior and intermediate pituitary lobes.";
RL Mol. Cell. Endocrinol. 103:101-108(1994).
RN [3]

[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=84239667; PubMed=6547437;
RA Oates E., Herbert E.;
RT "5' sequence of porcine and rat pro-opiomelanocortin mRNA. One porcine
and two rat forms.";
RL J. Biol. Chem. 259:7421-7425(1984).
RN [4]

[5]
RP SEQUENCE OF 136-174.
RA Shepherd R.G., Willson S.D., Howard K.S., Bell P.H., Davies D.S.,
RA Davis S.B., Eigner E.A., Shakespeare N.E.;
RT "Studies with corticotropin. III. Determination of the structure of
beta-corticotropin and its active degradation products.";
RL J. Am. Chem. Soc. 78:5067-5076(1956).
RN [5]

[6]
RP REVISIONS TO 160 AND 165.
RX MEDLINE=72114902; PubMed=4334191;
RA Riniker B., Sieber P., Rittel W., Zuber H.;
RT "Revised amino-acid sequences for porcine and human
adrenocorticotrophic hormone.";
RL Nature New Biol. 235:114-115(1972).
RN [6]

[7]
RP REVISIONS (CORTICOTROPIN).

RX MEDLINE=74306590; PubMed=4369114;
RA Graf L.;
RT "Re-examination of the sequence of the C-terminal tryptic fragment
from porcine adrenocorticotrophic hormone.";
RL Acta Biochim. Biophys. Acad. Sci. Hung. 7:293-297(1972).
RN [8]

RP SEQUENCE OF 136-174.
RX MEDLINE=91071194; PubMed=2174774;
RA Voigt K., Stegmaier W., McGregor G.P., Roesch H., Selliger H.;
RT "Isolation and full structural characterization of six
adrenocorticotropin-like peptides from porcine pituitary gland.
RT Identification of three novel fragments of adrenocorticotropin and of
two forms of a novel adrenocorticotropin-like peptide.";
RL Eur. J. Biochem. 194:225-236(1990).
RN [9]

RP SEQUENCE OF 136-148.
RA Harris J.I., Lerner A.B.;
RT "Amino-acid sequence of the alpha-melanocyte-stimulating hormone.";
RL Nature 179:1346-1347(1957).
RN [10]

RP SEQUENCE OF 177-267.
RX MEDLINE=71111231; PubMed=5543613;
RA Graf L., Barat E., Cseh G., Sejgo M.;
RT "Amino acid sequence of porcine beta-lipotrophic hormone.";
RL Biochim. Biophys. Acta 229:276-278(1971).
RN [11]

RP REVISIONS (LIPOTROPIN).
RA Gilardeau C., Chretien M.;
RT "Complete amino acid sequence of porcine beta-lipotrophic hormone
(beta-LPH).";
RL (In) Meienhofer J. (eds.);
RL Chemistry and biology of peptides, pp.609-611, Ann Arbor Sci. Pub.,
RL Ann Arbor (1972).
RN [12]

RP REVISION TO 211.
RX MEDLINE=73048217; PubMed=4673865;
RA Pankov Y.A., Yudaev N.A.;
RT "Complete amino acid sequence in the molecule of porcine beta-
lipotropin.";
RL Biokhimiia 37:991-1004(1972).
RN [13]

RP SEQUENCE OF 217-234.
RA Harris J.I., Roos P.;
RT "Amino-acid sequence of a melanophore-stimulating peptide.";
RL Nature 178:90-90(1956).
RN [14]

RP SEQUENCE OF 217-234.
RA Geschwind I.I., Li C.H., Barnafi L.;
RT "The structure of the beta-melanocyte-stimulating hormone.";
RL J. Am. Chem. Soc. 79:620-625(1957).
RN [15]

RP SEQUENCE OF 237-241.
RX MEDLINE=76100762; PubMed=1207728;
RA Hughes J., Smith T.W., Kosterlitz H.W., Fothergill L.A., Morgan B.A.,
RA Morris H.R.;
RT "Identification of two related pentapeptides from the brain with
potent opiate agonist activity.";
RL Nature 258:577-579(1975).
RN [16]

RP SEQUENCE OF 237-267.
RX MEDLINE=77084500; PubMed=1007884;
RA Graf L., Barat E., Patthy A.;
RT "Isolation of a COOH-terminal beta-lipotropin fragment (residues
61-91) with morphine-like analgesic activity from porcine pituitary
glands.";
RL Acta Biochim. Biophys. Acad. Sci. Hung. 11:121-122(1976).
RN [17]

CC -1- FUNCTION: ACTH STIMULATES THE ADRENAL GLANDS TO RELEASE CORTISOL.
CC -1- FUNCTION: MSH (MELANOCYTE-STIMULATING HORMONE) INCREASES THE
CC PIGMENTATION OF SKIN BY INCREASING MELANIN PRODUCTION IN
CC MELANOCYTES.
CC -1- FUNCTION: BETA-ENDORPHIN AND MET-ENKEPHALIN ARE ENDOGENOUS
CC OPIATES.
CC -1- TISSUE SPECIFICITY: ACTH AND MSH ARE PRODUCED BY THE PITUITARY

CC GLAND.
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
CC THE DIFFERENT ACTIVE PEPTIDES
CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
CC -----
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CC -----
CC EMBL; X03561; CAA27248.1; -
CC EMBL; X00135; CAA24968.1; -
CC EMBL; S73519; AAB32312.1; -
CC EMBL; K01879; AAB31104.1; -
CC FIC; A93496; CTPGP.
CC InterPro: IPR001941; Mcoctin_ACTH.
CC Pfam: PF00976; ACTH_domain; 1.
CC PRINTS: PR00383; MELANOCORTIN.
CC Endorphin; Hormone; Cleavage on pair of basic residues; Amidation;
CC Glycoprotein; Signal.
CC SIGNAL 1 26
CC PEPTIDE 27 106
CC PEPTIDE 77 87
CC PEPTIDE 136 174
CC PEPTIDE 136 148
CC PEPTIDE 134 174
CC PEPTIDE 177 267
CC PEPTIDE 177 234
CC PEPTIDE 217 234
CC PEPTIDE 237 267
CC PEPTIDE 237 241
CC MOD_RES 87 87
CC MOD_RES 148 148
CC CARBOHYD 91 91
CC VARIANT 143 143
CC CONFLICT 6 6
CC CONFLICT 15 15
CC CONFLICT 23 23
CC CONFLICT 49 49
CC SEQUENCE 267 AA; 28894 MW; A6DB487A5032B648 CRC64;

CC Query Match 25.0%; Score 6; DB 1; Length 267;
CC Best Local Similarity 100.0%; Pred. No. 38;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 16 GAEDEL 21
CC Db 161 GAEDEL 166

CC RESULT 10
CC TPMD2_DROME STANDARD; PRT; 284 AA.
CC AC P09491; P09490; Q24408; Q24427; Q24428; Q8S265; Q9VF95;
CC DT 01-WAR-1989 (Rel. 10, Created)
CC DT 01-WAR-1989 (Rel. 10, Last sequence update)
CC DE 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Tropomyosin 2 (Tropomyosin I).
CC TM2 OR TMI OR CG4843.
CC OS Drosophila melanogaster (Fruit fly).
CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC OC Ephydroidea; Drosophilidae; Drosophila.
CC OX NCBI_TaxID=7227;
CC RN [1]
CC RP SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
CC RC TISSUE=Embryo. Larva, and Pupae;
CC RX MEDLINE=84205681; PubMed=6202423;
CC RA Karlik C.C., Mahaffey J.W., Coutu M.D., Fyrberg E.A.;
CC "Organization of contractile protein genes within the 88F subdivision
RT

RT of the D. melanogaster third chromosome.";
RL Cell 37:469-481(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
RX MEDLINE=86085920; PubMed=3079761;
RA Basi G.S., Storti R.V.;
RT "Structure and DNA sequence of the tropomyosin I gene from Drosophila
RT melanogaster.";
RL J. Biol. Chem. 261:817-827(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S.Q.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [4]
RP REVISIONS.
RC STRAIN=Berkley;
RX MEDLINE=22426069; PubMed=12537572;
RA Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM EMBRYONIC).
RC STRAIN=Berkley; TISSUE=Embryo;
RX PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";


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QY 6 LRPEDG 11
Db 277 LRPEDG 282

RESULT 12
OPSD_LIMPA STANDARD; PRT; 289 AA.
AC 042431.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Rhodopsin (Fragment).
GN RHO.
OS Limnocottus pallidus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Scorpaeniformes;
OC Cottoidei; Abyssocottidae; Limnocottus.
OX NCBI_TaxID=61634;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98086781; PubMed=9417898;
RA Hunt D.M., Fitzgibbon J., Slobodyanyuk S.J., Bowmaker J.K.,
RA Dulai K.S.;
RT "Molecular evolution of the cottoid fish endemic to Lake Baikal
RT deduced from nuclear DNA evidence.";
RL Mol. Phylogenet. Evol. 8:415-422(1997).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES
CC VISION IN DIM LIGHT.
CC -!- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC -----
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CC -----
DR EMBL; U97271; AAB61725.1; -.
DR HSP; P02699; 1BQ7.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR001760; Opsin.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRRHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; FALSE_NEG.
DR PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS00238; OPSIN; 1.
DR PROSITE; PS00238; OPSIN; 1.
KW Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.
FT DOMAIN 1
FT TRANSMEM 1
FT TRANSMEM <1 7 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 8 32 1 (POTENTIAL).
FT TRANSMEM 33 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 69 2 (POTENTIAL).
FT TRANSMEM 70 84 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 85 104 3 (POTENTIAL).
FT TRANSMEM 105 123 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 124 147 4 (POTENTIAL).
FT TRANSMEM 148 173 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 174 201 5 (POTENTIAL).
FT TRANSMEM 202 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 247 6 (POTENTIAL).
FT TRANSMEM 248 255 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 256 280 7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
RETINAL CHROMOPHORE (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).

Query Match 25.0%; Score 6; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAGWLR 7
Db 143 LAGWLR 148

RESULT 13
PARB_HELPJ STANDARD; PRT; 290 AA.
AC Q92K75;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable chromosome partitioning protein parB.
GN PARB OR JHP1066.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- FUNCTION: INVOLVED IN CHROMOSOME PARTITION. LOCALIZE TO BOTH POLES
CC OF THE PREDIVISIONAL CELL FOLLOWING COMPLETION OF DNA REPLICATION.
CC BINDS TO THE DNA ORIGIN OF REPLICATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARB FAMILY.
CC -----
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CC -----
DR EMBL; AE001534; AAD06646.1; -.
DR FIR; H71852; H71852.
DR InterPro; IPR004437; ParB_part.
DR InterPro; IPR003115; ParBc.
DR Pfam; PF02195; ParBc; 1.
DR SMART; SM00470; ParB; 1.
DR TIGRFAMs; TIGR00180; parB_part; 1.
DR Chromosome partitioning; DNA-binding; Complete proteome.
KW Chromosome partitioning; DNA-binding; Complete proteome.
SQ SEQUENCE 290 AA; 33405 MW; 6709BA0547A55A4F CRC64;

Query Match 25.0%; Score 6; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AEDELE 22
Db 245 AEDELE 250

RESULT 14

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MTSA_STRP8
ID Q8P280; STANDARD; PRT; 310 AA.
AC
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metal ABC transporter substrate-binding lipoprotein precursor.
GN MTSA OR SPYM18_0494.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OC NCBI_TaxID=186103;
RN
RP
RC
RX STRAIN=MGAS8232 / Serotype M18;
RA MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC
CC -1- FUNCTION: Part of an ATP-driven transport system for a metal; this
CC protein has affinity for Zn(II), Fe(III) and Cu(II).
CC
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC
CC -1- SIMILARITY: Belongs to the bacterial solute-binding protein family
CC 9. Lipoprotein receptor antigen (Lrai) subfamily.
CC
CC
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CC
CC EMBL; AE009988; AAL97215.1; -
CC InterPro; IPR006128; Lipoprotein_4.
CC Pfam; PF01297; SBP_bac_9.1.
CC PRINTS; PR00690; ADHESNFAMILY.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Transport; zinc transport; iron transport; Copper; Membrane;
KW Lipoprotein; Signal; Complete proteome.
FT SIGNAL 1 20 PROBABLE.
FT CHAIN 21 310 METAL ABC TRANSPORTER SUBSTRATE-
FT LIPID 21 21 BINDING LIPOPROTEIN.
FT SEQUENCE 310 AA; 34330 MW; 40F613659AAD1768 CRC64;
Query Match 25.0%; Score 6; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 EDGQQA 14
DQ 94 EDGQQA 99
RESULT 15
MTSA_STRPY
ID MTSA_STRPY STANDARD; PRT; 310 AA.
AC Q9A157; Q9RNJ0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Metal ABC transporter substrate-binding lipoprotein precursor.
GN MTSA OR SPY0453 OR SPYM3_0318 OR SPS1539.
OS Streptococcus pyogenes, and
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

Streptococcus.
OX NCBI_TaxID=1314, 198466;
RN
RP
RC
RX SEQUENCE FROM N.A., SEQUENCE OF 30-39, AND CHARACTERIZATION.
RA STRAIN=SF370 / ATCC 700294 / Serotype M1, and API / Serotype M1;
RA MEDLINE=20032372; PubMed=10564500;
RA Janulczyk R., Pallon J., Bjoerck L.;
RT "Identification and characterization of a Streptococcus pyogenes ABC
RT transporter with multiple specificity for metal cations.";
RL Mol. Microbiol. 34:596-606(1999).
RN
RP
RC
RX SEQUENCE FROM N.A.
RA STRAIN=SF370 / ATCC 700294 / Serotype M1;
RA MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN
RP
RC
RX SEQUENCE FROM N.A.
RA STRAIN=MGAS315 / Serotype M3;
RA MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN
RP
RC
RX SEQUENCE FROM N.A.
RA STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: Part of an ATP-driven transport system for a metal; this
CC protein has affinity for Zn(II), Fe(III) and Cu(II).
CC
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC
CC -1- SIMILARITY: Belongs to the bacterial solute-binding protein family
CC 9. Lipoprotein receptor antigen (Lrai) subfamily.
CC
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; AF180520; AAD56936.1; -
CC EMBL; AF180521; AAD56939.1; -
CC EMBL; AE006505; AAK33468.1; -
CC EMBL; AE014143; AAM78925.1; ALT_INIT.
CC EMBL; AP005145; BAC64634.1; ALT_INIT.
CC HSPSP; P96116; ITOA.
CC InterPro; IPR006128; Lipoprotein_4.
CC InterPro; IPR006127; SBP_bac_9.
CC Pfam; PF01297; SBP_bac_9.1.
CC PRINTS; PR00690; ADHESNFAMILY.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Transport; zinc transport; iron transport; Copper; Membrane;
KW Lipoprotein; Signal; Complete proteome.
FT SIGNAL 1 20 PROBABLE.
FT CHAIN 21 310 METAL ABC TRANSPORTER SUBSTRATE-
FT LIPID 21 21 BINDING LIPOPROTEIN.
FT VARIANT 77 77 N-ACYL DIGLYCERIDE (PROBABLE).
FT VARIANT 77 77 V -> A (IN STRAIN API).

```
FT CONFLICT 26 26 T -> A (IN REF. 1).
FT CONFLICT 30 30 K -> E (IN REF. 1).
FT CONFLICT 44 44 A -> G (IN REF. 1).
FT CONFLICT 49 50 AI -> VM (IN REF. 1).
SQ SEQUENCE 310 AA; 34358 MW; B0F829EF1C72CADC CRC64;

Query Match 25.0%; Score 6; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 EDGGA 14
Db 94 EDGGA 99
```

Search completed: September 11, 2003, 17:52:40
Job time : 6.62032 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:02 ; Search time 22.9733 Seconds
(without alignments)
269.586 Million cell updates/sec

Title: US-09-853-253-4
Perfect score: 24
Sequence: 1 ALAGWLRPEDGGQAEAGDELEVR 24

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|-----------|--------------------|
| 1 | 20 | 83.3 | 117 | 4 Q8TAT9 | Q8tat9 homo sapien |
| 2 | 11 | 45.8 | 117 | 11 Q8CH53 | Q8ch53 meriones un |
| 3 | 8 | 33.3 | 433 | 10 Q93ZV7 | Q93zv7 arabidopsis |
| 4 | 8 | 33.3 | 433 | 10 Q8L7B4 | Q8l7e4 arabidopsis |
| 5 | 8 | 33.3 | 483 | 10 Q65529 | Q65529 arabidopsis |
| 6 | 7 | 29.2 | 103 | 16 Q9L063 | Q9l063 streptomyce |
| 7 | 7 | 29.2 | 313 | 2 Q8VP52 | Q8vp52 streptomyce |
| 8 | 7 | 29.2 | 433 | 16 Q8CNY4 | Q8cny4 staphylococ |
| 9 | 7 | 29.2 | 887 | 16 Q8XY49 | Q8xy49 ralstonia s |
| 10 | 7 | 29.2 | 910 | 16 Q9I3F5 | Q9i3f5 pseudomonas |
| 11 | 7 | 29.2 | 2376 | 5 Q9V5J0 | Q9v5j0 drosophila |
| 12 | 7 | 29.2 | 2376 | 5 Q966V1 | Q966v1 drosophila |
| 13 | 6 | 25.0 | 69 | 16 Q9A542 | Q9a542 caulobacter |
| 14 | 6 | 25.0 | 88 | 17 Q8Z2R1 | Q8zzr1 pyrobaculum |
| 15 | 6 | 25.0 | 98 | 5 P91785 | P91785 onchocerca |
| 16 | 6 | 25.0 | 100 | 16 Q8PBN4 | Q8pbn4 xanthomonas |

| | | | | | |
|----|---|------|-----|-----------|--------------------|
| 17 | 6 | 25.0 | 103 | 16 Q9KTL5 | Q9ktl5 vibrio chol |
| 18 | 6 | 25.0 | 106 | 10 P93359 | P93359 nicotiana t |
| 19 | 6 | 25.0 | 110 | 2 Q87801 | Q87801 pseudomonas |
| 20 | 6 | 25.0 | 112 | 5 Q26847 | Q26847 trypanosoma |
| 21 | 6 | 25.0 | 113 | 16 Q8G7N5 | Q8g7n5 bifidobacte |
| 22 | 6 | 25.0 | 117 | 12 Q65548 | Q65548 bovine herp |
| 23 | 6 | 25.0 | 129 | 4 Q43180 | Q43180 homo sapien |
| 24 | 6 | 25.0 | 133 | 13 Q8JFY6 | Q8jfy6 litoria cae |
| 25 | 6 | 25.0 | 137 | 4 Q8N8H9 | Q8n8h9 homo sapien |
| 26 | 6 | 25.0 | 138 | 16 Q9RD30 | Q9rd30 streptomyce |
| 27 | 6 | 25.0 | 142 | 16 Q8ZBU1 | Q8zbu1 yersinia pe |
| 28 | 6 | 25.0 | 147 | 5 Q25622 | Q25622 onchocerca |
| 29 | 6 | 25.0 | 148 | 5 Q8WT59 | Q8wt59 onchocerca |
| 30 | 6 | 25.0 | 154 | 5 Q8WT58 | Q8wt58 onchocerca |
| 31 | 6 | 25.0 | 154 | 5 Q8WT56 | Q8wt56 litomosolde |
| 32 | 6 | 25.0 | 154 | 5 Q8WT57 | Q8wt57 onchocerca |
| 33 | 6 | 25.0 | 159 | 3 Q05697 | Q05697 saccharomyc |
| 34 | 6 | 25.0 | 159 | 4 Q8N9A4 | Q8n9a4 homo sapien |
| 35 | 6 | 25.0 | 161 | 10 Q9LWY4 | Q9lwy4 oryza sativ |
| 36 | 6 | 25.0 | 163 | 17 Q8TMV7 | Q8tmv7 methanosarc |
| 37 | 6 | 25.0 | 165 | 2 Q9BNJ3 | Q9bnj3 zymomonas m |
| 38 | 6 | 25.0 | 165 | 16 Q8XXY6 | Q8xy6 ralstonia s |
| 39 | 6 | 25.0 | 171 | 5 Q25624 | Q25624 onchocerca |
| 40 | 6 | 25.0 | 175 | 13 Q8JFY7 | Q8jfy7 litoria cae |
| 41 | 6 | 25.0 | 175 | 16 Q9KQ90 | Q9kq90 vibrio chol |
| 42 | 6 | 25.0 | 177 | 11 Q8CI08 | Q8ciq8 rattus norv |
| 43 | 6 | 25.0 | 178 | 5 Q25619 | Q25619 onchocerca |
| 44 | 6 | 25.0 | 178 | 5 Q8MZJ8 | Q8mzj8 acanthochel |
| 45 | 6 | 25.0 | 178 | 16 Q98IM5 | Q98im5 rhizobium 1 |

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY; PRT; 117 AA.
AC Q8TAT9;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Ghrelin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025791; AAH25791.1; -
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
SQ SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;

Query Match 83.3%; Score 20; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.le-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAEAGDE 20
Db 52 ALAGWLRPEDGGQAEAGDE 71

RESULT 2

Q8CH53 PRELIMINARY; PRT; 117 AA.
AC Q8CH53;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)

```

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RL "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AAC00695.1; -
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 45.8%; Score 11; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GQAEAGDELE 22
Db 63 GQAEAGDELE 73
|||||
12 GQAEAGDELE 22
63 GQAEAGDELE 73

RESULT 3
Q932V7 PRELIMINARY; PRT; 433 AA.
ID AC Q932V7
DC Q932V7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DR 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative RNA-binding protein LAH1.
GN A74G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Koesena E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene A74G32720 (GI:7270219).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY056237; AAL07086.1; -
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 433 AA; 48095 MW; E58EBAF51C35A8F7 CRC64;

Query Match 33.3%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAED 20
Db 287 QAEGAED 294
|||||
13 QAEGAED 20
287 QAEGAED 294

RESULT 4
Q8L7E4 PRELIMINARY; PRT; 433 AA.
ID AC Q8L7E4
DC Q8L7E4
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DR 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN A74G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Shinn P., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
RA Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY136302; AAM96968.1; -
DR EMBL; BT000396; AAN15715.1; -
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 433 AA; 48126 MW; CFF6F611A29AA0318 CRC64;

Query Match 33.3%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAED 20
Db 287 QAEGAED 294
|||||
13 QAEGAED 20
287 QAEGAED 294

RESULT 5
O65529 PRELIMINARY; PRT; 483 AA.
ID AC O65529
DC O65529
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DR 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 54.1 kDa protein.
GN F4D11.80 OR A74G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoorge W., Hohelsel J.,
RA Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]

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RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoerge W., Mewes H.W., Lemcke K.,
RL Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022537; CAA18589.1; -.
DR EMBL; AL161582; CAB79989.1; -.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rtm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 483 AA; 54125 MW; 20840B34A0BC94E2 CRC64;

Query Match 33.3%; Score 8; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAED 20
DB 302 QAEGAED 309
|||||||

RESULT 6
Q9L063
ID Q9L063 PRELIMINARY; PRT; 103 AA.
AC Q9L063;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SC02791.
GN SCO2791 OR SCC105.22C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417.141-147(2002).
DR EMBL; AL939114; CAB87228.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 103 AA; 10639 MW; 9316F1F38C1BD492 CRC64;

Query Match 29.2%; Score 7; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAEG 16
DB 48 DGGQAEG 54
|||||||

RESULT 7

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Q8VP52
ID Q8VP52 PRELIMINARY; PRT; 313 AA.
AC Q8VP52;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE LysR-like transcriptional activator SnpR.
OS Streptomyces sp. C5.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=45212;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C5;
RA DeSanti C.L., Strohl W.R.;
RT "Characterization of the Streptomyces sp. strain C5 snp locus and
development of an snp-derived expression vector family.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
DR EMBL; AY072041; AAL61992.1; -.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; Transcription; Transcription regulation.
SQ SEQUENCE 313 AA; 34258 MW; C907C8AF51C3FA13 CRC64;

Query Match 29.2%; Score 7; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
DB 103 ALAGWLR 109
|||||||

RESULT 8
Q8CNY4
ID Q8CNY4 PRELIMINARY; PRT; 433 AA.
AC Q8CNY4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Trigger factor.
GN SE1350.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
RA Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016748; AAO04949.1; -.
KW Complete proteome.
SQ SEQUENCE 433 AA; 48732 MW; FF2490AD097F437D CRC64;

Query Match 29.2%; Score 7; DB 16; Length 433;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAEG 16
DB 180 DGGQAEG 186
|||||||

RESULT 9
Q8XY49
ID Q8XY49 PRELIMINARY; PRT; 887 AA.

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AC Q8XY49;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Probable phage-related tail transmembrane protein.
GN RSC1914 OR RS03483.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schliex T.,
RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002)
DR EMBL; AL646067; CAD15616.1; -.
KW Complete proteome.
SQ SEQUENCE 887 AA; 94105 MW; 9A8840E5362E740E CRC64;

Query Match 29.2%; Score 7; DB 16; Length 887;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GQAEAG 18
Db 290 GQAEAG 296
IIIIII

RESULT 10
Q913F5 Q913F5 PRELIMINARY; PRT; 910 AA.
AC Q913F5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aconitase hydratase 1.
GN ACNA OR PA1562.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004584; AAG04951.1; -.
DR HSP; P20004; IACO.
DR InterPro; IPR006249; Aconitase_1.
DR InterPro; IPR000573; Aconitase_C.
DR InterPro; IPR001030; Aconitase_N.
DR Pfam; PF00330; aconitase; 1.
DR Pfam; PF00694; Aconitase_C; 1.
DR PRINTS; PR00415; ACONITASE.
DR PRODOM; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR01341; aconitase_1; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.

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KW Complete proteome.
SQ SEQUENCE 910 AA; 99147 MW; C65F23CDB6FA0E1C CRC64;

Query Match 29.2%; Score 7; DB 16; Length 910;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7
Db 65 ALAGWLR 71
IIIIII

RESULT 11
Q9V5J0 Q9V5J0 PRELIMINARY; PRT; 2376 AA.
AC Q9V5J0;
DT 01-MAR-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG18408 protein.
GN REXIN OR CG3451 OR CG18408 OR CG18409.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=Berkelley;
RX MEDLINE=20196008; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RC SEQUENCE FROM N.A.
RP Celisner S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

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RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Gall R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Matteli B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.B., Bergman C., Bernan B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Milburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003830; AAF58816.2; -;
DR FlyBase; FBgn0033504; rexin.
DR InterPro; IPR001452; SH3.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000066; SH3; 3.
DR SMART; SM00326; SH3; 3.
DR PROSITE; PS50002; SH3; 3.
SQ SEQUENCE 2376 AA; 267666 MW; A5F2D0589B88695C CRC64;

Query Match 29.2%; Score 7; DB 5; Length 2376;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAEED 19
Db 37 QAEGAEED 43

RESULT 12
Q966V1 PRELIMINARY; PRT; 2376 AA.
AC Q966V1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Rexin Li.
GN REXIN OR RXN OR CG3451 OR CG18408 OR CG18409.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki H.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamazaki H., Willert K., Fish M., Nusse R.;
RT "Drosophila Rexin, a Novel SH3 Adaptor Protein of Axin and Arrow that
RT is Essential for Living in Late Stage Embryo."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: CONTAINS 3 SH3 DOMAINS.
DR EMBL; AB053478; BAB62017.1; -;
DR FlyBase; FBgn0033504; rexin.
DR InterPro; IPR002965; P_FICH_extensan.
DR Pfam; IPR001452; SH3.
DR Pfam; PF00018; SH3; 3.
DR PRINTS; PR01217; PRICHEXTENS.
DR ProDom; PD000066; SH3; 3.
DR SMART; SM00326; SH3; 3.
DR PROSITE; PS50002; SH3; 3.
KW SH3 domain.
SQ SEQUENCE 2376 AA; 267657 MW; 9C7BD6C7A705C888 CRC64;

Query Match 29.2%; Score 7; DB 5; Length 2376;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAEED 19
Db 37 QAEGAEED 43

RESULT 13
Q9A542 PRELIMINARY; PRT; 69 AA.
AC Q9A542;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cold-shock domain family protein.
GN CC2623.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=153892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE-21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR EMBL; AE005930; AAK24591.1; -;
DR HSP; F15277; IMJC.
DR TIGR; CC2623; -;
DR InterPro; IPR002059; Cold_shock.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000821; Cold_shock; 1.
DR SMART; SM00357; Csp; 1.
KW Activator; DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 69 AA; 7450 MW; 8EA80BE9EE56853C CRC64;

Query Match 25.0%; Score 6; DB 16; Length 69;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PEDGGQ 13
Db 20 PEDGGQ 25

RESULT 14
Q8Z2R1 PRELIMINARY; PRT; 88 AA.
ID Q8Z2R1

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AC Q82ZRI;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PAE0124.
GN PAE0124.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Muller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009752; AAL62578.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 88 AA; 9492 MW; 22091651B45CADD1 CRC64;

Query Match 25.0%; Score 6; DB 17; Length 88;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
DB 45 ALAGWL 50

RESULT 15
P91785
ID P91785 PRELIMINARY; PRT; 98 AA.
AC P91785;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Antigen maltose binding protein (Fragment).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94336252; PubMed=8058358;
RA Trenholme K.R., Tree T.I., Gillespie A.J., Guderian R., Maizels R.M.,
RA Bradley J.E.;
RT "Heterogeneity of IgG antibody responses to cloned Onchocerca volvulus
RT antigens in microfiladermia positive individuals from Esmeraldas
RT Province, Ecuador."
RL Parasite Immunol. 16:201-209(1994).
DR EMBL; S71371; AAC60510.2; -.
FT NON_TER 1 1
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11165 MW; 221BFEFE14DC76 CRC64;

Query Match 25.0%; Score 6; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LRPEDG 11
DB 51 LRPEDG 56

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Search completed: September 11, 2003, 17:55:48
 Job time : 25.9733 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 16.893 Seconds
(without alignments)
325.703 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 611

Sequence: 1 MPSPTGVCSSLLGLMLDL.....LGKFLQDILWEEAKEAPADK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----|-------------|
| 1 | 611 | 100.0 | 117 | 1 | GHRL_HUMAN |
| 2 | 524 | 85.8 | 117 | 1 | GHRL_MOUSE |
| 3 | 518 | 84.8 | 117 | 1 | GHRL_RAT |
| 4 | 476 | 77.9 | 117 | 1 | GHRL_CANFA |
| 5 | 472.5 | 77.3 | 118 | 1 | GHRL_PIG |
| 6 | 417.5 | 68.3 | 116 | 1 | GHRL_BOVIN |
| 7 | 92 | 15.1 | 115 | 1 | MOTI_MACMU |
| 8 | 88.5 | 14.5 | 115 | 1 | MOTI_HUMAN |
| 9 | 86.5 | 14.2 | 127 | 1 | MOTI_CAVPO |
| 10 | 86 | 14.1 | 92 | 1 | MOTI_HORSE |
| 11 | 82 | 13.4 | 119 | 1 | MOTI_PIG |
| 12 | 72.5 | 11.9 | 115 | 1 | MOTI_SHEEP |
| 13 | 72.5 | 11.9 | 482 | 1 | TYPH_HUMAN |
| 14 | 72 | 11.8 | 147 | 1 | H2B_GOSHI |
| 15 | 71 | 11.6 | 1236 | 1 | TOP2_LEICH |
| 16 | 70 | 11.5 | 116 | 1 | MOTI_FELCA |
| 17 | 70 | 11.5 | 220 | 1 | WFDL_HUMAN |
| 18 | 69 | 11.3 | 792 | 1 | NEKA_MOUSE |
| 19 | 69 | 11.3 | 2424 | 1 | CCAA_RABIT |
| 20 | 68.5 | 11.2 | 115 | 1 | MOTI_BOVIN |
| 21 | 68.5 | 11.2 | 133 | 1 | MOTI_RABIT |
| 22 | 68.5 | 11.2 | 340 | 1 | CBX2_XENLA |
| 23 | 68.5 | 11.2 | 533 | 1 | GUEQ_YERPE |
| 24 | 68 | 11.1 | 330 | 1 | NAG2_VIBCH |
| 25 | 67.5 | 11.0 | 416 | 1 | TC10_HUMAN |
| 26 | 67.5 | 11.0 | 1878 | 1 | BA2A_HUMAN |
| 27 | 67 | 11.0 | 2164 | 1 | CCAA_MOUSE |
| 28 | 67 | 11.0 | 2212 | 1 | CCAA_RAT |
| 29 | 66.5 | 10.9 | 575 | 1 | PT1_LACLA |
| 30 | 66.5 | 10.9 | 575 | 1 | PT1_LACIC |
| 31 | 66.5 | 10.9 | 577 | 1 | PT1_STRBO |
| 32 | 66 | 10.8 | 247 | 1 | MOG_HUMAN |
| 33 | 66 | 10.8 | 589 | 1 | IF2P_THEVO |

| | | | | | | |
|----|------|------|------|---|------------|---------------------|
| 34 | 66 | 10.8 | 770 | 1 | STA3_HUMAN | P40763 homo sapien |
| 35 | 66 | 10.8 | 770 | 1 | STA3_MOUSE | P42227 mus musculus |
| 36 | 66 | 10.8 | 770 | 1 | STA3_RAT | P52631 rattus norv |
| 37 | 66 | 10.8 | 3462 | 1 | RELN_RAT | P58751 rattus norv |
| 38 | 65.5 | 10.7 | 262 | 1 | TRUA_PYRHO | O58941 pyrococcus |
| 39 | 65.5 | 10.7 | 333 | 1 | TALI_KLULA | P34214 kluyveromyc |
| 40 | 65.5 | 10.7 | 692 | 1 | FLHA_SALTY | O40729 salmonella |
| 41 | 65 | 10.6 | 155 | 1 | RS15_HALMA | P05762 haloarcula |
| 42 | 65 | 10.6 | 458 | 1 | HN3B_RAT | P32182 rattus norv |
| 43 | 65 | 10.6 | 554 | 1 | SAP_RAT | P10960 rattus norv |
| 44 | 65 | 10.6 | 795 | 1 | SYFB_HAEIN | P43820 haemophilus |
| 45 | 64.5 | 10.6 | 447 | 1 | CPXU_RHISN | P55340 rhizobium s |

ALIGNMENTS

RESULT 1
GHRL_HUMAN
ID GHRL_HUMAN STANDARD; PRT; 117 AA.
AC Q9UBU3; O8TAT9; Q9H3R3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
DE releasing peptide)
GN GHRL OR MTLRP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
RX Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.; MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.; RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach.";
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Stomach;
RA Tomasetto C., Karam S.M., Rio M.-C.;
RL "Identification of a novel gastric protein m46.";
RN Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Wajnsrajch M.P., Ten I.S., Gertner J.M., Leibei R.L.;
RL "Genomic organization of the human Ghrelin gene.";
RN J. Endocrinol. Genet. 1:231-233(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RL MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Maman A., Rodrigues S., Sanchez A., Whitting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences."; www.ncbi.nlm.nih.gov/pubmed/116899
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [6]
 RP SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RT hormone: the motilin-related peptide."; www.ncbi.nlm.nih.gov/pubmed/119395405
 RL Gastroenterology 119:395-405(2000).
 RN [7]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor."; www.ncbi.nlm.nih.gov/pubmed/12118122
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -!- PTM: O-n-octanoylation is essential for activity.
 CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infoblog.fr/services/chromocancer/Genes/GhrelinID327.html".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB029434; BA89371.1; -;
 DR EMBL; AB035700; BAB19045.1; -;
 DR EMBL; AJ252278; CAB65733.1; -;
 DR EMBL; AF296558; AAG10300.1; -;
 DR EMBL; BC025791; AAR25791.1; -;
 DR PIR; A59316; A59316.
 DR MIM; 605353; -;
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005131; F:growth hormone receptor ligand activity; TAS.
 DR GO; GO:0007287; P:cell-cell signaling; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; TAS.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc.1.
 DR Pfam; PF04644; motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 23 GHRELIN.
 FT PEPTIDE 24 51 REMOVED IN MATURE FORM.
 FT PROPEP 52 117 N-OCTANOATE.
 FT LIPID 26 26 Missing (in Isoform 2).
 FT VARSPLIC 37 37 /FTid=VSP_003245.
 FT FT
 FT CONFLICT 72 72 L-> M (IN REF. 5).
 FT

SQ SEQUENCE 117 AA; 12911 MW; 39C0572BECA2755 CRC64;
 Query Match 100.0%; Score 611; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.1e-54;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MPSPTVCSTLLGLMLDLAMAGSSFLSPHORVQQRKESKPPAKLPQPRALAGWLRLPE 60
 Db 1 MPSPTVCSTLLGLMLDLAMAGSSFLSPHORVQQRKESKPPAKLPQPRALAGWLRLPE 60
 Qy 61 DGGQAEAEDELEVRNAPFDVGKLSGVQYQHSQALGKFLQDILWEEAKEAPADK 117
 Db 61 DGGQAEAEDELEVRNAPFDVGKLSGVQYQHSQALGKFLQDILWEEAKEAPADK 117
 RESULT 2
 GHRL_MOUSE STANDARD; PRT; 117 AA.
 ID GHRL_MOUSE
 AC Q9EQX0; Q9MUZ1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide) (Motilin-related peptide) (M46 protein).
 GN GHRL OR MTLRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
 RX TISSUE=Stomach;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RT hormone: the motilin-related peptide."; www.ncbi.nlm.nih.gov/pubmed/119395405
 RL Gastroenterology 119:395-405(2000).
 RN [2]
 RC SEQUENCE FROM N.A. (ISOFORM 1).
 RA Kojima M.;
 RT "Mouse mRNA for preproghrelin."; www.ncbi.nlm.nih.gov/pubmed/745555
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RC SEQUENCE FROM N.A. (ISOFORM 1).
 RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RC SEQUENCE FROM N.A. (ISOFORM 1).
 RX STRAIN=C57BL/6J; TISSUE=Stomach;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casanova H.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
 RA Schramm L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann C., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."; www.ncbi.nlm.nih.gov/pubmed/119395405
 RL Nature 409:685-690(2001).
 RN [5]
 RP REVIEW.


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RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulation of gastric acid secretion. Involved in
CC growth regulation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9EQX0-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9EQX0-2; Sequence=VSP_003246;
CC -!- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
CC with higher levels in the stomach, medium levels in the duodenum,
CC jejunum, ileum and colon. Low expression in the testis and brain.
CC Not detected in the salivary gland, pancreas, liver and lung.
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC
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CC
DR EMBL; AJ243503; CAB46500.1; -
DR EMBL; AB035701; BAB19046.1; -
DR EMBL; AB060078; BAB69857.1; -
DR EMBL; AK008658; BAB25814.1; -
DR EMBL; AK008860; BAB25934.1; -
DR MGI; MGI:1930008; Ghrl.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005576; C:extracellular; IDA.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc.1.
DR Pfam; PF04644; motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN
DR ProDom; PD332162; Preproghrelin; 1.
KW Hormone: Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23
FT PEPTIDE 24 51
FT PROPEP 52 117
FT LIPID 26 26
FT VARSPIC 37 37
FT /FTID=VSP_003246;
SQ SEQUENCE 117 AA; 13207 MW; EACB49D2E3CA7203 CRC64;

Query Match 85.8%; Score 524; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 1.le-45;
Matches 98; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MPSPGVCSLLLLGLMLDLAMAGSFLSPHQVRQKESKPPAKLPQALAGWLKPE 60
Db 1 MLSSCTICSLLLSLMLMDMAMAGSFLSPHQVQKESKPPAKLPQALAGWLKPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQVQOQSALGKFLQDILWEEKEAPADK 117
Db 61 DRGQAEETEELIRNAPFDVGIKLSGAQVQOQGRALGKFLQDILWEEKEAPADK 117

RESULT 3
GHRL_RAT STANDARD; PRT; 117 AA.
ID GHRL_RAT

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AG Q9QYH7: Q9ET69;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide).
GN GHRL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,
RP AND ACYLATION OF SER-26.
RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
RX MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from
RT stomach.";
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS
RP SPECTROMETRY, AND ACYLATION OF SER-26.
RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
RX MEDLINE=20357315; PubMed=10801861;
RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT "Purification and characterization of rat des-Gln14-ghrelin, a second
RT endogenous ligand for the growth hormone secretagogue receptor.";
RL J. Biol. Chem. 275:21995-22000(2000).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=21092536; PubMed=11162448;
RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
RT in gastrointestinal tissue.";
RL Biochem. Biophys. Res. Commun. 279:909-913(2000).
RN [4]
RP STRUCTURE-ACTIVITY RELATIONSHIP.
RX MEDLINE=21433488; PubMed=11549267;
RA Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
RT "Structure-activity relationship of ghrelin: pharmacological study of
RT ghrelin peptides.";
RL Biochem. Biophys. Res. Commun. 287:142-146(2001).
RN [5]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9QYH7-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9QYH7-2; Sequence=VSP_003248;
CC -!- TISSUE SPECIFICITY: Broadly expressed with higher expression in
CC the stomach. Very low levels are detected in the hypothalamus,
CC heart, lung, pancreas, intestine and adipose tissue.
CC -!- PTM: O-n-octanoylation is essential for activity. The replacement
CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.
CC -!- MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;
CC RANGE=24-51.
CC -!- MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;
CC RANGE=24-36, 38-51.
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.

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-----
EMBL: AB029433; BAA89370.1; -
EMBL: AB035699; BAB11956.1; -
PIR: B59316; B59316.
InterPro: IPR006737; motilin_assoc.
InterPro: IPR005441; Preproghrelin.
Pfam: PF04643; motilin_assoc; 1.
Pfam: PF04644; motilin_ghrelin; 1.
PRINTS: PR01624; GHRELIN.
ProDom: PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23 GHRELIN.
FT PEPTIDE 24 51 REMOVED IN MATURE FORM.
FT PROPEP 52 117 N-OCTANOATE.
FT LIPID 26 26 Missing (in isoform 2).
FT VARSPLIC 37 37 /FTid=VSP_003248.
SQ SEQUENCE 117 AA; 13176 MW; 8857546FE51A7691 CRC64;

Query Match 84.8%; Score 518; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 4.2e-45;
Matches 97; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MPSPTGTCVSLLLGLMLDLAMAGSSFLSPHEHQVQQRKSKPPAKLQPRALAGWLRLPE 60
DB 1 MVSATTCISLLLSMLMDMAMAGSSFLSPHEHQVQQRKSKPPAKLQPRALAGWLRLPE 60

QY 61 DGGQAEAGDELEVRFPDVGIKLSGVQYQHQHSGALGKFLQDLILWEEAKEAPADK 117
DB 61 DRGQAEAELEIRFNAPFDVGIKLSGVQYQHQHSGALGKFLQDLILWEEAKEAPANK 117

RESULT 4
GHRLL_CANFA STANDARD; PRT; 117 AA.
ID GHRLL_CANFA Q9BEF8; Q9BEF7;
AC Q9BEF8; Q9BEF7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (growth hormone secretagogue) (growth hormone
releasing peptide) (Motilin-related peptide).
GN GHRLL OR MTLRP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
[1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RN RA Tomasetto C., Wendling C., Rio M.-C., Poltras P.;
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
fundus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Specific ligand for the growth hormone secretagogue
receptor type 1 (GHSR) inducing the release of growth hormone from
the pituitary. Has an appetite-stimulating effect, induces
adiposity and stimulates gastric acid secretion. Involved in
growth regulation (By similarity).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9BEF8-1; Sequence=Displayed;

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Name=2; Synonyms=del-Gln14-ghrelin;
IsoId=Q9BEF8-2; Sequence=VSP_003244;
-|- PFM: O-n-octanoylation is essential for activity (By similarity).
-|- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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-----
EMBL: AJ298295; CAC29155.1; -
EMBL: AJ298296; CAC29156.1; -
InterPro: IPR006737; motilin_assoc.
InterPro: IPR006738; motilin_ghrelin.
InterPro: IPR005441; Preproghrelin.
Pfam: PF04643; motilin_assoc; 1.
Pfam: PF04644; motilin_ghrelin; 1.
PRINTS: PR01624; GHRELIN.
ProDom: PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPLIC 37 37 Missing (in isoform 2).
FT /FTid=VSP_003244.
SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;

Query Match 77.9%; Score 476; DB 1; Length 117;
Best Local Similarity 77.8%; Pred. No. 6.7e-41;
Matches 91; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 MPSPTGTCVSLLLGLMLDLAMAGSSFLSPHEHQVQQRKSKPPAKLQPRALAGWLRLPE 60
DB 1 MPSLGTCSLLLSVLDLMDMAMAGSSFLSPHEHQVQQRKSKPPAKLQPRALAGWLRLPE 60

QY 61 DGGQAEAGDELEVRFPDVGIKLSGVQYQHQHSGALGKFLQDLILWEEAKEAPADK 117
DB 61 DTSQVEAEDELEIRFNAPFDVGIKLSGVQYQHQHSGALGKFLQDLILWEEAKEAPADK 117

RESULT 5
GHRLL_PIG STANDARD; PRT; 118 AA.
ID GHRLL_PIG Q9GKY5; Q9BGD8; Q9GKY4;
AC Q9GKY5; Q9BGD8; Q9GKY4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (growth hormone secretagogue) (growth hormone
releasing peptide).
GN GHRLL.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RN RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Stomach;
RA Roussellet J., Lacroix D., Dubreuil P.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Specific ligand for the growth hormone secretagogue
receptor type 1 (GHSR) inducing the release of growth hormone from
the pituitary. Has an appetite-stimulating effect, induces
adiposity and stimulates gastric acid secretion. Involved in
growth regulation (By similarity).
CC

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DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Motilin precursor [Contains: Motilin; Motilin associated peptide
(MAP)].
GN MLN.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=2109894; PubMed=11172801;
RA Xu L., Depoortere I., Tang M., Peeters T.L.;
RT "Identification and expression of the motilin precursor in the guinea
pig".
RL FEBS Lett. 490:7-10(2001).
CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF
INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Present in the gut mucosa with the exception
of the gastric corpus. Also present in medulla oblongata, nucleus
of the solitary tract, hypophysis, spinal cord, hypothalamus, and
cerebellum but not in the cerebral cortex.
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
CC EMBL: AF323752; AAK07442.1; -
DR InterPro: IPR006737; motilin_assoc.
DR InterPro: IPR006738; motilin_ghrelin.
DR Pfam: PF04643; motilin_assoc; 1.
DR Pfam: PF04644; motilin_ghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT PEPTIDE 26 47 MOTILIN.
FT PEPTIDE 50 127 MOTILIN ASSOCIATED PEPTIDE.
SQ SEQUENCE 127 AA; 14156 MW; A46E90C0E7EFC220 CRC64;
Query Match 14.2%; Score 86.5; DB 1; Length 127;
Best Local Similarity 27.6%; Pred. No. 0.072;
Matches 32; Conservative 23; Mismatches 44; Indels 17; Gaps 5;
QY 1 MFPGTVCGLLLGLMLDLAMAGSS-----FLSPHQVQQRKSK--KPPAKLQPR 51
DB 1 MLRSKRAVALLVHV-----TAMLASQTEGFVIFTYSELRRTQREQNKRLRSURVQOR 56
QY 52 A-LAGLRLPEDGQAGAEDELEVRNAPFDVIGIKLSGVQYQOHSQALGKFLQDIL 106
DB 57 SKAAGRLRPQ---EVNREEENGVIKLTAPVEIGVGLSSRLQLEKRAVLEALLSEAL 109
RESULT 10
MOTIL_HORSE
ID MOTI_HORSE STANDARD; PRT; 92 AA.
AC O46617;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Motilin precursor [Contains: Motilin; Motilin associated peptide
(MAP)] (Fragment).
GN MLN.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=DuoDenal mucosa;
RX MEDLINE=20033365; PubMed=10564829;
RA Huang Z., Depoortere I., De Clercq P., Peeters T.;
RT "Sequence and characterization of cDNA encoding the motilin precursor
from chicken, dog, cow and horse. Evidence of mosaic evolution in
premotilin".
RL Gene 240:217-226(1999).
CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF
INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF047520; AAC03790.1; -
DR InterPro: IPR006737; motilin_assoc.
DR InterPro: IPR006738; motilin_ghrelin.
DR Pfam: PF04643; motilin_assoc; 1.
DR Pfam: PF04644; motilin_ghrelin; 1.
KW Hormone; Cleavage on pair of basic residues.
FT NON_TER 1 1
FT PEPTIDE 1 22 MOTILIN.
FT PEPTIDE 25 92 MOTILIN ASSOCIATED PEPTIDE.
SQ SEQUENCE 92 AA; 10410 MW; 99DCA503EAFE4C8 CRC64;
Query Match 14.1%; Score 86; DB 1; Length 92;
Best Local Similarity 28.9%; Pred. No. 0.057;
Matches 24; Conservative 19; Mismatches 34; Indels 6; Gaps 3;
QY 27 FLSPHQVQ--QRKSKPPAKLQPR--LAGLRLPEDGQAGAEDELEVRNAPFDVIG 83
DB 5 FTYSRLQRMQERKRNQKSLGLQORSEEVGSLDPTAEAEKGEK---VIKLTAPVEIG 61
QY 84 IKLSGVQYQOHSQALGKFLQDIL 106
DB 62 MRNRSQLEKYRAALEGLLEVL 84
RESULT 11
MOTI_PIG
ID MOTI_PIG STANDARD; PRT; 119 AA.
AC P01307;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Motilin precursor [Contains: Motilin; Motilin associated peptide
(MAP)].
GN MLN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8828831; PubMed=2456453;
RA Bond C.T., Nilaver G., Godfrey B., Zimmerman E.A., Adelman J.P.;
RT "Characterization of complementary deoxyribonucleic acid for
precursor of porcine motilin".
RL Mol. Endocrinol. 2:175-180(1988).
RN [2]
RP SEQUENCE OF 26-47.
RX MEDLINE=73184120; PubMed=4706833;

```

Db          90 DSRQLEKYRATLERLL 105

RESULT 12
MOTIL_SHEEP
ID MOTI_SHEEP STANDARD; PRT; 115 AA.
AC Q18845;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Motilin precursor [Contains: Motilin; Motilin associated peptide
DE (MAP)].
DE
GN MLN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RC MEDLINE=98087436; PubMed=9427564;
RA De Clercq P., Depoortere I., Peeters T.L.;
RT "Isolation and sequencing of the cDNA encoding the motilin precursor
RT from sheep intestine.";
RL Gene 202187-191(1997).
CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF
CC INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
CC RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF022771; AAB80930.1; -
CC PIR; JC6511; JC6511.
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC Pfam; PF04643; motilin_assoc.1.
CC Pfam; PF04644; motilin_ghrelin.1.
CC Hormone; Cleavage on pair of basic residues; Signal.
KW SIGNAL
FT SIGNAL 1 25 BY SIMILARITY.
FT PEPTIDE 26 47 MOTILIN.
FT PEPTIDE 50 115 MOTILIN ASSOCIATED PEPTIDE.
SQ SEQUENCE 115 AA; 12956 MW; 383892C2AD7EC5D CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 115;
Best Local Similarity 25.0%; Pred. No.1.6;
Matches 21; Conservative 21; Mismatches 33; Indels 9; Gaps 2;

QY 27 FLSPHQVRQVRKSKPPAKLQPRLAGWLRPEDGQAGAEDELE----VRFNAPFOV 82
Db 30 FTYGEVQRMQEKERYKG----QKSLSVQQRSEEVGPDPAEPREKQEVKLTAPVEI 84
QY 83 GIKLSGVQVQOHSQALGKGLQDIL 106
Db 85 GMRMNSRQLEKYQATLEGLLRKAL 108

RESULT 13
TYPH_HUMAN
ID TYPH_HUMAN STANDARD; PRT; 482 AA.
AC P19971; Q13390;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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Db 60 AVVNGSAQAQIGAML-----MAIRLRGMDLETSVLTOALASGQGLEWPEAWRQOL 112
Qy 115 ADK 117
    ||
Db 113 VDK 115

RESULT 14
H2B_GOSHI
ID H2B_GOSHI STANDARD; PRT; 147 AA.
AC O22582;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histone H2B.
GN HIS2B.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Deltapine 62; TISSUE=Etiolated cotyledon;
RA Turley R.B.;
RT "cDNA clones encoding histone H3 and histone H2B from upland cotton
  (Gossypium hirsutum L.).";
RL (In) Plant Gene Register PGR97-182.
CC -1- SUBUNIT: The nucleosome is an octamer containing two molecules
  each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
  BP of DNA.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the histone H2B family.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF025667; AAB97163.1; -.
DR PIR; T09722; T09722.
DR InterPro; IPR004822; Histone_Core.
DR InterPro; IPR000558; Histone_H2B.
DR Pfam; PF00125; histone.1
DR PRINTS; PR00621; HISTONEH2B.
DR PRODOM; PD000497; Histone_H2B; 1.
DR SMART; SM00427; H2B; 1.
DR PROSITE; PS00357; HISTONE_H2B; 1.
DR KW Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
SQ SEQUENCE 147 AA; 16087 MW; CEFDS5C774E6E11F6 CRC64;

Query Match 11.8%; Score 72; DB 1; Length 147;
Best Local Similarity 25.2%; Pred. No. 2.4;
Matches 28; Conservative 22; Mismatches 31; Indels 30; Gaps 5;

Qy 22 MAGSFFLSPEHORVQORKE--SKKPPAKLOPRALAGWLRPEDGGQAGEDELEVRFNAP 79
Db 1 MAPKAEEKPAEAKPAEKKAVAEKPK--AGKKLPKEGGAAGDKKKRKKVSVE 58
Qy 80 F-----DVGIRLSGVQYQOHSQALG---KFLQDILWEAEKA 113
    |||
Db 59 TYKIYIPKLVKQVHPDIGIS-----SKAMGIMNSFINDIFEKLAQEA 100

RESULT 15
TOP2_LEICH
ID TOP2_LEICH STANDARD; PRT; 1236 AA.
AC O61078;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA topoisomerase II (EC 5.99.1.3).
GN TOP2.
OS Leishmania chagasi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=44271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MHOM/BR/86/L669;
RA Tepe-Lansdell T., Mann B.J., Labombard M., Macdonald T., Slunt K.M.,
  Pearson R.D.;
RT "Isolation of a gene encoding a DNA topoisomerase II of Leishmania
  (Leishmania) chagasi.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
  BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
  MAKES DOUBLE-STRAND BREAKS.
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
  of double-stranded DNA.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
  NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
  RELAX ONLY NEGATIVE SUPERCOILS.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF051307; AAC05295.2; -.
DR HSP; P06786; IBGW.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR001241; DNA_topoisoII.
DR InterPro; IPR002205; DNA_topoisoIV.
DR Pfam; PF00204; DNA_gyrase; 1.
DR Pfam; PF00521; DNA_topoisoIV; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR PRODOM; PD000742; DNA_topoisoIV; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00433; TOP2c; 1.
DR SMART; SM00434; TOP4c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
DR KW Isomerase; Topoisomerase; ATP-binding.
FT NP_BIND 137 142 ATP (POTENTIAL).
FT ACT_SITE 775 775 DNA CLEAVAGE (BY SIMILARITY).
SQ SEQUENCE 1236 AA; 138968 MW; A3209B95A078045C CRC64;

Query Match 11.6%; Score 71; DB 1; Length 1236;
Best Local Similarity 27.4%; Pred. No. 30;
Matches 26; Conservative 13; Mismatches 48; Indels 8; Gaps 2;

Qy 20 LAMAGSFFLSPEHORVQORKE--SKKPPAKLOPRALAGWLRPED-----GGQAGEDELE 73
    |||
Db 1141 LLMLGASAKGATAYRVHACQYERPPPSKRRPGESVGGARPSDSAAARTVGRKRLVGRSEFK 1200
Qy 74 VR--FNAPFDVGKLSGVQYQOHSQALGKFLQDIL 106
    |||
Db 1201 NKKPMRSKKNVKSLSLSTRTVAQPCGAQLGRLLPHVL 1235

Search completed: September 11, 2003, 17:21:41
Job time : 18.893 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 25.0267 Seconds
(without alignments)
152.215 Million cell updates/sec

Title: US-09-853-253-4

Perfect score: 126

Sequence: 1 ALAGWLRPEDGGQAEAGAELEVR 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_15Jun03.*

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7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
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9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------------------|
| 1 | 126 | 100.0 | 24 | 23 | AAE23839 Human zsig33-linker |
| 2 | 126 | 100.0 | 24 | 23 | AAE15884 Human zsig33-linker |
| 3 | 126 | 100.0 | 91 | 24 | AAE33410 Human exon 3-delet |
| 4 | 126 | 100.0 | 116 | 22 | AAE60517 Human des-Gln14-gh |
| 5 | 126 | 100.0 | 117 | 20 | AAW87991 Protein designated |
| 6 | 126 | 100.0 | 117 | 21 | AAW87236 Human signal pepti |
| 7 | 126 | 100.0 | 117 | 22 | AAW38890 Human polypeptide |
| 8 | 126 | 100.0 | 117 | 22 | AAE62649 Human zsig33 polyp |
| 9 | 126 | 100.0 | 117 | 22 | AAE20101 Zsig33 protein. H |

| | | | | | |
|----|------|-------|------|----|-----------------------------|
| 10 | 126 | 100.0 | 117 | 22 | AAE60511 Human ghrelin prep |
| 11 | 126 | 100.0 | 117 | 23 | ABW78319 Amino acid sequenc |
| 12 | 126 | 100.0 | 117 | 23 | AAE23838 Human zsig33 prote |
| 13 | 126 | 100.0 | 117 | 23 | AAE15883 Human zsig33 prote |
| 14 | 126 | 100.0 | 117 | 24 | ABU66790 Human PRO polypept |
| 15 | 126 | 100.0 | 117 | 24 | ABU67066 Human secreted/tr |
| 16 | 126 | 100.0 | 117 | 24 | ABU59871 Novel secreted and |
| 17 | 126 | 100.0 | 117 | 24 | ABU59124 Novel human secret |
| 18 | 126 | 100.0 | 117 | 24 | ABU59271 Human secreted/tr |
| 19 | 126 | 100.0 | 117 | 24 | ABU59420 Novel human secret |
| 20 | 126 | 100.0 | 117 | 24 | ABU60555 Human secreted/tr |
| 21 | 126 | 100.0 | 117 | 24 | ABU58046 Human PRO polypept |
| 22 | 126 | 100.0 | 117 | 24 | ABU58977 Human secreted/tr |
| 23 | 126 | 100.0 | 117 | 24 | AAE33409 Human preproghreli |
| 24 | 126 | 100.0 | 117 | 24 | ABU13937 Human PRO1066 poly |
| 25 | 126 | 100.0 | 117 | 24 | ABU10892 Human PRO polypept |
| 26 | 126 | 100.0 | 118 | 21 | AAE66708 Membrane-bound pro |
| 27 | 126 | 100.0 | 118 | 22 | AAU12392 Human PRO1066 poly |
| 28 | 126 | 100.0 | 118 | 22 | AAE65231 Human PRO1066 (UNQ |
| 29 | 126 | 100.0 | 126 | 22 | AAE40676 Human polypeptide |
| 30 | 121 | 96.0 | 23 | 23 | AAE23840 Human zsig33-linke |
| 31 | 121 | 96.0 | 23 | 23 | AAE23841 Human zsig33-linke |
| 32 | 121 | 96.0 | 23 | 23 | AAE15885 Human zsig33-linke |
| 33 | 121 | 96.0 | 23 | 23 | AAE15886 Human zsig33-linke |
| 34 | 95 | 75.4 | 90 | 23 | ABP08975 Human ORFX protein |
| 35 | 95 | 75.4 | 116 | 22 | AAE60516 Rat des-Gln14-ghre |
| 36 | 95 | 75.4 | 117 | 22 | AAE60510 Rat ghrelin prepro |
| 37 | 92 | 73.0 | 117 | 22 | AAE60521 Porcine des-Gln14- |
| 38 | 92 | 73.0 | 118 | 22 | AAE60520 Porcine ghrelin pr |
| 39 | 67.5 | 53.6 | 89 | 22 | AAE60523 Bovine ghrelin pre |
| 40 | 54 | 42.9 | 200 | 24 | ABP58240 Xenopus laevis nuc |
| 41 | 50 | 39.7 | 653 | 17 | AAE98903 Murine APLP1. Mus |
| 42 | 48 | 38.1 | 82 | 22 | AAE73526 Human colon cancer |
| 43 | 48 | 38.1 | 287 | 22 | ABG15575 Novel human diagno |
| 44 | 48 | 38.1 | 570 | 22 | ABG20671 Novel human diagno |
| 45 | 48 | 38.1 | 2836 | 22 | ABE62719 Drosophila melanog |

ALIGNMENTS

RESULT 1

AAE23839

ID AAE23839 standard; peptide; 24 AA.

XX AAE23839;

AC AAE23839;

XX 10-SEP-2002 (first entry)

DT Human zsig33-linker peptide #1.

DE Human zsig33-linker peptide #1.

XX Human; zsig33-like peptide; gastric contractility; nutrient uptake;

KW growth hormone; digestive enzyme; restorative therapy; gene therapy;

KW protein therapy; gastrointestinal; endocrine; anabolic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 7..18

FT /note= "Hydrophilic region"

XX US2002055156-A1.

PN 09-MAY-2002.

PD 10-MAY-2001; 2001US-0853253.

XX 11-MAY-2000; 2000US-203300P.

XX (JASP/) JASPERS S R.

PA (SHEP/) SHEPPARD P O.

PA (DEIS/) DEISHER T A.

PA (BISH/) BISHOP P D.

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XX PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX WPI: 2002-443750/47.
XX DR N-PSDB; AAD38239.
XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
XX contractility, nutrient uptake, growth hormones and/or secretion of
XX digestive/pancreatic enzymes and hormones.
XX Claim 1; Page 28; 34pp; English.
XX The invention relates to zsig33-like peptides and their corresponding
XX nucleic acids and methods for modulating gastric contractility, nutrient
XX uptake, growth hormones, secretion of digestive enzymes and hormones.
XX The sequences of the invention are used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate ZSIG33 expression.
XX The nucleic acids of the invention and their complements are used as
XX DNA probes in diagnostic assays to detect and quantitate the presence
XX of similar nucleic acids in samples, and therefore which patients may be
XX in need of restorative therapy. The ZSIG33 peptides are used as antigens
XX in the production of antibodies against ZSIG33 and in assays to identify
XX modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
XX and antagonists are used to down regulate expression and activity. The
XX anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
XX the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
XX assay (ELISA)). The peptides and nucleic acids of the invention are used
XX to modulate gastric contractility, nutrient uptake, growth hormones, the
XX secretion of digestive enzymes and hormones, and/or secretion of enzymes
XX and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
XX and zsig33-like peptide is used in protein therapy. The present sequence
XX is human zsig33-like peptide, zsig33-linker peptide.
XX SQ Sequence 24 AA;
XX Query Match 100.0%; Score 126; DB 23; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 5.7e-12;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
XX Db 1 ALAGWLRPEDGGQAGAEDELEVR 24
XX RESULT 2
XX AAEL15884
XX ID AAEL15884 standard; peptide; 24 AA.
XX AC AAEL15884;
XX XX 26-MAR-2002 (first entry)
XX XX Human zsig33-linker peptide #1.
XX XX Human: zsig33-like peptide; ZS33LP; immunity; developmental process;
XX KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
XX KW adsorption enhancer; gastrointestinal disease; growth related disease;
XX KW inflammation; gene therapy; growth regulation; blood vessel formation;
XX KW HIV; zsig33-linker peptide.
XX XX Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Region 6..22
XX FT /note= "Hydrophilic antigenic site"
XX FT Region 7..18
XX FT /note= "Hydrophilic region"
XX XX WO200187933-A2.
XX PN 22-NOV-2001.
XX PD 10-MAY-2001; 2001WO-US15091.
XX PF

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XX 11-MAY-2000; 2000US-0569271.
XX (ZYMO ) ZYMOGENETICS INC.
XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX WPI: 2002-082982/11.
XX DR N-PSDB; AAD25760.
XX New polypeptides, useful for modulating gastric contractility, nutrient
XX uptake, pancreatic secretion of hormones, digestive enzymes and
XX treating gastrointestinal and growth related diseases, comprises
XX zsig33-like peptides.
XX Claim 1a; Page 81; 89pp; English.
XX The invention relates to zsig33-like peptides (ZS33LP) including
XX zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and
XX zsig33-epsilon peptides and nucleic acid molecules encoding such
XX zsig33-like peptides. ZS33LP peptides activate the immune system
XX in boosting immunity to infectious diseases, treating immunocompromised
XX patients such as human immunodeficiency virus (HIV) patients, in
XX improving vaccines and in treatment of bacterial, viral, protozoal and
XX fungal infections. Peptides of the invention are used to identify and
XX isolate receptors involved in growth regulation in the liver, blood
XX vessel formation and other developmental processes. They are useful for
XX evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
XX growth and/or differentiation of tumour cells, as additives to anti-
XX hypoglycaemic preparations containing glucose and as adsorption
XX enhancers for oral drugs which require fast nutrient action and to
XX stimulate glucose-induced insulin release. They are also useful as
XX research reagents for the expansion, differentiation, growth factor and
XX hormone secretion and/or cell-cell interactions of tissues associated
XX with gastrointestinal system, brain and central nervous system. These
XX molecules are useful for treating dysfunction associated with contractile
XX tissues or to suppress or enhance contractility in vivo and to treat
XX gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
XX acids and/or antibodies are useful for treating disorders associated
XX with gastrointestinal contractility, secretion of digestive enzymes,
XX hormone and acids, secretion of hormones in the pancreas and/or brain,
XX gastrointestinal motility, recruitment of digestive enzymes, inflammation
XX and regulation of nutrient absorption. Sequences of the invention are
XX useful in gene therapy. The present sequence is human zsig33-linker
XX peptide.
XX SQ Sequence 24 AA;
XX Query Match 100.0%; Score 126; DB 23; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 5.7e-12;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
XX Db 1 ALAGWLRPEDGGQAGAEDELEVR 24
XX RESULT 3
XX AAEL33410
XX ID AAEL33410 standard; Protein; 91 AA.
XX AC AAEL33410;
XX XX 02-APR-2003 (first entry)
XX DT Human exon 3-deleted ghrelin protein.
XX DE Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
XX KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
XX KW cancer; human.
XX XX Homo sapiens.
XX OS
XX

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PN WO200290387-A1.
XX 14-NOV-2002.
XX 10-MAY-2002; 2002WO-AU00582.
XX 10-MAY-2001; 2001AU-0004919.
PR 17-DEC-2001; 2001AU-0009567.
XX (UYOU-) UNIV QUEENSLAND TECHNOLOGY.
XX Chopin LK, Jeffery PL, Herington AC;
XX WPI; 2003-1111957/10.
DR N-PSDB; AAD50726.
XX Identifying a cancer cell or tissue for treating prostate, ovarian,
PT breast cancer, or benign prostatic hyperplasia, by detecting the
PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
PT 1b proteins or nucleic acids -
XX Claim 14; Page 34; 50pp; English.
XX The invention relates to a method for identifying a cancer cell or
CC tissue of the reproductive system by detecting expression of a ghrelin,
CC an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic
CC acids. The antibodies, exon 3-deleted form of preproghrelin and
CC antagonists are useful for treating cancer of the reproductive system
CC such as prostate, ovarian, breast, cervical or uterine cancer,
CC choriocarcinoma or benign prostatic hyperplasia. The present sequence
CC is human exon 3-deleted ghrelin protein.
XX Sequence 91 AA;
SQ Query Match 100.0%; Score 126; DB 24; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRLPEDGGQAGAEDELEVR 24
Db 52 ALAGWLRLPEDGGQAGAEDELEVR 75
RESULT 4
AAB60517
ID AAB60517 standard; Protein; 116 AA.
XX AAB60517;
XX 24-APR-2001 (first entry)
XX Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
KW calcium concentration elevation; infant growth disorder;
KW growth hormone deficiency.
XX Homo sapiens.
XX WO200107475-A1.
XX 01-FEB-2001.
XX 24-JUL-2000; 2000WO-JP04907.
XX 23-JUL-1999; 99JP-0210002.
PR 29-NOV-1999; 99JP-0338841.
PR 26-APR-2000; 2000JP-0126623.
XX (KANG/) KANGAWA K.
XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
PI WPI; 1999-070071/06.
DR

DR WPI; 2001-159704/16.
DR N-PSDB; AAF59647.
XX New peptide compounds which induce growth hormone secretion and
PT elevate cell calcium concentrations, useful in treatment and diagnosis
PT of infant growth disorders -
XX Claim 3; Page 186-187; 210pp; Japanese.
XX The invention relates to a novel peptide compound or its salt which
CC induces the secretion of growth hormone and/or elevates calcium ion
CC concentration in cells. The peptides are ghrelin homologues and are
CC characterised in that at least one amino acid has been substituted by
CC a modified amino acid and/or a non-amino acid compound. The invention
CC also encompasses the unmodified peptides; the DNA encoding the peptides;
CC vectors and host cells comprising such DNA; a method of producing the
CC peptides comprising recombinant production, optionally followed by
CC chemical modification; an antibody specific for a peptide of the
CC invention; and an assay and kit for detecting the peptides. The peptides
CC of the invention are useful for treating and/or diagnosing diseases
CC caused by a deficiency in growth hormone expression or activity. In
CC particular, they are useful for promoting infant growth due to growth
CC hormone deficiency. The compounds of the invention are safe with
CC no accompanying side effects. The present sequence represents a
CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
CC of the invention.
XX Sequence 116 AA;
SQ Query Match 100.0%; Score 126; DB 22; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRLPEDGGQAGAEDELEVR 24
Db 51 ALAGWLRLPEDGGQAGAEDELEVR 74
RESULT 5
AAW87991
ID AAW87991 standard; Protein; 117 AA.
XX AAW87991;
XX 07-APR-1999 (first entry)
XX Protein designated zsig33.
XX Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
KW nutrient absorption regulation; obesity; metabolic disorder.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..23
FT /note= "signal peptide"
FT Protein 24..117
FT /note= "mature protein"
XX WO9842840-A1.
XX 01-OCT-1998.
XX 23-MAR-1998; 98WO-US05620.
XX 24-MAR-1997; 97US-0822897.
PR 24-MAR-1997; 97US-0041102.
XX (ZYMO) ZYMOGENETICS INC.
XX Delsher TA, Sheppard PO;
XX WPI; 1999-070071/06.
DR

DR N-PSDB; AAX04550.

XX Human polypeptide having homology to motilin, zsig33 - useful e.g.

PT to treat gastrointestinal motility disorders, obesity etc. and to

PT identify antagonists to treat gastrointestinal hypermotility

XX

PS Claim 13; Page 55-56; 69pp; English.

XX

CC The present sequence represents a protein designated zsig33. The nucleic

CC acids are strongly expressed in stomach tissue. The polypeptide (or

CC allelic variants/orthologs) can be used to stimulate gastric motility,

CC measured as increased transit time or gastric emptying of an ingested

CC substance in mammals. The products are used to treat disorders associated

CC with gastrointestinal cell contractility, secretion of digestive

CC enzymes/acids, gastrointestinal motility, recruitment of digestive

CC enzymes, gastrointestinal inflammation, reflux disease and nutrient

CC absorption regulation. Zsig33 polypeptides may also be important

CC neurologically, since the family of gut-brain peptides to which the

CC homologous protein motilin belongs has been associated with neurological

CC and CNS functions. They may therefore be used e.g. to regulate satiety

CC or treat obesity and other metabolic disorders where neurological

CC feedback modulates nutritional absorption. They are useful to identify

CC zsig33 agonists, antagonists and ligands and to produce antibodies.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 126; DB 20; Length 117;

Best Local Similarity 100.0%; Pred. NO. 3.4e-11;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24

DB 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 6

AAAY87236

ID AAY87236 standard; Protein; 117 AA.

XX

AC AAY87236;

XX

DT 11-MAY-2000 (first entry)

XX

DE Human signal peptide containing protein HSPP-13 SEQ ID NO:13.

XX

KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;

KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;

KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;

KW antischismatic; gene therapy; cell proliferation; neurological disorder;

KW reproductive disorder; developmental disorder; arteriosclerosis;

KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;

KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;

KW Parkinson's disease; Huntington's diseases; ovulatory defect;

KW muscular dystrophy.

XX

OS Homo sapiens.

XX

PN WO200000610-A2.

XX

PD 06-JAN-2000.

XX

PF 25-JUN-1999; 99WO-US14484.

XX

XX 26-JUN-1998; 98US-0090762.

PR 31-JUL-1998; 98US-0094983.

PR 01-OCT-1998; 98US-0102686.

PR 11-DEC-1998; 98US-0112129.

XX

PA (INCY-) INCYTE PHARM INC.

XX

XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;

PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;

PI Bandman O;

XX WPI; 2000-160673/14.

DR N-PSDB; AAZ98121.

XX

XX New human signal peptide-containing proteins useful in treatment,

PT prevention and diagnosis of e.g. cancer, inflammation and

PT cardiovascular disease

XX

PS Claim 1; Page 168-169; 327pp; English.

XX

CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the

CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have

CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,

CC neuroprotective, cardiovascular and antischismatic activities, and can

CC be used in gene therapy. HSPPs can be used to treat or prevent disorders

CC associated with decreased activity or function of HSPP. Antagonists of

CC HSPP are used to treat or prevent disorders associated with increased

CC activity or function of HSPP. Such diseases include cell proliferation

CC (including cancer), inflammation, cardiovascular, neurological,

CC reproductive or developmental disorders, (e.g. arteriosclerosis,

CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,

CC asthma, Crohn's disease, microbial or other infections, congestive or

CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's

CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP

CC nucleic acids can be used for the recombinant production of HSPP, for

CC detecting HSPP in standard hybridisation and amplification assays (for

CC diagnosis and monitoring), in gene therapy, as antisense,

CC triplex-forming or ribozyme therapeutics, for detecting related sequences

CC or genetic variations, and for chromosomal mapping. HSPP are also used

CC to raise specific antibodies (Ab) and to screen for agonists and

CC antagonists (potential therapeutic agents). Ab are used to diagnose, or

CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic

CC antagonists, in competitive drug screens, and for purification of HSPP

CC from natural sources.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 126; DB 21; Length 117;

Best Local Similarity 100.0%; Pred. NO. 3.4e-11;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24

DB 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 7

AAAM38890

ID AAM38890 standard; Protein; 117 AA.

XX

AC AAM38890;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 2035.

XX

XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

PD 26-JUL-2001.

XX

XX 26-DEC-2000; 2000WO-US34263.

PF 21-JAN-2000; 2000US-0488725.

PR 23-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB; AAI58046.
 XX
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 PT
 PS Example 3; SEQ ID NO 2035; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAW42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: the sequence data for this patent did not form part of the printed
 CC specification.
 XX
 XX Sequence 117 AA;
 Query Match 100.0%; Score 126; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPDDGGQAGAEDELEVR 24
 Db 52 ALAGWLRPDDGGQAGAEDELEVR 75
 RESULT 8
 AAB62649
 ID AAB62649 standard; Protein; 117 AA.
 XX
 AC AAB62649;
 XX
 XX 23-JUL-2001 (first entry)
 XX Human zsig33 polypeptide.
 XX
 KW zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
 KW G-protein coupled receptor.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH 24..37
 FT /note= "specifically claimed fragment that binds to
 FT the GHS-R"
 XX
 PN WO200138355-A2.

XX 31-MAY-2001.
 PD
 XX 22-NOV-2000; 2000WO-US32074.
 PF
 XX 22-NOV-1999; 99US-0166765.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 PI WPI: 2001-355879/37.
 DR N-PSDB; AAF83678.
 XX
 XX Forming reversible peptide receptor complex for purifying cell and
 PT peptides, stimulating signal transduction and modulating hormone
 PT secretion, involves contacting a receptor with zsig33 polypeptide -
 PT
 PS Claim 1; Page 93-94; 111pp; English.
 XX
 CC The invention relates to a method of forming a reversible peptide-
 CC receptor complex that involves providing an immobilized receptor, and
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
 CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
 CC is useful for purifying cells, purifying a peptide, stimulating signal
 CC transduction in a cell expressing a receptor. It is also useful for
 CC modulating secretion of hormones, neural development and/or utilization,
 CC gastric contractility, nutrient uptake, secretion of digestive and
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
 CC hormone secretion in a mammal having a disease associated with abnormal
 CC levels of growth hormone, such as osteoporosis, bone repair, bone
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,
 CC protein catabolic responses after surgery, cachexia, protein loss,
 CC dwarfism, wound healing and ovulation induction, treating a mammal having
 CC a metabolic disorder requiring neurological feedback, such as satiety
 CC regulation, glucose absorption and metabolism and neuropathy-associated
 CC gastrointestinal disorders, and stimulating glucose-induced insulin
 CC release in a mammal. The present sequence represents the human zsig33
 CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
 XX
 XX Sequence 117 AA;
 Query Match 100.0%; Score 126; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPDDGGQAGAEDELEVR 24
 Db 52 ALAGWLRPDDGGQAGAEDELEVR 75
 RESULT 9
 AAB20101
 ID AAB20101 standard; Protein; 117 AA.
 XX
 AC AAB20101;
 XX
 XX 23-APR-2001 (first entry)
 DT Zsig33 protein.
 XX
 DE SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
 KW nutritional absorption modulator; growth hormone secretagogue;
 KW therapy; human.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH 1..23
 FT /label= signal_peptide
 FT 24..117
 FT Protein

```

FT Peptide /label= Mature_protein
FT 24..34
FT /label= SGIP_peptide
FT /note= "this peptide is claimed in Claim 1"
PN WO200100830-A1.
XX
XX
XX 04-JAN-2001.
XX
XX 30-JUN-2000; 2000WO-US18306.
XX
XX 30-JUN-1999; 99US-0345157.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
XX WPI; 2001-123010/13.
XX N-PSDB; AAF30033.
XX
XX Novel variants of SGIP peptides for modulating contractility in
XX duodenum or jejunum tissue, pancreatic secretion of hormones and
XX digestive enzymes, inducing growth hormone secretion or modulating
XX gastric emptying -
XX
XX Disclosure: 54; 61pp; English.
XX
XX The present sequence is that of zsig33, a secreted protein with
XX homology to motilin (see AAB20102). Zsig33 is expressed at high
XX levels in the stomach, and at lower levels in the small intestine
XX and pancreas. A novel peptide fragment of zsig33, termed SGIP (see
XX AAB20100), is claimed. SGIP is a ligand for growth hormone
XX secretagogue receptor, and is therefore useful for modulating
XX secretion of growth hormone and insulin like growth factor 1.
XX SGIP, and variant SGIP peptides, are used in claimed methods for
XX stimulating contractility in duodenum or jejunum tissue,
XX modulating pancreatic secretion of hormones and digestive enzymes,
XX inducing growth hormone secretion, and modulating gastric emptying.
XX
XX Sequence 117 AA;

Query Match 100.0%; Score 126; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. NO. 3.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24
DB 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 10
AAB60511
ID AAB60511 standard; Protein; 117 AA.
XX
XX AAB60511;
XX
XX 24-APR-2001 (first entry)
XX
XX Human ghrelin preproprotein, SEQ ID NO:5.
XX
XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
XX calcium concentration elevation; infant growth disorder;
XX growth hormone deficiency.
XX
XX Homo sapiens.
XX
XX WO200107475-A1.
XX
XX 01-FEB-2001.
XX
XX 24-JUL-2000; 2000WO-JP04907.
XX
XX 23-JUL-1999; 99JP-0210002.
XX

PR 29-NOV-1999; 99JP-0338841.
PR 26-APR-2000; 2000JP-0126623.
XX
XX (KANG/) KANGAWA K.
XX
XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
XX
XX WPI; 2001-159704/16.
XX N-PSDB; AAF59645.
XX
XX New peptide compounds which induce growth hormone secretion and
XX elevate cell calcium concentrations, useful in treatment and diagnosis
XX of infant growth disorders -
XX
XX Claim 3; Page 182; 210pp; Japanese.
XX
XX The invention relates to a novel peptide compound or its salt which
XX induces the secretion of growth hormone and/or elevates calcium ion
XX concentration in cells. The peptides are ghrelin homologues and are
XX characterised in that at least one amino acid has been substituted by
XX a modified amino acid and/or a non-amino acid compound. The invention
XX also encompasses the unmodified peptides; the DNA encoding the peptides;
XX vectors and host cells comprising such DNA; a method of producing the
XX peptides comprising recombinant production, optionally followed by
XX chemical modification; an antibody specific for a peptide of the
XX invention; and an assay and kit for detecting the peptides. The peptides
XX of the invention are useful for treating and/or diagnosing diseases
XX caused by a deficiency in growth hormone expression or activity. In
XX particular, they are useful for promoting infant growth due to growth
XX hormone deficiency. The compounds of the invention are safe with
XX no accompanying side effects. The present sequence represents a
XX ghrelin-type growth hormone secretagogue (GHS) precursor protein
XX of the invention.
XX
XX Sequence 117 AA;

Query Match 100.0%; Score 126; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. NO. 3.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24
DB 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 11
AAB78319
ID ABB78319 standard; Protein; 117 AA.
XX
XX ABB78319;
XX
XX 05-DEC-2002 (first entry)
XX
XX Amino acid sequence of a human zsig33.
XX
XX Short gastrointestinal peptide; SGIP; zsig33; motilin.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX /note= "signal peptide"
XX Protein 24..119
XX /note= "mature protein"
XX
XX US6420521-B1.
XX
XX 16-JUL-2002.
XX
XX 30-JUN-2000; 2000US-0608810.
XX
XX 30-JUN-1999; 99US-141592P.
XX

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PA (ZYMO) ZYMOGENETICS INC.
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 PI
 XX WPI: 2002-634794/68.
 DR N-PSDB; ABV72214.
 XX
 XX New Short Gastrointestinal Peptide, which has homology to motilin,
 PT useful for preventing, diagnosing and treating gastrointestinal
 PT disorders
 XX
 XX Disclosure: Columns 39-40; 23pp; English.
 PS
 XX The present sequence represents human zsig33. The specification describes
 CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.
 CC SGIP has homology to motilin. The SGIP peptide may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate SGIP expression. For example, SGIP may be used to treat
 CC disorders associated with decreased expression by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of SGIP by
 CC expressing inactive proteins or to supplement the patient's own production
 CC of SGIP. SGIP may also be used as an antigen in the production of
 CC antibodies against SGIP and in assays to identify modulators of SGIP
 CC expression and activity. The anti-SGIP antibodies, agonists and
 CC antagonists may also be used to regulate expression and activity. The
 CC anti-SGIP antibodies may also be used as diagnostic agents for detecting
 CC the presence of SGIP in samples.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 126; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. NO. 3.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 DB 52 ALAGWLRPEDGGQAGAEDELEVR 75
 RESULT 12
 AAE15883
 ID AAE15838 standard; Protein; 117 AA.
 XX
 AC AAE15838;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human zsig33 protein.
 XX
 KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
 KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
 KW protein therapy; gastrointestinal; endocrine; anabolic.
 XX
 OS Homo sapiens.
 XX
 XX US2002055156-A1.
 PN
 XX
 XX 09-MAY-2002.
 PD
 XX
 XX 10-MAY-2001; 2001US-0853253.
 PF
 XX
 XX 11-MAY-2000; 2000US-203300P.
 PR
 XX
 XX (JASP/) JASPERS S R.
 PA (SHEP/) SHEPPARD P O.
 PA (DEIS/) DEISHER T A.
 PA (BISH/) BISHOP P D.
 XX
 XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 PI
 XX WPI: 2002-443750/47.
 DR N-PSDB; AAD38238.
 XX

PT ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
 PT contractility, nutrient uptake, growth hormones and/or secretion of
 PT digestive/pancreatic enzymes and hormones -
 XX
 PS Disclosure: Page 27; 34pp; English.
 XX
 XX The invention relates to zsig33-like peptides and their corresponding
 CC nucleic acids and methods for modulating gastric contractility, nutrient
 CC uptake, growth hormones, secretion of digestive enzymes and hormones.
 CC The sequences of the invention are used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate ZSIG33 expression.
 CC The nucleic acids of the invention and their complements are used as
 CC DNA probes in diagnostic assays to detect and quantitate the presence
 CC of similar nucleic acids in samples, and therefore which patients may be
 CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
 CC in the production of antibodies against ZSIG33 and in assays to identify
 CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
 CC and antagonists are used to down regulate expression and activity. The
 CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
 CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
 CC assay (ELISA)). The peptides and nucleic acids of the invention are used
 CC to modulate gastric contractility, nutrient uptake, growth hormones, the
 CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
 CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
 CC and zsig33-like peptide is used in protein therapy. The present sequence
 CC is human zsig33 protein.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 126; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. NO. 3.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 DB 52 ALAGWLRPEDGGQAGAEDELEVR 75
 RESULT 13
 AAE15883
 ID AAE15893 standard; Protein; 117 AA.
 XX
 AC AAE15893;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human zsig33 protein.
 XX
 KW Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
 KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
 KW adsorption enhancer; gastrointestinal disease; growth related disease;
 KW inflammation; gene therapy; growth regulation; blood vessel formation;
 KW HIV; zsig33 protein.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT Protein /label= signal_peptide
 FT 24..117
 FT /note= "Human mature zsig33 protein"
 XX
 XX WO200187933-A2.
 PN
 XX
 XX 22-NOV-2001.
 PD
 XX
 XX 10-MAY-2001; 2001WO-US15091.
 PF
 XX
 XX 11-MAY-2000; 2000US-0569271.
 PR
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 PI

XX WPI; 2002-082982/11.
DR N-PSDB; AAD25759.
XX
XX New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and
PT treating gastrointestinal and growth related diseases, comprises
PT zsig33-like peptides -
XX
XX Disclosure; Page 80-81; 89pp; English.
XX
CC The invention relates to zsig33-like peptides (ZS33LP) including
CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and
CC zsig33-epsilon peptides and nucleic acid molecules encoding such
CC zsig33-like peptides. ZS33LP peptides activate the immune system
CC in boosting immunity to infectious diseases, treating immunocompromised
CC patients such as human immunodeficiency virus (HIV) patients, in
CC improving vaccines and in treatment of bacterial, viral, protozoal and
CC fungal infections. Peptides of the invention are used to identify and
CC isolate receptors involved in growth regulation in the liver, blood
CC vessel formation and other developmental processes. They are useful for
CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
CC growth and/or differentiation of tumour cells, as additives to anti-
CC hypoglycaemic preparations containing glucose and as adsorption
CC enhancers for oral drugs which require fast nutrient action and to
CC stimulate glucose-induced insulin release. They are also useful as
CC research reagents for the expansion, differentiation, growth factor and
CC hormone secretion and/or cell-cell interactions of tissues associated
CC with gastrointestinal system, brain and central nervous system. These
CC molecules are useful for treating dysfunction associated with contractile
CC tissues or to suppress or enhance contractility in vivo and to treat
CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
CC acids and/or antibodies are useful for treating disorders associated
CC with gastrointestinal contractility, secretion of digestive enzymes,
CC hormone and acids, secretion of hormones in the pancreas and/or brain,
CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
CC and regulation of nutrient absorption. Sequences of the invention are
CC useful in gene therapy. The present sequence is human zsig33 protein.
XX
XX Sequence 117 AA;
SQ

Query Match 100.0%; Score 126; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ALAGWLRPEDGGQAGAEDELEVR 24
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEVR 75
|||||

RESULT 14
ABU66790
ID ABU66790 standard; Protein; 117 AA.
XX
AC ABU66790;
XX
XX 23-MAY-2003 (first entry)
XX
XX Human PRO polypeptide #221.
XX
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytosolic.
XX
XX Homo sapiens.
OS
XX US2003036180-A1.
PN
XX
XX 20-FEB-2003.
PD
XX
XX 09-MAY-2002; 2002US-0143114.
PF
XX

31-MAR-1997; 97WO-US05230.
12-JUN-1998; 98WO-US12456.
14-JUL-1998; 98WO-US14552.
28-AUG-1998; 98WO-US17888.
10-SEP-1998; 98WO-US18824.
14-SEP-1998; 98WO-US19093.
14-SEP-1998; 98WO-US19094.
14-SEP-1998; 98WO-US19177.
16-SEP-1998; 98WO-US19330.
17-SEP-1998; 98WO-US19437.
07-OCT-1998; 98WO-US21141.
29-OCT-1998; 98WO-US22991.
29-OCT-1998; 98WO-US22992.
20-NOV-1998; 98WO-US24855.
01-DEC-1998; 98WO-US25108.
05-JAN-1999; 98WO-US00106.
08-MAR-1999; 98WO-US05028.
10-MAR-1999; 98WO-US05190.
20-APR-1999; 98WO-US08615.
14-MAY-1999; 98WO-US10733.
02-JUN-1999; 98WO-US12252.
01-SEP-1999; 98WO-US20111.
08-SEP-1999; 98WO-US20594.
13-SEP-1999; 98WO-US20944.
15-SEP-1999; 98WO-US21090.
15-SEP-1999; 98WO-US21547.
05-OCT-1999; 98WO-US23089.
29-NOV-1999; 98WO-US28214.
30-NOV-1999; 98WO-US28313.
30-NOV-1999; 98WO-US28409.
01-DEC-1999; 98WO-US28301.
01-DEC-1999; 98WO-US28634.
02-DEC-1999; 98WO-US28551.
02-DEC-1999; 98WO-US28564.
02-DEC-1999; 98WO-US28565.
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20-DEC-1999; 98WO-US30911.
20-DEC-1999; 98WO-US30999.
22-DEC-1999; 98WO-US30720.
30-DEC-1999; 98WO-US31243.
30-DEC-1999; 98WO-US31274.
05-JAN-2000; 2000WO-US00219.
06-JAN-2000; 2000WO-US00277.
06-JAN-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US03565.
18-FEB-2000; 2000WO-US04341.
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000WO-US04414.
24-FEB-2000; 2000WO-US04914.
01-MAR-2000; 2000WO-US05004.
01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05746.
02-MAR-2000; 2000WO-US05841.
10-MAR-2000; 2000WO-US06319.
15-MAR-2000; 2000WO-US06884.
20-MAR-2000; 2000WO-US07377.
31-MAR-2000; 2000WO-US07532.
21-MAR-2000; 2000WO-US08439.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-JUN-2000; 2000WO-US15264.
28-JUL-2000; 2000WO-US20710.
11-AUG-2000; 2000WO-US22031.
23-AUG-2000; 2000WO-US23522.
24-AUG-2000; 2000WO-US23328.
08-NOV-2000; 2000WO-US30952.
10-NOV-2000; 2000WO-US30873.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-US06520.
01-MAR-2001; 2001WO-US06666.
25-MAY-2001; 2001WO-US17092.

PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
 XX
 DR WPI: 2003-332040/31.
 DR N-PSDB: ACA03823.

XX
 PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification

XX Claim 12; Fig 442; 660pp: English.

XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. ABU66570-ABU66844 represent the human
 CC PRO polypeptides of the invention.

CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsdEntry.html.

XX Sequence 117 AA;

Query Match 100.0%; Score 126; DB 24; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALAGWLRPDGGGQAGAELEVR 24
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 DB 52 ALAGWLRPDGGGQAGAELEVR 75

RESULT 15
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 ID ABU67066 standard; Protein; 117 AA.
 XX
 AC ABU67066;
 XX
 DT 27-MAY-2003 (first entry)
 DE Human secreted/transmembrane, PRO, protein SEQ ID 442.
 XX
 KW Human; secreted protein; transmembrane protein; PRO;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioindicator; tumour.
 XX
 OS Homo sapiens.
 XX
 PN US2003032155-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 03-MAY-2002; 2002US-0137865.
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 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 21-JUN-2001; 2001US-0886342.
 PR 18-JUL-2001; 2001US-0887879.
 PR 06-AUG-2001; 2001US-0908827.
 PR 09-AUG-2001; 2001US-0924419.
 PR 16-AUG-2001; 2001US-0927796.
 PR 19-DEC-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX

DR WPI: 2003-331925/31.
 DR N-PSDB: ACA04244.
 XX

XX New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer
 XX

PS Claim 12: Fig 442: 659pp; English.
 XX

XX The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited

CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.
 XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 126; DB 24; Length 117;
 Best Local Similarity 100.0%; Pred. NO. 3.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ALAGWLRPEDGGQAGAEDELEVR 24

|||||

Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

Search completed: September 11, 2003, 17:25:02
 Job time : 25.0267 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 6.41711 Seconds
(without alignments)
158.243 Million cell updates/sec

Title: US-09-853-253-4
Perfect score: 126
Sequence: 1 ALAGWLRPEDGGQAEGBEDEVLR 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
 - 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
 - 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
 - 5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
 - 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 126 | 100.0 | 117 | 4 | US-08-822-897C-2 |
| 3 | 126 | 100.0 | 117 | 4 | US-09-608-810A-4 |
| 4 | 126 | 100.0 | 117 | 4 | US-09-996-243-268 |
| 5 | 52 | 41.3 | 233 | 4 | US-09-252-991A-27758 |
| 6 | 50 | 39.7 | 518 | 4 | US-09-252-991A-23604 |
| 7 | 50 | 39.7 | 634 | 1 | US-08-339-152A-17 |
| 8 | 50 | 39.7 | 653 | 1 | US-08-339-152A-16 |
| 9 | 50 | 39.7 | 653 | 2 | US-08-007-999B-3 |
| 10 | 50 | 39.7 | 653 | 2 | US-08-689-276A-3 |
| 11 | 49 | 38.9 | 139 | 2 | US-08-039-1988-10 |
| 12 | 48 | 38.1 | 428 | 4 | US-09-252-991A-19723 |
| 13 | 47 | 37.3 | 283 | 4 | US-09-252-991A-29700 |
| 14 | 47 | 37.3 | 405 | 4 | US-09-252-991A-20326 |
| 15 | 47 | 37.3 | 468 | 4 | US-09-252-991A-24394 |
| 16 | 46 | 36.5 | 517 | 4 | US-09-252-991A-27327 |
| 17 | 46 | 36.5 | 341 | 4 | US-09-252-991A-25921 |
| 18 | 46 | 36.5 | 1044 | 4 | US-09-252-991A-18853 |
| 19 | 45.5 | 36.1 | 551 | 4 | US-09-252-991A-20358 |
| 20 | 45.5 | 36.1 | 579 | 3 | US-08-704-711A-1 |
| 21 | 45.5 | 36.1 | 579 | 4 | US-09-521-220-1 |
| 22 | 45.5 | 36.1 | 582 | 3 | US-08-704-711A-2 |
| 23 | 45.5 | 36.1 | 582 | 3 | US-08-448-489-1 |
| 24 | 45.5 | 36.1 | 582 | 3 | US-09-211-704A-9 |
| 25 | 45.5 | 36.1 | 582 | 4 | US-09-521-220-2 |
| 26 | 45.5 | 36.1 | 582 | 4 | US-09-391-104-28 |
| 27 | 45.5 | 36.1 | 591 | 2 | US-08-889-402-1 |

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| 28 | 45 | 35.7 | 174 | 4 | US-09-252-991A-18600 | Sequence 18600, A |
| 29 | 45 | 35.7 | 494 | 1 | US-08-464-340A-4 | Sequence 4, Appl1 |
| 30 | 45 | 35.7 | 494 | 5 | PCT-US94-08449A-4 | Sequence 4, Appl1 |
| 31 | 45 | 35.7 | 1059 | 4 | US-09-394-272-5 | Sequence 5, Appl1 |
| 32 | 45 | 35.7 | 1185 | 3 | US-08-664-962B-2 | Sequence 2, Appl1 |
| 33 | 45 | 35.7 | 1185 | 3 | US-09-311-743-2 | Sequence 2, Appl1 |
| 34 | 44 | 34.9 | 298 | 4 | US-09-252-991A-32302 | Sequence 32302, A |
| 35 | 43 | 34.1 | 118 | 3 | US-08-482-304-12 | Sequence 12, Appl |
| 36 | 43 | 34.1 | 118 | 3 | US-08-483-474-12 | Sequence 12, Appl |
| 37 | 43 | 34.1 | 140 | 3 | US-08-482-304-9 | Sequence 9, Appl1 |
| 38 | 43 | 34.1 | 140 | 3 | US-08-483-474-9 | Sequence 9, Appl1 |
| 39 | 43 | 34.1 | 162 | 4 | US-09-252-991A-24838 | Sequence 24838, A |
| 40 | 43 | 34.1 | 191 | 4 | US-09-252-991A-21437 | Sequence 21437, A |
| 41 | 43 | 34.1 | 212 | 3 | US-09-154-083-4 | Sequence 4, Appl1 |
| 42 | 43 | 34.1 | 247 | 4 | US-09-252-991A-27419 | Sequence 27419, A |
| 43 | 43 | 34.1 | 268 | 4 | US-09-252-991A-27950 | Sequence 27950, A |
| 44 | 43 | 34.1 | 281 | 2 | US-08-900-565-1 | Sequence 1, Appl1 |
| 45 | 43 | 34.1 | 281 | 4 | US-09-149-534-1 | Sequence 1, Appl1 |

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: zymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 100.0%; Score 126; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 |||||
 Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 2

US-08-822-897C-2
 ; Sequence 2, Application US/08822897C
 ; Patent No. 6380158
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Deisher, Theresa A.
 ; TITLE OF INVENTION: MOTILIN HOMOLOGS
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZymoGenetics, Inc.
 ; STREET: 1201 Eastlake Avenue East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/822,897C
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sawistak, Deborah A.
 ; REGISTRATION NUMBER: 37,438
 ; REFERENCE/DOCKET NUMBER: 97-04
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-442-6672
 ; TELEFAX: 206-442-6678
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 117 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-822-897C-2

Query Match 100.0%; Score 126; DB 4; Length 117;
 Best Local Similarity 100.0%; Pred. No. 9.9e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 |||||
 Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 3

US-09-608-810A-4
 ; Sequence 4, Application US/09608810A
 ; Patent No. 6420521
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Jaspers, Stephen R.
 ; APPLICANT: Deisher, Theresa A.
 ; APPLICANT: Bishop, Paul D.
 ; TITLE OF INVENTION: SGIP PEPTIDES
 ; FILE REFERENCE: 99-51
 ; CURRENT APPLICATION NUMBER: US/09/608,810A
 ; CURRENT FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 60/141,592
 ; PRIOR FILING DATE: 1999-06-30
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 117
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(23)
 ; US-09-608-810A-4

Query Match 100.0%; Score 126; DB 4; Length 117;
 Best Local Similarity 100.0%; Pred. No. 9.9e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 |||||
 Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 4

US-09-996-243-268
 ; Sequence 268, Application US/09996243
 ; Patent No. 6478825
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PLC13
 ; CURRENT APPLICATION NUMBER: US/09/996,243
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/075945
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/084600

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|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 524 | 525 |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 126; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPDGGGAGAEDELEVR 24
|||||
Db 52 ALAGWLRPDGGGAGAEDELEVR 75

RESULT 5

US-09-252-991A-27758
; Sequence 27758, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27758
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27758

Query Match 41.3%; Score 52; DB 4; Length 233;
Best Local Similarity 72.7%; Pred. No. 2*8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GWLRPDGGQA 14
|||||
Db 203 GWLRPDGSGRA 213

RESULT 6

US-09-252-991A-23604
; Sequence 23604, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23604
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23604

Query Match 39.7%; Score 50; DB 4; Length 518;
Best Local Similarity 45.5%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 3 AGWLRPDGGGAGAEDELEVR 24

Db 412 AGWAQPEPGCGGGAERLHRR 433
||| :||| | | : | |

RESULT 7

US-08-339-152A-17
; Sequence 17, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/339,152A
APPLICATION NUMBER: US/08/339,152A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 0609.4120000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 634 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-339-152A-17

Query Match 39.7%; Score 50; DB 1; Length 634;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGQAGGADELEV 23
||:|||||

Db 213 GGRAEGGEDEEV 225
||:|||||

RESULT 8

US-08-339-152A-16
; Sequence 16, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,152A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 0609.4120000
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-152A-16

Query Match 39.7%; Score 50; DB 1; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGAAGAEDELEV 23
||:|||||
Db 233 GGAEGGEDEV 245

RESULT 9
US-08-007-999B-3
Sequence 3, Application US/08007999B
Patent No. 5851787
GENERAL INFORMATION:
APPLICANT: Masco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Tanzil, Rudolph
APPLICANT: Solomon, Frank
TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,999B
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,642
FILING DATE: 20-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 0609.3520002/JAG/GKT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2571
TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-007-999B-3

Query Match 39.7%; Score 50; DB 2; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGAAGAEDELEV 23
||:|||||
Db 233 GGAEGGEDEV 245

RESULT 10
US-08-689-276A-3
Sequence 3, Application US/08689276A
Patent No. 5891991
GENERAL INFORMATION:
APPLICANT: Masco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Tanzil, Rudolph
APPLICANT: Solomon, Frank
TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,276A
FILING DATE: 06-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,999
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,642
FILING DATE: 20-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3520003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2571
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-689-276A-3

Query Match 39.7%; Score 50; DB 2; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGAGGAEDELEV 23
11:111 111 11
Db 233 GGAGGEGDEEV 245

RESULT 11

US-08-039-1988-10
; Sequence 10, Application US/080391988
; Patent No. 5858725
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PREPARATION OF CHIMAERIC ANTIBODIES
; TITLE OF INVENTION: RECOMBINANT PCR STRATEGY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/039,1988
; APPLICATION NUMBER: US/08/039,1988
; FILING DATE: 29-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01744
; FILING DATE: 08-OCT-91
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-86
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-039-1988-10

Query Match 38.9%; Score 49; DB 2; Length 139;
Best Local Similarity 61.5%; Pred. No. 4.4;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGGAG 16
11:11111 1
Db 68 GWIDPEDGGTKY 80

RESULT 12

US-09-252-991A-19723
; Sequence 19723, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19723
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19723

Query Match 38.1%; Score 48; DB 4; Length 428;
Best Local Similarity 52.2%; Pred. No. 22;
Matches 12; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LAGWLRPEDGGGAEDELEVR 24
11:111 111 111 1
Db 293 LALWSLPEDPRPADWADELSDR 315

RESULT 13

US-09-252-991A-29700
; Sequence 29700, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29700
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29700

Query Match 37.3%; Score 47; DB 4; Length 283;
Best Local Similarity 58.8%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 AGWLRPEDGGGAG 19
11:111 111 111
Db 86 AAGLRQEDGADGTGAED 102

RESULT 14

US-09-252-991A-20326
; Sequence 20326, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20326
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20326

Query Match 37.3%; Score 47; DB 4; Length 405;
Best Local Similarity 45.5%; Pred. No. 29;
Matches 10; Conservative 2; Mismatches 8; Indels 2; Gaps 1;

QY 5 WLRPEDGG--QAEGAEDELEVR 24
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 Db 154 WLRPEGGADQOQGVHQPAAQR 175

RESULT 15

US-09-252-991A-24394
 ; Sequence 24394, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24394
 ; LENGTH: 468
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24394

Query Match 37.3%; Score 47; DB 4; Length 468;
 Best Local Similarity 57.9%; Pred. No. 34;
 Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 6 LRPEDGGQAEDELEVR 24
 || : | || ||| ||
 Db 122 LRRSEGLAGGAGDELVR 140

Search completed: September 11, 2003, 17:27:17
 Job time : 7.41711 secs

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| Result No. | Query | | | ID | Description |
|------------|-------|-------|--------|-------------------|-------------------|
| | Score | Match | Length | | |
| 1 | 126 | 100.0 | 24 | US-09-853-253-4 | Sequence 4, Appli |
| 2 | 126 | 100.0 | 117 | US-09-794-987-2 | Sequence 2, Appli |
| 3 | 126 | 100.0 | 117 | US-09-853-253-2 | Sequence 2, Appli |
| 4 | 126 | 100.0 | 117 | US-09-989-722-268 | Sequence 268, App |
| 5 | 126 | 100.0 | 117 | US-09-989-723-268 | Sequence 268, App |
| 6 | 126 | 100.0 | 117 | US-09-989-279-268 | Sequence 268, App |
| 7 | 126 | 100.0 | 117 | US-09-989-727-268 | Sequence 268, App |
| 8 | 126 | 100.0 | 117 | US-09-989-731-268 | Sequence 268, App |
| 9 | 126 | 100.0 | 117 | US-09-989-732-268 | Sequence 268, App |
| 10 | 126 | 100.0 | 117 | US-09-931-073-268 | Sequence 268, App |
| 11 | 126 | 100.0 | 117 | US-09-990-442-268 | Sequence 268, App |
| 12 | 126 | 100.0 | 117 | US-09-991-163-268 | Sequence 268, App |
| 13 | 126 | 100.0 | 117 | US-09-993-604-268 | Sequence 268, App |
| 14 | 126 | 100.0 | 117 | US-09-990-456-268 | Sequence 268, App |
| 15 | 126 | 100.0 | 117 | US-09-989-721-268 | Sequence 268, App |

; Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

Query Match 100.0%; Score 126; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 3

US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. US2002005156A1
; GENERAL INFORMATION:
; APPLICANT: JASPEERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-2

Query Match 100.0%; Score 126; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 4

US-09-989-722-268
; Sequence 268, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04

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; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
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; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952

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; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 126; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAELEVR 24

Db 52 ALAGWLRPEDGGGAEGAELEVR 75

RESULT 5

US-09-989-723-268
; Sequence 268, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989, 723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
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Query Match 100.0%; Score 126; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 52 ALAGWLRPEDGGQAEGADELEVR 75

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; Sequence 268, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
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;; APPLICANT: Gurney, Austin L.
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;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730PIC56
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;; CURRENT FILING DATE: 2001-11-19
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

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APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Napier, Mary A.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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FILE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 126; DB 9; Length 117;

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US-09-989-731-268

; Sequence 268, Application US/09989731

; Patent No. US20020103125A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C70
 ; CURRENT FILING DATE: 2001-11-20
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 126; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24
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Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75
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RESULT 9
US-09-989-732-268
; Sequence 268, Application US/09989732
; Patent No US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Ben L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC57
CURRENT FILING DATE: 2001-11-19
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 126; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 1,1e-09;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ALAGWLRPEDGGQAGAELEVR 24
Db 52 ALAGWLRPEDGGQAGAELEVR 75
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RESULT 10

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US-09-991-073-268
; Sequence 268, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073

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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0% Score 126; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
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Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 11

US-09-990-442-268
; Sequence 268, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990.442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 126; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.le-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 12
US-09-991-163-268
; Sequence 268, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991.163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 126; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.le-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGAGAEDELEVR 24
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DB 52 ALAGWLRPEDGGAGAEDELEVR 75

RESULT 13
US-09-993-604-268
; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Pao, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993,604
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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| 14 | PRIOR APPLICATION NUMBER: 60/090252 |
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| 27 | PRIOR FILING DATE: 1998-06-24 |
| 28 | PRIOR APPLICATION NUMBER: 60/090444 |
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| 31 | PRIOR FILING DATE: 1998-06-24 |
| 32 | PRIOR APPLICATION NUMBER: 60/090472 |
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| 58 | PRIOR APPLICATION NUMBER: 60/091360 |
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| 61 | PRIOR FILING DATE: 1998-07-02 |
| 62 | PRIOR APPLICATION NUMBER: 60/091633 |
| 63 | PRIOR FILING DATE: 1998-07-02 |
| 64 | PRIOR APPLICATION NUMBER: 60/091978 |
| 65 | PRIOR FILING DATE: 1998-07-07 |
| 66 | PRIOR APPLICATION NUMBER: 60/091982 |
| 67 | PRIOR FILING DATE: 1998-07-07 |

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 126; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. NO. 1.le-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAEGADELEVR 24
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Db 52 ALAGWLRPDGGQAEGADELEVR 75

RESULT 14
US-09-990-456-268
; Sequence 268, Application us/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC22
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; PRIOR APPLICATION NUMBER: 60/049787
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 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
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GenCore version 5.1.6
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
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; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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US-09-046-479-2

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US-09-134-001C-3033
; Sequence 3033, Application US/09134001C
; Patent No. 6380370

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GFC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3033

LENGTH: 442

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3033

Query Match 30.4%; Score 7; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAG 16
Db |||||||

189 DGGQAG 195

RESULT 6

US-09-252-991A-27032
; Sequence 27032, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27032

LENGTH: 552

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-27032

Query Match 30.4%; Score 7; DB 4; Length 552;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAG 16

Db |||||||

22 DGGQAG 28

RESULT 7

US-09-252-991A-20368
; Sequence 20368, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20368

LENGTH: 599

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-20368

Query Match 30.4%; Score 7; DB 4; Length 599;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGQAEGA 17

|||||||

383 GGQAEGA 389

RESULT 8

US-09-252-991A-16798
; Sequence 16798, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 16798

LENGTH: 981

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-16798

Query Match 30.4%; Score 7; DB 4; Length 981;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7

|||||||

136 ALAGWLR 142

RESULT 9

US-08-428-488-13
; Sequence 13, Application US/08428488
; Patent No. 5624894

GENERAL INFORMATION:

; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE

;; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
;; NUMBER OF SEQUENCES: 107
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/428,488
;; FILING DATE: 27-APR-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Baumeister, Mary Katherine
;; REGISTRATION NUMBER: 26,254
;; REFERENCE/DOCKET NUMBER: 028724-087
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 39 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1
;; OTHER INFORMATION: /note= "Position 1 - H-Ser."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 39
;; OTHER INFORMATION: /note= "Position 39 - Phe-OH."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 30
;; OTHER INFORMATION: /note= "Position 30 - Glu-NH2."
US-08-428-488-13

Query Match 26.1%; Score 6; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 GAEDEL 21
DB 26 GAEDEL 31

RESULT 10
US-08-403-852D-31
; Sequence 31, Application US/08403852D
; Patent No. 5891695

;; GENERAL INFORMATION:
;; APPLICANT: Blanc, Veronique
;; APPLICANT: Blanc, Francis
;; APPLICANT: Crouzet, Joel
;; APPLICANT: Jacques, Nathalie
;; APPLICANT: Lacroix, Patricia
;; APPLICANT: Thibaut, Denis
;; APPLICANT: Zagorec, Monique
;; APPLICANT: Debussche, Laurent
;; APPLICANT: De Crecy-Lagard, Valerie
;; TITLE OF INVENTION: Polypeptides Involved In The
;; Biosynthesis Of Streptogramins, Nucleotide Sequences
;; AND Their Use
;; NUMBER OF SEQUENCES: 43

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/403,852D
;; FILING DATE: 10-MAY-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR 93/00923
;; FILING DATE: 25-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 92/11441
;; FILING DATE: 25-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03806.0054-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 97 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-403-852D-31

Query Match 26.1%; Score 6; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 QAEGAE 18
DB 2 QAEGAE 7

RESULT 11
US-08-510-646B-32
; Sequence 32, Application US/08510646B
; Patent No. 6077699

;; GENERAL INFORMATION:
;; APPLICANT: Blanc, Veronique
;; APPLICANT: Blanc, Francis
;; APPLICANT: Crouzet, Joel
;; APPLICANT: Jacques, Nathalie
;; APPLICANT: Lacroix, Patricia
;; APPLICANT: Thibaut, Denis
;; APPLICANT: Zagorec, Monique
;; APPLICANT: Debussche, Laurent
;; APPLICANT: De Crecy-Lagard, Valerie
;; TITLE OF INVENTION: Polypeptides Involved In The
;; Biosynthesis Of Streptogramins, Nucleotide Sequences
;; AND Their Use
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,646B
; FILING DATE: 03-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-510-646B-32

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Query Match      25.1%; Score 6; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 QAEGAE 18
Db      2 QAEGAE 7

```

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RESULT 12
US-09-231-818-31
; Sequence 31, Application US/09231818
; Patent No. 6171846
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,818
; FILING DATE:
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/08/403,852
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-231-818-31

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Query Match      26.1%; Score 6; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 QAEGAE 18
Db      2 QAEGAE 7

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RESULT 13
US-09-135-994-12
; Sequence 12, Application US/09135994A
; Patent No. 6280938
; GENERAL INFORMATION:
; APPLICANT: Ranum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/135,994A
; CURRENT FILING DATE: 1998-08-18
; EARLIER APPLICATION NUMBER: 60/056,170
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-135-994-12

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Query Match      26.1%; Score 6; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 RPEDGG 12
Db      57 RPEDGG 62

```

```

RESULT 14
US-09-684-843A-12
; Sequence 12, Application US/09684843A
; Patent No. 6514755
; GENERAL INFORMATION:
; APPLICANT: Ranum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: Regents of the University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/684,843A
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/056,170
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 09/135,994

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; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-843A-12

Query Match 26.1%; Score 6; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RPEDGG 12
|
|
|
|
Db 57 RPEDGG 62

RESULT 15
US-09-198-452A-612
; Sequence 612, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffalls, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 612
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-612

Query Match 26.1%; Score 6; DB 4; Length 183;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AEGAED 19
|
|
|
|
Db 155 AEGAED 160

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-09-853-253-5

Perfect score: 23

Sequence: 1 ALAGWLRPEDGGQAEAEDELEV 23

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Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 23 | 100.0 | 23 | AAE23840 | Human zsig33-linker |
| 2 | 23 | 100.0 | 23 | AAE23841 | Human zsig33-linker |
| 3 | 23 | 100.0 | 23 | AAE15885 | Human zsig33-linker |
| 4 | 23 | 100.0 | 23 | AAE15886 | Human zsig33-linker |
| 5 | 23 | 100.0 | 24 | AAE23839 | Human zsig33-linker |
| 6 | 23 | 100.0 | 24 | AAE15884 | Human zsig33-linker |
| 7 | 23 | 100.0 | 91 | AAE33410 | Human exon 3-delet |
| 8 | 23 | 100.0 | 116 | AAE60517 | Human des-Gln14-gh |
| 9 | 23 | 100.0 | 117 | AAW87991 | Protein designated |

| | | | | | | |
|----|----|-------|------|----|----------|--------------------|
| 10 | 23 | 100.0 | 117 | 21 | AAE87236 | Human signal pepti |
| 11 | 23 | 100.0 | 117 | 22 | AAE38890 | Human polypeptide |
| 12 | 23 | 100.0 | 117 | 22 | AAE62649 | Human zsig33 poly |
| 13 | 23 | 100.0 | 117 | 22 | AAE20101 | Zsig33 protein. H |
| 14 | 23 | 100.0 | 117 | 22 | AAE60511 | Human ghrelin prep |
| 15 | 23 | 100.0 | 117 | 23 | ABE78319 | Amino acid sequenc |
| 16 | 23 | 100.0 | 117 | 23 | AAE23838 | Human zsig33 prote |
| 17 | 23 | 100.0 | 117 | 23 | AAE15883 | Human zsig33 prote |
| 18 | 23 | 100.0 | 117 | 23 | AAE15883 | Human PRO polypept |
| 19 | 23 | 100.0 | 117 | 24 | ABU66790 | Human secreted/tra |
| 20 | 23 | 100.0 | 117 | 24 | ABU67066 | Novel secreted and |
| 21 | 23 | 100.0 | 117 | 24 | ABU59871 | Novel human secret |
| 22 | 23 | 100.0 | 117 | 24 | ABU59124 | Human secreted/tra |
| 23 | 23 | 100.0 | 117 | 24 | ABU59271 | Novel human secret |
| 24 | 23 | 100.0 | 117 | 24 | ABU59420 | Human secreted/tra |
| 25 | 23 | 100.0 | 117 | 24 | ABU60555 | Human PRO polypept |
| 26 | 23 | 100.0 | 117 | 24 | ABU58046 | Human secreted/tra |
| 27 | 23 | 100.0 | 117 | 24 | ABU58977 | Human secreted/tra |
| 28 | 23 | 100.0 | 117 | 24 | AAE33409 | Human preproghreli |
| 29 | 23 | 100.0 | 117 | 24 | ABU13937 | Human PRO1066 poly |
| 30 | 23 | 100.0 | 117 | 24 | ABU10892 | Human PRO polypept |
| 31 | 23 | 100.0 | 118 | 21 | AAE66708 | Membrane-bound pro |
| 32 | 23 | 100.0 | 118 | 22 | AAU12392 | Human PRO1066 poly |
| 33 | 23 | 100.0 | 118 | 22 | AAE65231 | Human PRO1066 (UNQ |
| 34 | 10 | 43.5 | 89 | 22 | AAE60523 | Human polypeptide |
| 35 | 8 | 34.8 | 334 | 21 | AAE29677 | Bovine ghrelin pre |
| 36 | 8 | 34.8 | 428 | 21 | AAE29676 | Arabidopsis thalia |
| 37 | 8 | 34.8 | 483 | 21 | AAE29675 | Arabidopsis thalia |
| 38 | 7 | 30.4 | 311 | 19 | AAW36129 | Snpr activator pro |
| 39 | 7 | 30.4 | 311 | 21 | AAE30494 | Amino acid sequenc |
| 40 | 7 | 30.4 | 442 | 23 | ABP38188 | Staphylococcus epi |
| 41 | 7 | 30.4 | 1931 | 22 | ABE66948 | Drosophila melanog |
| 42 | 6 | 26.1 | 14 | 22 | AAE66893 | Human peptide #168 |
| 43 | 6 | 26.1 | 26 | 24 | AAE33406 | PD-1-ctail2 peptid |
| 44 | 6 | 26.1 | 26 | 24 | ABJ18534 | PD-1-related pepti |
| 45 | 6 | 26.1 | 39 | 20 | AAE50239 | Neutrophil-activat |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | |
| AAE23840 | |
| ID | AAE23840 standard; peptide; 23 AA. |
| XX | |
| AC | AAE23840; |
| XX | |
| DT | 10-SEP-2002 (first entry) |
| XX | |
| DE | Human zsig33-linker peptide #2. |
| XX | |
| KW | Human; zsig33-like peptide; gastric contractility; nutrient uptake; |
| KW | growth hormone; digestive enzyme; restorative therapy; gene therapy; |
| KW | protein therapy; gastrointestinal; endocrine; anabolic. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | US2002055156-A1. |
| XX | |
| PD | 09-MAY-2002. |
| XX | |
| PF | 10-MAY-2001; 2001US-0853253. |
| XX | |
| PR | 11-MAY-2000; 2000US-203300P. |
| XX | |
| PA | (JASP/) JASPERS S R. |
| PA | (SHEP/) SHEPPARD P O. |
| PA | (DEIS/) DEISHER T A. |
| PA | (BISH/) BISHOP P D. |
| XX | |
| PI | Jaspers SR, Sheppard PO, Delsher TA, Bishop PD; |
| XX | |
| DR | WPI; 2002-443750/47. |

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
 PT contractility, nutrient uptake, growth hormones and/or secretion of
 PT digestive/pancreatic enzymes and hormones -
 PT
 XX
 PS Claim 1; Page 28; 34pp; English.
 XX
 CC The invention relates to zsig33-like peptides and their corresponding
 CC nucleic acids and methods for modulating gastric contractility, nutrient
 CC uptake, growth hormones, secretion of digestive enzymes and hormones.
 CC The sequences of the invention are used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate ZSIG33 expression.
 CC The nucleic acids of the invention and their complements are used as
 CC DNA probes in diagnostic assays to detect and quantitate the presence
 CC of similar nucleic acids in samples, and therefore which patients may be
 CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
 CC in the production of antibodies against ZSIG33 and in assays to identify
 CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
 CC and antagonists are used to down regulate expression and activity. The
 CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
 CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
 CC assay (ELISA)). The peptides and nucleic acids of the invention are used
 CC to modulate gastric contractility, nutrient uptake, growth hormones, the
 CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
 CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
 CC and zsig33-like peptide is used in protein therapy. The present sequence
 CC is human zsig33-like peptide, zsig33-linker peptide.
 XX

SQ Sequence 23 AA;

Query Match 100.0%; Score 23; DB 23; Length 23;

Best Local Similarity 100.0%; Pred. No. 5.9e-15;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQGAEGAEDELEV 23

DB 1 ALAGWLRPEDGGQGAEGAEDELEV 23

RESULT 2

AAE23841

ID AAE23841 standard; peptide; 23 AA.

XX AAE23841;

AC AAE23841;

DT 10-SEP-2002 (first entry)

DE Human zsig33-linker peptide #3.

XX Human; zsig33-like peptide; gastric contractility; nutrient uptake;
 KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
 KW protein therapy; gastrointestinal; endocrine; anabolic.

XX Homo sapiens.

XX US2002055156-A1.

XX 09-MAY-2002.

XX 10-MAY-2001; 2001US-0853253.

XX 11-MAY-2000; 2000US-203300P.

XX (JASP/) JASPERS S R.

PA (SHEP/) SHEPPARD P O.

PA (DEIS/) DEISHER T A.

PA (BISH/) BISHOP P D.

XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PB;
 XX WPI; 2002-443750/47.

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
 PT contractility, nutrient uptake, growth hormones and/or secretion of
 PT digestive/pancreatic enzymes and hormones -

PT contractility, nutrient uptake, growth hormones and/or secretion of
 PT digestive/pancreatic enzymes and hormones -
 PT
 PS Claim 1; Page 28; 34pp; English.
 XX

CC The invention relates to zsig33-like peptides and their corresponding
 CC nucleic acids and methods for modulating gastric contractility, nutrient
 CC uptake, growth hormones, secretion of digestive enzymes and hormones.
 CC The sequences of the invention are used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate ZSIG33 expression.
 CC The nucleic acids of the invention and their complements are used as
 CC DNA probes in diagnostic assays to detect and quantitate the presence
 CC of similar nucleic acids in samples, and therefore which patients may be
 CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
 CC in the production of antibodies against ZSIG33 and in assays to identify
 CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
 CC and antagonists are used to down regulate expression and activity. The
 CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
 CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
 CC assay (ELISA)). The peptides and nucleic acids of the invention are used
 CC to modulate gastric contractility, nutrient uptake, growth hormones, the
 CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
 CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
 CC and zsig33-like peptide is used in protein therapy. The present sequence
 CC is human zsig33-like peptide, zsig33-linker peptide.

SQ Sequence 23 AA;

Query Match 100.0%; Score 23; DB 23; Length 23;

Best Local Similarity 100.0%; Pred. No. 5.9e-15;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQGAEGAEDELEV 23

DB 1 ALAGWLRPEDGGQGAEGAEDELEV 23

RESULT 3

AAE15885

ID AAE15885 standard; peptide; 23 AA.

XX AAE15885;

AC AAE15885;

DT 26-MAR-2002 (first entry)

DE Human zsig33-linker peptide #2.

XX Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
 KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
 KW adsorption enhancer; gastrointestinal disease; growth related disease;
 KW inflammation; gene therapy; growth regulation; blood vessel formation;
 KW HIV; zsig33-linker peptide.

XX Homo sapiens.

XX WO200187933-A2.

XX 22-NOV-2001.

XX 10-MAY-2001; 2001WO-US15091.

XX 11-MAY-2000; 2000US-0569271.

XX (ZYMO) ZYMOGENETICS INC.

XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI; 2002-082982/11.

XX N-PSDB; AAD25760.

XX New polypeptides, useful for modulating gastric contractility, nutrient
 PT uptake, pancreatic secretion of hormones, digestive enzymes and
 PT treating gastrointestinal and growth related diseases, comprises


```

PT zsig33-like peptides -
XX Claim 1b; Page 81; 89pp; English.
XX
XX The invention relates to zsig33-like peptides (ZS33LP) including
CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and
CC zsig33-epsilon peptides and nucleic acid molecules encoding such
CC zsig33-like peptides. ZS33LP peptides activate the immune system
CC in boosting immunity to infectious diseases, treating immunocompromised
CC patients such as human immunodeficiency virus (HIV) patients, in
CC improving vaccines and in treatment of bacterial, viral, protozoal and
CC fungal infections. Peptides of the invention are used to identify and
CC isolate receptors involved in growth regulation in the liver, blood
CC vessel formation and other developmental processes. They are useful for
CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
CC growth and/or differentiation of tumour cells, as additives to anti-
CC hypoglycaemic preparations containing glucose and as adsorption
CC enhancers for oral drugs which require fast nutrient action and to
CC stimulate glucose-induced insulin release. They are also useful as
CC research reagents for the expansion, differentiation, growth factor and
CC hormone secretion and/or cell-cell interactions of tissues associated
CC with gastrointestinal system, brain and central nervous system. These
CC molecules are useful for treating dysfunction associated with contractile
CC tissues or to suppress or enhance contractility in vivo and to treat
CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
CC acids and/or antibodies are useful for treating disorders associated
CC with gastrointestinal contractility, secretion of digestive enzymes,
CC hormone and acids, secretion of hormones in the pancreas and/or brain,
CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
CC and regulation of nutrient absorption. Sequences of the invention are
CC useful in gene therapy. The present sequence is human zsig33-linker
CC peptide.
XX
XX Sequence 23 AA;
SQ
Query Match 100.0%; Score 23; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ALAGWLRLPEDGGGAEGAEDELEV 23
DB 1 ALAGWLRLPEDGGGAEGAEDELEV 23
|||||
RESULT 4
AAE15886
ID AAE15886 standard; peptide; 23 AA.
AC AAE15886;
XX
XX 26-MAR-2002 (first entry)
DT
DE Human zsig33-linker peptide #3.
XX
KW Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
KW adsorption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33-linker peptide.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 23 /note= "C-terminal amide"
FT
XX
XX W0200187933-A2.
PN
XX
XX 22-NOV-2001.
PD
XX
XX 10-MAY-2001; 2001WO-US15091.
PF
XX
XX 11-MAY-2000; 2000US-0569271.
PR

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(ZYMO) ZYMOGENETICS INC.

Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

WPI; 2002-082982/11.

N-PSDB; AAD25760.

New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises zsig33-like peptides -

Claim 1c; Page 82; 89pp; English.

The invention relates to zsig33-like peptides (ZS33LP) including zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and zsig33-epsilon peptides and nucleic acid molecules encoding such zsig33-like peptides. ZS33LP peptides activate the immune system in boosting immunity to infectious diseases, treating immunocompromised patients such as human immunodeficiency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and fungal infections. Peptides of the invention are used to identify and isolate receptors involved in growth regulation in the liver, blood vessel formation and other developmental processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic preparations containing glucose and as adsorption enhancers for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation, growth factor and hormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These molecules are useful for treating dysfunction associated with contractile tissues or to suppress or enhance contractility in vivo and to treat gastrointestinal and growth related diseases. ZS33LP peptides, nucleic acids and/or antibodies are useful for treating disorders associated with gastrointestinal contractility, secretion of digestive enzymes, hormone and acids, secretion of hormones in the pancreas and/or brain, gastrointestinal motility, recruitment of digestive enzymes, inflammation and regulation of nutrient absorption. Sequences of the invention are useful in gene therapy. The present sequence is human zsig33-linker peptide.

Query Match 100.0%; Score 23; DB 23; Length 23; Best Local Similarity 100.0%; Pred. No. 5.9e-15; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALAGWLRLPEDGGGAEGAEDELEV 23

DB 1 ALAGWLRLPEDGGGAEGAEDELEV 23

|||||

RESULT 5

AAE23839

ID AAE23839 standard; peptide; 24 AA.

XX AAE23839;

AC AAE23839;

XX

XX 10-SEP-2002 (first entry)

DT

DE Human zsig33-linker peptide #1.

XX

KW Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.

KW

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT

FT 7.18

FT XX. /note= "Hydrophilic region"
 PN US2002055156-A1.
 XX 09-MAY-2002.
 PD 10-MAY-2001; 2001US-0853253.
 XX 11-MAY-2000; 2000US-203300P.
 XX (JASP/) JASPERS S R.
 PA (SHEP/) SHEPPARD P O.
 PA (DEIS/) DEISHER T A.
 PA (BISH/) BISHOP P D.
 XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 PI WPI; 2002-443750/47.
 XX N-PSDB; AAD38239.
 DR ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
 PT contractility, nutrient uptake, growth hormones and/or secretion of
 PT digestive/pancreatic enzymes and hormones -
 XX
 PS Claim 1; Page 28; 34pp; English.
 XX The invention relates to zsig33-like peptides and their corresponding
 CC nucleic acids and methods for modulating gastric contractility, nutrient
 CC uptake, growth hormones, secretion of digestive enzymes and hormones.
 CC The sequences of the invention are used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate ZSIG33 expression.
 CC The nucleic acids of the invention and their complements are used as
 CC DNA probes in diagnostic assays to detect and quantitate the presence
 CC of similar nucleic acids in samples, and therefore which patients may be
 CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
 CC in the production of antibodies against ZSIG33 and in assays to identify
 CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
 CC and antagonists are used to down regulate expression and activity. The
 CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
 CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
 CC assay (ELISA)). The peptides and nucleic acids of the invention are used
 CC to modulate gastric contractility, nutrient uptake, growth hormones, the
 CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
 CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
 CC and zsig33-like peptide is used in protein therapy. The present sequence
 CC is human zsig33-like peptide, zsig33-linker peptide.
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 23; DB 23; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.1e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAEAEDELEV 23
 Db 1 ALAGWLRPEDGGQAEAEDELEV 23
 RESULT 6
 AAE15884
 ID AAE15884 standard; peptide; 24 AA.
 AC AAE15884;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX Human zsig33-linker peptide #1.
 DE
 XX Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
 KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
 KW adsorption enhancer; gastrointestinal disease; growth related disease;
 KW inflammation; gene therapy; growth regulation; blood vessel formation;
 KW HIV; zsig33-linker peptide.

XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Region 6..22
 FT /note= "Hydrophilic antigenic site"
 FT Region 7..18
 FT /note= "Hydrophilic region"
 XX
 PN WO200187933-A2.
 XX
 XX 22-NOV-2001.
 PD
 XX
 XX 10-MAY-2001; 2001WO-US15091.
 XX
 XX 11-MAY-2000; 2000US-0569271.
 PR (ZYMO) ZYMOGENETICS INC.
 XX
 XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 PI WPI; 2002-082982/11.
 DR N-PSDB; AAD25760.
 DR
 XX
 XX New polypeptides, useful for modulating gastric contractility, nutrient
 PT uptake, pancreatic secretion of hormones, digestive enzymes and
 PT treating gastrointestinal and growth related diseases, comprises
 PT zsig33-like peptides -
 XX
 PS Claim 1a; Page 81; 89pp; English.
 XX The invention relates to zsig33-like peptides (ZS33LP) including
 CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and
 CC zsig33-epsilon peptides and nucleic acid molecules encoding such
 CC zsig33-like peptides. ZS33LP peptides activate the immune system
 CC in boosting immunity to infectious diseases, treating immunocompromised
 CC patients such as human immunodeficiency virus (HIV) patients, in
 CC improving vaccines and in treatment of bacterial, viral, protozoal and
 CC fungal infections. Peptides of the invention are used to identify and
 CC isolate receptors involved in growth regulation in the liver, blood
 CC vessel formation and other developmental processes. They are useful for
 CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
 CC growth and/or differentiation of tumour cells, as additives to anti-
 CC hypoglycaemic preparations containing glucose and as adsorption
 CC enhancers for oral drugs which require fast nutrient action and to
 CC stimulate glucose-induced insulin release. They are also useful as
 CC research reagents for the expansion, differentiation, growth factor and
 CC hormone secretion and/or cell-cell interactions of tissues associated
 CC with gastrointestinal system, brain and central nervous system. These
 CC molecules are useful for treating dysfunction associated with contractile
 CC tissues or to suppress or enhance contractility in vivo and to treat
 CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
 CC acids and/or antibodies are useful for treating disorders associated
 CC with gastrointestinal contractility, secretion of digestive enzymes,
 CC hormone and acids, secretion of hormones in the pancreas and/or brain,
 CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
 CC and regulation of nutrient absorption. Sequences of the invention are
 CC useful in gene therapy. The present sequence is human zsig33-linker
 CC peptide.
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 23; DB 23; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.1e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAEAEDELEV 23
 Db 1 ALAGWLRPEDGGQAEAEDELEV 23
 RESULT 7
 AAE33410

ID AAE33410 standard; Protein: 91 AA.
 XX AC AAE33410;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human exon 3-deleted ghrelin protein.
 XX
 KW Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
 KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
 KW cancer; human.
 OS Homo sapiens.
 XX
 PN WO200290387-A1.
 XX
 PD 14-NOV-2002.
 XX
 PF 10-MAY-2002; 2002WO-AU00582.
 XX
 PR 10-MAY-2001; 2001AU-0004919.
 XX
 PR 17-DEC-2001; 2001AU-0009567.
 XX
 PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 PI Chopin LK, Jeffery PL, Herington AC;
 XX
 DR WPI: 2003-1111957/10.
 DR N-PSDB; AAD50726.
 XX
 PT Identifying a cancer cell or tissue for treating prostate, ovarian,
 PT breast cancer, or benign prostatic hyperplasia, by detecting the
 PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
 PT 1b proteins or nucleic acids -
 XX
 PS Claim 14; Page 34; 50pp; English.
 XX
 CC The invention relates to a method for identifying a cancer cell or
 CC tissue of the reproductive system by detecting expression of a ghrelin,
 CC an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic
 CC acids. The antibodies, exon 3-deleted form of preproghrelin and
 CC antagonists are useful for treating cancer of the reproductive system
 CC such as prostate, ovarian, breast, cervical or uterine cancer,
 CC choriocarcinoma or benign prostatic hyperplasia. The present sequence
 CC is human exon 3-deleted ghrelin protein.
 XX
 SQ Sequence 91 AA;
 Query Match 100.0%; Score 23; DB 24; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 8
 AAB60517
 ID AAB60517 standard; Protein: 116 AA.
 XX
 AC AAB60517;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
 XX
 KW Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX

PN WO200107475-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-JP04907.
 XX
 PR 23-JUL-1999; 99JP-0210002.
 PR 29-NOV-1999; 99JP-0338841.
 PR 26-APR-2000; 2000JP-0126623.
 XX
 PA (KANG/) KANGAWA K.
 XX
 PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 XX
 DR WPI: 2001-1159704/16.
 DR N-PSDB; AAF59647.
 XX
 PT New peptide compounds which induce growth hormone secretion and
 PT elevate cell calcium concentrations, useful in treatment and diagnosis
 PT of infant growth disorders -
 XX
 PS Claim 3; Page 186-187; 210pp; Japanese.
 XX
 CC The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX
 SQ Sequence 116 AA;
 Query Match 100.0%; Score 23; DB 22; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 51 ALAGWLRPEDGGQAGAEDELEV 73
 RESULT 9
 AAW87991
 ID AAW87991 standard; Protein: 117 AA.
 XX
 AC AAW87991;
 XX
 DT 07-APR-1999 (first entry)
 XX
 DE Protein designated zsig33.
 XX
 KW Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
 KW nutrient absorption regulation; obesity; metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT Protein /note= "signal peptide"
 FT /note= "mature protein"
 XX

PN W09842840-A1.
 XX 01-OCT-1998.
 XX 23-MAR-1998; 98WO-US05620.
 XX 24-MAR-1997; 97US-0822897.
 XX 24-MAR-1997; 97US-0041102.
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Delsler TA, Sheppard PO;
 PI WPI; 1999-070071/06.
 DR N-PSDB; AAX04550.
 XX
 XX Human polypeptide having homology to motilin, zsi933 - useful e.g.
 PT to treat gastrointestinal motility disorders, obesity etc. and to
 PT identify antagonists to treat gastrointestinal hypermotility
 XX
 XX Claim 13; Page 55-56; 69pp; English.
 XX
 CC The present sequence represents a protein designated Zsi933. The nucleic
 CC acids are strongly expressed in stomach tissue. The polypeptide (or
 CC allelic variants/orthologs) can be used to stimulate gastric motility,
 CC measured as increased transit time or gastric emptying of an ingested
 CC substance in mammals. The products are used to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes/acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
 CC absorption regulation. Zsi933 polypeptides may also be important
 CC neurologically, since the family of gut-brain peptides to which the
 CC homologous protein motilin belongs has been associated with neurological
 CC and CNS functions. They may therefore be used e.g. to regulate satiety
 CC or treat obesity and other metabolic disorders where neurological
 CC feedback modulates nutritional absorption. They are useful to identify
 CC zsi933 agonists, antagonists and ligands and to produce antibodies.
 XX
 XX Sequence 117 AA;
 XX
 Query Match 100.0%; Score 23; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRLPEDGGQAGAEDELEV 23
 |||||
 DB 52 ALAGWLRLPEDGGQAGAEDELEV 74
 RESULT 10
 AAY87236
 ID AAY87236 standard; Protein; 117 AA.
 XX
 AC AAY87236;
 XX
 XX 11-MAY-2000 (first entry)
 XX
 XX Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
 XX
 KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiaesthmic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 XX W0200000610-A2.
 PN
 XX

PD 06-JAN-2000.
 XX 25-JUN-1999; 99WO-US14484.
 XX 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX (INCY-) INCYTE PHARM INC.
 XX
 XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX
 DR WPI; 2000-160673/14.
 DR N-PSDB; AAZ98121.
 XX
 XX New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease -
 PT
 XX
 PS Claim 1; Page 168-169; 327pp; English.
 XX
 CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
 CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiaesthmic activities, and can
 CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPP. Antagonists of
 CC HSPP are used to treat or prevent disorders associated with increased
 CC activity or function of HSPP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
 CC nucleic acids can be used for the recombinant production of HSPP, for
 CC detecting HSPP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPP
 CC from natural sources.
 XX
 XX Sequence 117 AA;
 XX
 Query Match 100.0%; Score 23; DB 21; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRLPEDGGQAGAEDELEV 23
 |||||
 DB 52 ALAGWLRLPEDGGQAGAEDELEV 74
 RESULT 11
 AAM38890
 ID AAM38890 standard; Protein; 117 AA.
 XX
 AC AAM38890;
 XX
 XX 22-OCT-2001 (first entry)
 XX
 XX Human polypeptide SEQ ID NO 2035.
 DE
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX Homo sapiens.
 OS WO200153312-A1.
 PN 26-JUL-2001.
 PD 26-DEC-2000; 2000WO-US34263.
 PF 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX WPI: 2001-442253/47.
 DR N-PSDB; AAI58046.
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 PS Example 3; SEQ ID NO 2035; 10078pp; English.
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytosstatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX Sequence 117 AA;
 SQ
 Query Match 100.0%; Score 23; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 12
 AAB62649
 ID AAB62649 standard; Protein; 117 AA.
 XX AAB62649;
 AC
 XX 23-JUL-2001 (first entry)
 DT
 XX Human zsig33 polypeptide.
 DE
 XX

KW zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R;
 KW G-protein coupled receptor.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 24..37
 FT /note= "specifically claimed fragment that binds to
 FT the GHS-R"
 XX WO200138355-A2.
 PN 31-MAY-2001.
 PD 22-NOV-2000; 2000WO-US32074.
 PF 22-NOV-1999; 99US-0166765.
 PR 22-NOV-1999;
 XX (ZYMO) ZYMOGENETICS INC.
 PA Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 PI WPI: 2001-355879/37.
 DR N-PSDB; AAF83678.
 DR Forming reversible peptide receptor complex for purifying cell and
 PT peptides, stimulating signal transduction and modulating hormone
 PT secretion, involves contacting a receptor with zsig33 polypeptide -
 XX Claim 1; Page 93-94; 111pp; English.
 PS The invention relates to a method of forming a reversible peptide-
 CC receptor complex that involves providing an immobilized receptor, and
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
 CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
 CC is useful for purifying cells, purifying a peptide, stimulating signal
 CC transduction in a cell expressing a receptor. It is also useful for
 CC modulating secretion of hormones, neural development and/or utilization,
 CC gastric contractility, nutrient uptake, secretion of digestive and
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
 CC hormone secretion in a mammal having a disease associated with abnormal
 CC levels of growth hormone, such as osteoporosis, bone repair, bone
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,
 CC protein catabolic responses after surgery, cachexia, protein loss,
 CC dwarfism, wound healing and ovulation induction, treating a mammal having
 CC a metabolic disorder requiring neurological feedback, such as satiety
 CC regulation, glucose absorption and metabolism and neuropathy-associated
 CC gastrointestinal disorders, and stimulating glucose-induced insulin
 CC release in a mammal. The present sequence represents the human zsig33
 CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
 XX Sequence 117 AA;
 SQ
 Query Match 100.0%; Score 23; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 13
 AAB20101
 ID AAB20101 standard; Protein; 117 AA.
 XX
 AC AAB20101;
 XX

DT 23-APR-2001 (first entry)
 XX Zsig33 protein.
 DE
 XX SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
 KW nutritional absorption modulator; growth hormone secretagogue;
 KW therapy; human.
 XX
 OS Homo sapiens.
 XX
 FH Location/Qualifiers
 XX
 FT Peptide
 FT 1..23
 FT /label= Signal_peptide
 FT Protein
 FT 24..117
 FT /label= Mature_protein
 FT Peptide
 FT 24..34
 FT /label= SGIP_peptide
 FT /note= "this peptide is claimed in Claim 1"
 XX
 PN WO200100830-A1.
 XX
 PN 04-JAN-2001.
 XX
 PF 30-JUN-2000; 2000WO-US18306.
 XX
 PR 30-JUN-1999; 99US-0345157.
 XX
 XX (ZVMO) ZYMOGENETICS INC.
 XX
 PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 XX
 DR WPI: 2001-123010/13.
 DR N-PSDB; AAF30033.
 XX
 XX Novel variants of SGIP peptides for modulating contractility in
 PT duodenum or jejunum tissue, pancreatic secretion of hormones and
 PT digestive enzymes, inducing growth hormone secretion or modulating
 PT gastric emptying -
 XX
 XX Disclosure; 54; 61pp; English.
 PS
 CC The present sequence is that of zsig33, a secreted protein with
 CC homology to motilin (see AAB20102). Zsig33 is expressed at high
 CC levels in the stomach, and at lower levels in the small intestine
 CC and pancreas. A novel peptide fragment of zsig33, termed SGIP (see
 CC AAB20100), is claimed. SGIP is a ligand for growth hormone
 CC secretagogue receptor, and is therefore useful for modulating
 CC secretion of growth hormone and insulin like growth factor 1.
 CC SGIP, and variant SGIP peptides, are used in claimed methods for
 CC stimulating contractility in duodenum or jejunum tissue,
 CC modulating pancreatic secretion of hormones and digestive enzymes,
 CC inducing growth hormone secretion, and modulating gastric emptying.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 23; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 14
 AAB50511
 ID AAB60511 standard; Protein; 117 AA.
 XX
 AC AAB60511;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human ghrelin preproprotein, SEQ ID NO:5.

XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX
 PN WO200107475-A1.
 XX
 PN 01-FEB-2001.
 XX
 PD 24-JUL-2000; 2000WO-JF04907.
 XX
 PF 23-JUL-1999; 99JP-0210002.
 XX
 PR 29-NOV-1999; 99JP-0338841.
 PR
 PR 26-APR-2000; 2000JP-0126623.
 XX
 XX (KANG/) KANGAWA K.
 PA
 XX
 XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 PI
 PI WPI: 2001-159704/16.
 XX
 DR N-PSDB; AAF59645.
 DR
 XX New peptide compounds which induce growth hormone secretion and
 PT elevate cell calcium concentrations, useful in treatment and diagnosis
 PT of infant growth disorders -
 PT
 XX
 PS Claim 3; Page 182; 210pp; Japanese.
 XX
 CC The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 23; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 15
 ABB78319
 ID ABB78319 standard; Protein; 117 AA.
 XX
 XX ABB78319;
 AC
 XX
 DT 05-DEC-2002 (first entry)
 XX
 DE Amino acid sequence of a human zsig33.
 XX
 KW Short gastrointestinal peptide; SGIP; zsig33; motilin.
 XX
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
FT Peptide 1..23
FT /note= "signal peptide"
FT Protein 24..119
FT /note= "mature protein"
XX
PN US6420521-B1.
XX
PD 16-JUL-2002.
XX
PF 30-JUN-2000; 2000US-0608810.
XX
PR 30-JUN-1999; 99US-141592P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
DR WPI: 2002-634794/68.
DR N-PSDB; ABV72214.
XX
PT New Short Gastrointestinal Peptide, which has homology to motilin,
PT useful for preventing, diagnosing and treating gastrointestinal
PT disorders -
XX
PS Disclosure; Columns 39-40; 23pp; English.
XX
CC The present sequence represents human zsig33. The specification describes
CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.
CC SGIP has homology to motilin. The SGIP peptide may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate SGIP expression. For example, SGIP may be used to treat
CC disorders associated with decreased expression by rectifying mutations
CC or deletions in a patient's genome that affect the activity of SGIP by
CC expressing inactive proteins or to supplement the patients own production
CC of SGIP. SGIP may also be used as an antigen in the production of
CC antibodies against SGIP and in assays to identify modulators of SGIP
CC expression and activity. The anti-SGIP antibodies, agonists and
CC antagonists may also be used to regulate expression and activity. The
CC anti-SGIP antibodies may also be used as diagnostic agents for detecting
CC the presence of SGIP in samples.
XX
SQ Sequence 117 AA;
Query Match 100.0%; Score 23; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-14; Mismatches 0; Gaps 0;
Matches 23; Conservative 0; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDGGQAGAEDELEV 23
DB 52 ALAGWLRPEDGGQAGAEDELEV 74

Search completed: September 11, 2003, 17:51:54
Job time : 24.2299 secs

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 : Search time 22.8449 Seconds
(without alignments)
271.100 Million cell updates/sec

Title: US-09-853-253-4
Perfect score: 126
Sequence: 1 ALAGWLRPEDGGQAGAEDELEVR 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | ID | Description |
|------------|-------|-------------|---------------|--------------------|
| 1 | 124 | 98.4 | 117 4 Q8TAT9 | Q8tat9 homo sapien |
| 2 | 97 | 77.0 | 117 11 Q8CH53 | Q8ch53 meriones un |
| 3 | 59 | 46.8 | 1208 5 Q8I5T3 | Q8i5t3 plasmodium |
| 4 | 59 | 46.8 | 1264 5 Q9U445 | Q9u445 plasmodium |
| 5 | 55 | 43.7 | 183 10 Q8NL6 | Q8nl6 oryza sativ |
| 6 | 53 | 42.1 | 202 15 Q90P58 | Q90p58 human immun |
| 7 | 53 | 42.1 | 1228 5 Q27724 | Q27724 plasmodium |
| 8 | 52 | 41.3 | 201 15 Q90P50 | Q90p50 human immun |
| 9 | 52 | 41.3 | 232 16 Q9I6L1 | Q9i6l1 pseudomonas |
| 10 | 52 | 41.3 | 249 12 Q82036 | Q82036 hiram rhab |
| 11 | 52 | 41.3 | 392 12 Q9L89 | Q9l89 hiram rhab |
| 12 | 52 | 41.3 | 977 6 Q9S169 | Q9s169 capra hircu |
| 13 | 51.5 | 40.9 | 436 5 Q9N638 | Q9n638 caenorhabdi |
| 14 | 51 | 40.5 | 158 16 Q8XW90 | Q8xw90 ralstonia s |
| 15 | 51 | 40.5 | 201 15 Q90NL5 | Q90nl5 human immun |
| 16 | 51 | 40.5 | 604 16 Q8UFA5 | Q8ufa5 agrobacteri |

| | | | | | | |
|----|------|------|-----|----|--------|--------------------|
| 17 | 51 | 40.5 | 609 | 2 | Q9RH77 | Q9rh77 bradyrhizob |
| 18 | 50 | 39.7 | 131 | 16 | Q9RV90 | Q9rv90 deinococcus |
| 19 | 50 | 39.7 | 202 | 15 | Q90P76 | Q90p76 human immun |
| 20 | 50 | 39.7 | 202 | 15 | Q90P77 | Q90p77 human immun |
| 21 | 50 | 39.7 | 472 | 10 | Q8LRD5 | Q8lrd5 oryza sativ |
| 22 | 50 | 39.7 | 582 | 6 | Q9XSP0 | Q9xsp0 capra hircu |
| 23 | 50 | 39.7 | 582 | 6 | Q9GLE4 | Q9gle4 bos taurus |
| 24 | 49.5 | 39.3 | 484 | 16 | Q9RZ17 | Q9rz17 deinococcus |
| 25 | 49 | 38.9 | 201 | 15 | Q90P55 | Q90p55 human immun |
| 26 | 49 | 38.9 | 201 | 15 | Q90NK8 | Q90nk8 human immun |
| 27 | 49 | 38.9 | 286 | 12 | Q8QRU5 | Q8qr5 chimpanzee |
| 28 | 48.5 | 38.5 | 110 | 10 | Q93VB3 | Q93vb3 oryza sativ |
| 29 | 48.5 | 38.5 | 172 | 2 | Q9RBY2 | Q9rby2 pseudomonas |
| 30 | 48.5 | 38.5 | 172 | 2 | Q9R2S2 | Q9r2s2 pseudomonas |
| 31 | 48.5 | 38.5 | 269 | 2 | Q9ETM8 | Q9etm8 pseudomonas |
| 32 | 48 | 38.1 | 106 | 16 | Q8ELH4 | Q8elh4 oceanobacil |
| 33 | 48 | 38.1 | 115 | 10 | Q8LI79 | Q8li79 oryza sativ |
| 34 | 48 | 38.1 | 120 | 15 | Q78494 | Q78494 human immun |
| 35 | 48 | 38.1 | 201 | 15 | Q90P53 | Q90p53 human immun |
| 36 | 48 | 38.1 | 201 | 15 | Q90NL3 | Q90nl3 human immun |
| 37 | 48 | 38.1 | 201 | 15 | Q90NL6 | Q90nl6 human immun |
| 38 | 48 | 38.1 | 201 | 15 | Q90NLO | Q90nlo human immun |
| 39 | 48 | 38.1 | 201 | 15 | Q90NLI | Q90nli human immun |
| 40 | 48 | 38.1 | 201 | 15 | Q90NM1 | Q90nm1 human immun |
| 41 | 48 | 38.1 | 201 | 15 | Q90NM2 | Q90nm2 human immun |
| 42 | 48 | 38.1 | 201 | 15 | Q90NL9 | Q90nl9 human immun |
| 43 | 48 | 38.1 | 202 | 15 | Q90P31 | Q90p31 human immun |
| 44 | 48 | 38.1 | 202 | 15 | Q90P37 | Q90p37 human immun |
| 45 | 48 | 38.1 | 211 | 10 | Q943L4 | Q943l4 oryza sativ |

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY; PRT; 117 AA.
 AC Q8TAT9
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Ghrelin.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025791; AAH25791.1; -
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR Pfam; PF04643; motilin_assoc.1.
 DR Pfam; PF04644; motilin_ghrelin.1.
 SQ SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;

Query Match 98.4%; Score 124; DB 4; Length 117;
 Best Local Similarity 95.8%; Pred. No. 3.5e-10;
 Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 |||||
 DB 52 ALAGWLRPEDGGQAGAEDEMEVR 75

RESULT 2

Q8CH53 PRELIMINARY; PRT; 117 AA.
 AC Q8CH53;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)

```

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AAC06965.1; -.
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 77.08; Score 97; DB 11; Length 117;
Best Local Similarity 75.08; Pred. No. 2.6e-06;
Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEVR 24
II III I: |||||IIIIII:
Db 52 ALEGWLRHPDGGGAEGAEDELEIR 75

RESULT 3
Q815T3 ID Q815T3 PRELIMINARY; PRT; 1208 AA.
AC Q815T3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P-type ATPase, putative.
GN PFL0590C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Perteaux M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.W., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014846; AAN36207.1; -.
SQ SEQUENCE 1208 AA; 133873 MW; 25AA7752E707E621 CRC64;

Query Match 46.88; Score 59; DB 5; Length 1208;
Best Local Similarity 52.68; Pred. No. 9;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGGAEGAEDELE 22
II III: :I ||||
Db 1072 GWCRPKDNKTSQGYNDELE 1090

RESULT 4
Q9U445 ID Q9U445 PRELIMINARY; PRT; 1264 AA.
AC Q9U445;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P-type ATPase4.

```

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GN ATPASE4.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Krishna S., Woodrow C., Webb R., Penny J., Takeyasu K., Kimura M.,
RA East J.M.;
RT "Expression and Functional Characterization of a Plasmodium falciparum
RT Ca2+-ATPase (PfATP4) Belonging to a Subclass Unique to Apicomplexan
RT Organisms.";
RL J. Biol. Chem. 276:10782-10787(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
CC ATPASES).
DR EMBL; AF203980; AAF17245.1; -.
DR HSSP; P04191; IEUL.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 5.
DR PROSITE; PS00154; ATPASE_E1-E2; 1.
KW ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SQ SEQUENCE 1264 AA; 140261 MW; 638142BB1B433640 CRC64;

Query Match 46.88; Score 59; DB 5; Length 1264;
Best Local Similarity 52.68; Pred. No. 9.4;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGGAEGAEDELE 22
II III: :I ||||
Db 1128 GWCRPKDNKTSQGYNDELE 1146

RESULT 5
Q8LNL6 ID Q8LNL6 PRELIMINARY; PRT; 183 AA.
AC Q8LNL6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OSJNBA0071120.2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA McCombie W.R., Spiegel L., de la Bastide M., Preston R., Ferraro K.,
RA Kuit K., Nascimento L., Zutavern T., Ballia V., Bell M., Baker J.,
RA Miller B., Katzenberger F., Muller S., King L., Sullivan P., Yang C.,
RA Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone
RT OSJNba0071120, from chromosome 10, complete sequence.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC074355; AAM74240.1; -.
DR Gramene; Q8LNL6; -.
KW Hypothetical protein.
SQ SEQUENCE 183 AA; 20492 MW; DE73BD8607292D7B CRC64;

Query Match 43.78; Score 55; DB 10; Length 183;
Best Local Similarity 47.68; Pred. No. 4.6;
Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

```

```
QY 3 AGWLRPEDGGQGAEGAEDELEV 23
   ||| ||| | | | |
Db 53 AGWIETEDGSDSESDSEV 73

RESULT 6
Q90P58 PRELIMINARY; PRT; 202 AA.
AC Q90P58;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Nickle D.C.;
RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF370911; AAK66310.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 22572 MW; 4CB8ACAFBF14314 CRC64;

Query Match 42.1%; Score 53; DB 15; Length 202;
Best Local Similarity 45.5%; Pred. No. 9.9;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQGAEGAEDELEV 23
   : | | | | | | | |
Db 180 ITGLLLTRDGGGQGDGTSETV 201

RESULT 7
Q27724 PRELIMINARY; PRT; 1228 AA.
AC Q27724;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P-type ATPase.
GN PFATPASE4.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=96408665; PubMed=8813672;
RA Dyer M., Jackson M., McWhinney C., Zhao G., Mikkelsen R.;
RT "Analysis of a cation-transporting ATPase of Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 78:1-12(1996).
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES).
CC EMBL: U39298; AAC47167.1; -
DR HSSP: P04131; IEUL.
DR InterPro: IPR001757; ATPase_E1-E2.
DR InterPro: IPR006068; Cation_ATPase_C.
DR InterPro: IPR004014; Cation_ATPase_N.
DR InterPro: IPR005834; Hydrolyase.
DR InterPro: IPR000695; H_ATPase.
DR Pfam: PF00689; Cation_ATPase_C; 1.
DR Pfam: PF00690; Cation_ATPase_N; 1.
DR Pfam: PF00122; E1-E2_ATPase; 1.
DR Pfam: PF00702; Hydrolyase; 1.
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DR PRINTS; PRO0119; CATATPASE.
DR PRINTS; PRO0120; HATPASE.
DR TIGRFS; TIGR01494; ATPase_P-type; 5.
DR PROSITE; PS00154; ATPASE_E1-E2; 1.
KW ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SQ SEQUENCE 1228 AA; 135989 MW; 32C3CFD324964CBE CRC64;

Query Match 42.1%; Score 53; DB 5; Length 1228;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 WLRPEDGGQGAEGAEDELE 22
   | | | | |
Db 1131 WCRPKDNKTSQDYNDELE 1148

RESULT 8
Q90P50 PRELIMINARY; PRT; 201 AA.
AC Q90P50;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Nickle D.C.;
RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF370919; AAK66318.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 201
SQ SEQUENCE 201 AA; 22550 MW; 6CAF6C460A9BA517 CRC64;

Query Match 41.3%; Score 52; DB 15; Length 201;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQGAEGAEDELEV 23
   : | | | | | | | |
Db 179 ITGLLLTRDGGGQGDGTNETEV 200

RESULT 9
Q916L1 PRELIMINARY; PRT; 232 AA.
AC Q916L1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Probable transcriptional regulator.
GN PA0279.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.;
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
```

RT *Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RL opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 CC -1- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL: AE004466; AAC03668.1; -.
 DR InterPro: IPR001845; HTH_ArsR.
 DR Pfam: PF01022; HTH_5; 1.
 DR PRINTS: PR00778; HTHARSR.
 DR SMART: SM00418; HTH_ArsR; 1.
 KW DNA-binding; Transcription regulation; Complete proteome.
 SQ SEQUENCE 232 AA; 24440 MW; E3C29187694CF936 CRC64;

Query Match 41.3%; Score 52; DB 16; Length 232;
 Best Local Similarity 72.7%; Pred. No. 16;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GWLRPDGGQA 14
 Db 202 GWLRPDGSGRA 212
 |||||: ||: |

RESULT 10

Q82036 PRELIMINARY; PRT; 249 AA.
 AC Q82036;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Nucleocapsid protein.
 GN N.
 OS Hirame rhabdovirus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Novirhabdovirus.
 OX NCBI_TaxID=38142;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8401-H;
 RA Nishizawa T.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D45422; BAA08261.1; -.
 DR InterPro: IPR004902; Rhabdo_ncap_2.
 DR Pfam: PF03216; Rhabdo_ncap_2; 1.
 SQ SEQUENCE 249 AA; 26936 MW; 62FF2BFA5D47DB89 CRC64;

Query Match 41.3%; Score 52; DB 12; Length 249;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 EDGGQAEAGDE 20
 Db 235 EDGEGEGGEDE 246
 |||||: || |||

RESULT 11

Q90L89 PRELIMINARY; PRT; 392 AA.
 AC Q90L89;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Nucleocapsid protein.
 GN N.
 OS Hirame rhabdovirus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Novirhabdovirus.
 OX NCBI_TaxID=38142;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CA 9703;
 RA Oh H.K., Choi T.J.;
 RL Submitted (NOV-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF104985; AAF14116.1; -.

DR InterPro: IPR004902; Rhabdo_ncap_2.
 DR Pfam: PF03216; Rhabdo_ncap_2; 1.
 SQ SEQUENCE 392 AA; 42465 MW; C5A282238FC7A638 CRC64;

Query Match 41.3%; Score 52; DB 12; Length 392;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 EDGGQAEAGDE 20
 Db 378 EDGEGEGGEDE 389
 |||||: || |||

RESULT 12

Q95169 PRELIMINARY; PRT; 977 AA.
 AC Q95169;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Skeletal muscle voltage-gated chloride channel gC1c-1 (Fragment).
 DE Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97008165; PubMed=8855341;
 RA Beck C.L., Fahke C., George A.L.;
 RT "Molecular basis for decreased muscle chloride conductance in the
 RT myotonic goat.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:11248-11252(1996).
 DR EMBL: U60275; AAC48666.1; -.
 DR InterPro: IPR000644; CBS_domain.
 DR InterPro: IPR001807; Cl-channel_volt.
 DR InterPro: IPR005829; Sug_transporter.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00654; voltage_CLC; 1.
 DR PRINTS: PR00762; CLCHANNEL.
 DR PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 977 AA; 107894 MW; 1E462B3CB307A148 CRC64;

Query Match 41.3%; Score 52; DB 6; Length 977;
 Best Local Similarity 62.5%; Pred. No. 73;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWLRPDGGQAEAGD 19
 Db 895 GWSLPEDGAGATGAGD 910
 || |||||: || |||

RESULT 13

Q9N638 PRELIMINARY; PRT; 436 AA.
 AC Q9N638;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE F37D6.6 protein.
 GN F37D6.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilkinson J.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;

RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; 279600; CAB70221.1; -;
DR EMBL; 275540; CAB70221.1; JOINED.
DR EMBL; 275540; CAB70215.1; -;
DR EMBL; 275540; CAB70215.1; JOINED.
DR WormPep; F37D6.6; CE24960.
DR InterPro; IPR001132; DwarfIn.
DR InterPro; IPR003619; DwarfIn_A.
DR Pfam; PF03166; MH2; 1.
DR SMART; SM00523; DMB; 1.
DR SMART; SM00524; DMB; 1.
SQ SEQUENCE 436 AA; 49496 MW; E0C71263BC580FEE CRC64;

Query Match 40.9%; Score 51.5; DB 5; Length 436;
Best Local Similarity 52.9%; Pred. No. 37;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
QY 5 WLRPE-DGGQAGAEDE 20
I:III :II :I:II:
DB 169 WIRPETNGDDGSEDK 185

RESULT 14
QBXX90
ID QBXX90 PRELIMINARY; PRT; 158 AA.
AC QBXX90;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein RSC2585.
GN RSC2585 OR RS00797.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
Siguler P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
RL Nature 415:497-502(2002).
DR EMBL; AL646070; CAD16292.1; -;
DR InterPro; IPR002145; HTH_CopG.
DR Pfam; PF01402; HTH 4; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 158 AA; 17814 MW; C9BA42BF9C10E1BC CRC64;

Query Match 40.5%; Score 51; DB 16; Length 158;
Best Local Similarity 58.8%; Pred. No. 15;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDDGQAGGA 17
III I I I I I
DB 36 ALASWLSPDAGDQREAA 52

RESULT 15
Q90NL5
ID Q90NL5 PRELIMINARY; PRT; 201 AA.
AC Q90NL5;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Nickle D.C.;
RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF371104; AAK66503.1; -;
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein.
KW NON_TER 1
FT NON_TER 1 201
SQ SEQUENCE 201 AA; 22470 MW; E1993A2A412EC118 CRC64;
Query Match 40.5%; Score 51; DB 15; Length 201;
Best Local Similarity 40.9%; Pred. No. 19;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
QY 2 LAGWLRPEDDGQAGAEDELEV 23
I:III :II :I:II:
DB 179 ITGLLLTTRDGGGNGTNDNETEI 200
Search completed: September 11, 2003, 17:30:27
Job time : 25.8449 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 3.46524 Seconds
(without alignments)
325.703 Million cell updates/sec

Title: US-09-853-253-4

Perfect score: 126

Sequence: 1 ALAGWLPRDPGQAEAELEVR 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|---------------------|
| 1 | 126 | 100.0 | 117 | GHRL_HUMAN | Q9ub33 homo sapien |
| 2 | 95 | 75.4 | 117 | GHRL_RAT | Q9qyh7 rattus norv |
| 3 | 92 | 73.0 | 118 | GHRL_PIG | Q9gky5 sus scrofa |
| 4 | 91 | 72.2 | 117 | GHRL_MOUSE | Q9eqx0 mus musculus |
| 5 | 77 | 61.1 | 116 | GHRL_BOVIN | Q9bdj6 bos taurus |
| 6 | 73 | 57.9 | 117 | GHRL_CANFA | Q9bef8 canis famil |
| 7 | 54 | 42.9 | 200 | NUPF_XENLA | P05221 xenopus lae |
| 8 | 51 | 40.5 | 91 | ACYP_BACSU | Q03031 bacillus su |
| 9 | 50 | 39.7 | 653 | APPL_MOUSE | Q03157 mus musculus |
| 10 | 49 | 38.9 | 300 | NRX1_BISBI | Q06383 bison bison |
| 11 | 49 | 38.9 | 1216 | NRX1_BOVIN | Q28139 bos taurus |
| 12 | 48 | 38.1 | 668 | SYM_METKA | P05019 homo sapien |
| 13 | 47.5 | 37.7 | 195 | IGFB_HUMAN | Q8tx28 methanopyru |
| 14 | 47 | 37.3 | 380 | OPRK_CAVPO | P05019 homo sapien |
| 15 | 47 | 37.3 | 1168 | DDX8_ARATH | P41144 cavia porce |
| 16 | 46.5 | 36.9 | 740 | POLB_MAIZE | Q38953 arabidopsis |
| 17 | 46 | 36.5 | 516 | SYM_AGR5 | P15718 zea mays (m |
| 18 | 45.5 | 36.1 | 580 | MM14_PIG | Q8ufa2 agrobacteri |
| 19 | 45.5 | 36.1 | 582 | MM14_HUMAN | Q9xt90 sus scrofa |
| 20 | 45.5 | 36.1 | 582 | MM14_MOUSE | P50281 homo sapien |
| 21 | 45.5 | 36.1 | 582 | MM14_RAT | P53690 mus musculus |
| 22 | 45.5 | 36.1 | 591 | PAXI_HUMAN | Q10739 rattus norv |
| 23 | 45 | 35.7 | 190 | RS9A_SCHPO | P49023 homo sapien |
| 24 | 45 | 35.7 | 242 | HAP5_YEAST | Q09757 schizosacch |
| 25 | 45 | 35.7 | 349 | WZEE_ECOLI | Q02516 saccharomyc |
| 26 | 45 | 35.7 | 494 | KCFI_HUMAN | P25905 escherichia |
| 27 | 45 | 35.7 | 544 | PYRG_DEIRA | Q9h3m0 homo sapien |
| 28 | 45 | 35.7 | 852 | SRCH_RABIT | Q9ru23 deinococcus |
| 29 | 45 | 35.7 | 864 | KLTK_HUMAN | P16230 oryctolagus |
| 30 | 45 | 35.7 | 992 | SNXJ_HUMAN | P29376 homo sapien |
| 31 | 45 | 35.7 | 1059 | SPS_VICFA | Q92543 homo sapien |
| 32 | 44.5 | 35.3 | 777 | RGL2_HUMAN | Q43876 vicia faba |
| 33 | 44.5 | 35.3 | 1233 | VLI1_REOVD | O15211 homo sapien |
| | | | | | P15024 reovirus (t |

| | | | | |
|----------|---|-----------|------|---------|
| RESULT 1 | | | | |
| ID | GHRL_HUMAN | STANDARD; | PRT; | 117 AA. |
| AC | Q9UBU3; Q8TAT9; Q9H3R3; | | | |
| DT | 28-FEB-2003 (Rel. 41, Created) | | | |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein). | | | |
| GN | GHRL OR MTLRP. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26. | | | |
| RX | MEDLINE=20067959; PubMed=10604470; | | | |
| RT | Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.; | | | |
| RT | "Ghrelin is a growth-hormone-releasing acylated peptide from stomach."; | | | |
| RL | Nature 402:656-660(1999). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). | | | |
| RA | Kojima M.; | | | |
| RL | Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). | | | |
| RC | TISSUE=Stomach; | | | |
| RA | Tomasetto C., Karam S.M., Rio M.-C.; | | | |
| RT | "Identification of a novel gastric protein m46."; | | | |
| RT | Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases. | | | |
| RL | [4] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). | | | |
| RA | Wajnrach M.P., Ten I.S., Gertner J.M., Leibel R.L.; | | | |
| RT | "Genomic organization of the human Ghrelin gene."; | | | |
| RL | J. Endocrinol. Genet. 1:231-233(2000). | | | |
| RN | [5] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). | | | |
| RC | TISSUE=Blood; | | | |
| RX | MEDLINE=22388857; PubMed=12477932; | | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., | | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., | | | |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., | | | |
| RA | Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., | | | |
| RA | Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., | | | |
| RA | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., | | | |
| RA | Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | | | |
| RA | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., | | | |
| RA | Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | | | |
| RA | Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A., | | | |
| RA | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., | | | |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., | | | |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., | | | |
| RA | Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., | | | |

| | | | | | | |
|----|------|------|------|---|------------|---------------------|
| 34 | 44 | 34.9 | 115 | 1 | INS_VERMO | Q9W7r2 verasper mo |
| 35 | 44 | 34.9 | 168 | 1 | TCTP_BRAOL | Q944w6 brassica ol |
| 36 | 44 | 34.9 | 273 | 1 | NK22_MOUSE | P42586 mus musculus |
| 37 | 44 | 34.9 | 301 | 1 | TS2A_MOUSE | Q8vlg3 mus musculus |
| 38 | 44 | 34.9 | 449 | 1 | CMGA_BOVIN | P05059 bos taurus |
| 39 | 44 | 34.9 | 4447 | 1 | PKSK_BACSU | P40803 bacillus su |
| 40 | 43.5 | 34.5 | 525 | 1 | SYK_DEIRA | Q9rxel deinococcus |
| 41 | 43.5 | 34.5 | 582 | 1 | MM14_RABIT | Q95220 oryctolagus |
| 42 | 43 | 34.1 | 281 | 1 | WS22_HUMAN | Q43709 homo sapien |
| 43 | 43 | 34.1 | 365 | 1 | SYAP_MOUSE | Q9d5v6 mus musculus |
| 44 | 43 | 34.1 | 380 | 1 | OPRK_HUMAN | P41145 homo sapien |
| 45 | 43 | 34.1 | 579 | 1 | SYQ_XANAC | Q8pzn5 xanthomonas |

ALIGNMENTS

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6].
 RP SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RT hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [7].
 RP REVIEW.
 RC MEDLINE=21203998; PubMed=11306336;
 RX Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RA "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect. Induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named Isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3.1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3.2; Sequence=VSP_003245;
 CC IsoId=Q9UBU3.2; Sequence=VSP_003245;
 CC -1- PTM: O-n-octanoylation is essential for activity.
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/GhrelinID327.html".
 CC -----
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 CC -----
 DR EMBL; AB029434; BAA89371.1; -.
 DR EMBL; AB035700; BAB19045.1; -.
 DR EMBL; AJ252278; CAB65733.1; -.
 DR EMBL; AF296558; AAG10300.1; -.
 DR EMBL; BC025791; AAH25791.1; -.
 DR PIR; A59316; A59316.
 DR MIM; 605353; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005331; F:growth hormone receptor ligand activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc; 1.
 DR Pfam; PF04644; motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 23
 FT PEPTIDE 24 51 GHRELIN.
 FT PROPEP 52 117 REMOVED IN MATURE FORM.
 FT LIPID 26 26 N-OCTANOATE.
 FT VARSPIC 37 37 Missing (in Isoform 2).
 FT /FTId=VSP_003245.
 FT CONFLICT 72 72 L -> M (IN REF. 5).

SQ SEQUENCE 117 AA; 12911 MW; 39C0572BECA2755 CRC64;
 Query Match 100.0%; Score 126; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.8e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24
 DB 52 ALAGWLRPEDGGGAEGAEDELEVR 75
 RESULT 2
 GHRL_RAT
 ID GHRL_RAT STANDARD; PRT; 117 AA.
 AC OQYH7; O9ET69;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (growth hormone secretagogue) (growth hormone
 DE releasing peptide).
 GN GHRL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,
 RP AND ACYLATION OF SER-26.
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
 RX MEDLINE=20067959; PubMed=10604470;
 RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
 RT "Ghrelin is a growth-hormone-releasing acylated peptide from
 RT stomach.";
 RL Nature 402:656-660(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS
 RP SPECTROMETRY, AND ACYLATION OF SER-26.
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
 RX MEDLINE=20357315; PubMed=10801861;
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
 RT "Purification and characterization of rat des-Gln14-ghrelin, a second
 RT endogenous ligand for the growth hormone secretagogue receptor.";
 RL J. Biol. Chem. 275:21995-22000(2000).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=21092536; PubMed=11162448;
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
 RT "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
 RT in gastrointestinal tissue.";
 RL Biochem. Biophys. Res. Commun. 279:909-913(2000).
 RN [4]
 RP STRUCTURE-ACTIVITY RELATIONSHIP.
 RX MEDLINE=21433488; PubMed=11549267;
 RA Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
 RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
 RT "Structure-activity relationship of ghrelin: pharmacological study of
 RT ghrelin peptides.";
 RL Biochem. Biophys. Res. Commun. 287:142-146(2001).
 RN [5]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect. Induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named Isoforms=2;

CC Name=1; Synonyms=Ghrelin;
 CC IsoID-Q9QYH7-1; Sequence-Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoID-Q9QYH7-2; Sequence-VSP_003248;
 CC TISSUE SPECIFICITY: Broadly expressed with higher expression in
 CC the stomach. Very low levels are detected in the hypothalamus,
 CC heart, lung, pancreas, intestine and adipose tissue.
 CC -1- PTM: O-n-octanoylation is essential for activity. The replacement
 CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.
 CC -1- MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;
 CC RANGE=24-51.
 CC -1- MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;
 CC RANGE=24-36, 38-51.
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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 CC -----
 CC EMBL; AB029433; BAA89370.1; -;
 CC EMBL; AB035699; BAB11956.1; -;
 CC FIRM; B59316; B59316.
 CC InterPro: IPR006737; motilin_assoc.
 CC InterPro: IPR006738; motilin_ghrelin.
 CC InterPro: IPR005441; Preproghrelin.
 CC Pfam: PF04643; motilin_assoc; 1.
 CC Pfam: PF04644; motilin_ghrelin; 1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom; PD332162; Preproghrelin; 1.
 CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW alternative splicing.
 FT SIGNAL 1 23 GHRELIN.
 FT PEPTIDE 24 51 REMOVED IN MATURE FORM.
 FT PROPEP 52 117 N-OCTANOATE.
 FT LIPID 26 26 Missing (in isoform 2).
 FT VARSPLIC 37 37 /FTID-VSE_003248.
 FT SEQUENCE 117 AA; 13176 MW; 8857546F51A7691 CRC64;
 Query Match 75.4%; Score 95; DB 1; Length 117;
 Best Local Similarity 75.0%; Pred. No. 9.8e-07;
 Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAEAELEVR 24
 DB 52 ALEGWLHPEDRGQAEAELEIR 75
 RESULT 3
 GHRL_PIG.
 ID GHRL_PIG STANDARD; PRT; 118 AA.
 AC Q9GKY5; Q9BDG8; Q9GKY4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide).
 GN GHRL.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA Kojima M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Stomach;

RA Rousselle J., Lacroix D., Dubreuil P.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=GhrelIn;
 CC IsoID-Q9GKY5-1; Sequence-Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoID-Q9GKY5-2; Sequence-VSP_003247;
 CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB035703; BAB19048.1; -;
 CC EMBL; AB035704; BAB19049.1; -;
 CC EMBL; AF308930; AAK19243.1; -;
 CC EMBL; AY028942; AAK30002.1; -;
 CC InterPro: IPR006737; motilin_assoc.
 CC InterPro: IPR006738; motilin_ghrelin.
 CC InterPro: IPR005441; Preproghrelin.
 CC Pfam: PF04643; motilin_assoc; 1.
 CC Pfam: PF04644; motilin_ghrelin; 1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom; PD332162; Preproghrelin; 1.
 CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW alternative splicing.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT PEPTIDE 25 52 GHRELIN.
 FT PROPEP 53 118 REMOVED IN MATURE FORM (BY SIMILARITY).
 FT LIPID 27 27 N-OCTANOATE (BY SIMILARITY).
 FT VARSPLIC 38 38 Missing (in isoform 2).
 FT SEQUENCE 118 AA; 12785 MW; 856D3E1D6DAB1A76 CRC64;
 Query Match 73.0%; Score 92; DB 1; Length 118;
 Best Local Similarity 66.7%; Pred. No. 2.7e-06;
 Matches 16; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAEAELEVR 24
 DB 53 ALEGWLGPDSGEVEGDKLEIR 76
 RESULT 4
 GHRL_MOUSE
 ID GHRL_MOUSE STANDARD; PRT; 117 AA.
 AC Q9EQX0; Q9WU21;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide) (Motilin-related peptide) (M46 protein).
 GN GHRL OR MTLRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.

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CC TISSUE=Stomach;
RX MEDLINE=20389976; PubMed=10930375;
RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT "Identification and characterization of a novel gastric peptide
RT hormone: the motilin-related peptide.";
RL Gastroenterology 119:395-405(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Kojima M.;
RL "Mouse mRNA for preproghrelin.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX STRAIN=C57BL/6J; TISSUE=Stomach;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schraml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lysons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1; Synonyms=Ghrelin;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC Name=3; Synonyms=VSP_003246;
CC -1- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
CC with higher levels in the stomach, medium levels in the duodenum,
CC jejunum, ileum and colon. Low expression in the testis and brain.
CC Not detected in the salivary gland, pancreas, liver and lung.
CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC EMBL; AJ243503; CAB46500.1; -
DR EMBL; AB035701; BAB19046.1; -
DR EMBL; AB060078; BAB69857.1; -
DR EMBL; AK008658; BAB25814.1; -
DR EMBL; AK008860; BAB25934.1; -
DR MG; MG1:1930008; Ghrl.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005576; C:extracellular; IDA.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrel.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrel; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23
FT PEPTIDE 24 51
FT PROPEP 52 117
FT LIPID 26 26
FT VAPSPIC 37 37
SQ SEQUENCE 117 AA; 13207 MW; EACB49D2E3CA7203 CRC64;
Query Match 72.28; Score 91; DB 1; Length 117;
Best Local Similarity 70.88; Pred. No. 3.6e-06;
Matches 1; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
Db 52 ALEGWLHPDRGQAEETEELR 75
RESULT 5
GHRL_BOVIN STANDARD; PRT; 116 AA.
AC Q9BDJ6; Q9GKY6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ghrelin precursor (growth hormone secretagogue) (growth hormone
DE releasing peptide).
GN GHRL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Kita K., Harada K., Yokota H.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 24-99 FROM N.A.
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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DR EMBL: X04766: CAA28460.1: -

RN [2] SEQUENCE FROM N.A.
 RC TISSUE-Retina;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muny D.K., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RX COLLAGEN-BINDING.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I";
 RJ J. Biol. Chem. 271:1613-1620(1996).
 RN [4]
 RX INTERACTION WITH DAB1.
 RX MEDLINE=99389880; PubMed=10460257;
 RA Hameyouni R., Rice D.S., Sheldon M., Curran T.;
 RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
 RT protein 1";
 RJ J. Neurosci. 19:7507-7515(1999).
 RN [5]
 RX INTERACTION WITH MAPK8IP1.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niihara T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/Islet-brain-1
 RT scaffolds Alzheimer's amyloid precursor protein with JNK";
 RJ J. Neurosci. 21:6597-6607(2001).
 RN [6]
 RX GAMMA-SECRETASE PROCESSING, INTERACTION WITH APPB1, AND MUTAGENESIS OF
 RX TYR-641.
 RX MEDLINE=22313598; PubMed=12228233;
 RA Scheinfeld M.H., Gherzi E., Laky K., Fowlkes B.J., D'Adamo L.;
 RT "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
 RT secretase regulates transcription";
 RJ J. Biol. Chem. 277:44195-44201(2002).
 RN [7]
 RX FUNCTION: May play a role in postsynaptic function. The C-terminal
 RX gamma-secretase processed fragment, ALDI, activates transcription
 RX activation through APPB1 (Ref5) binding. Couples to JIP signal
 RX transduction through C-terminal binding. May interact with
 RX cellular G-protein signaling pathways. Can regulate neurite
 RX outgrowth through binding to components of the extracellular
 RX matrix such as heparin and collagen I.
 RX FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
 RX neuronal apoptosis (By similarity).
 RX SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 RX cytoplasmic proteins, including APPB and APPA family members,
 RX MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
 RX serine phosphorylation.
 RX SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
 RX processed in the Golgi complex.
 RX DOMAIN: The NPXY sequence motif found in many tyrosine-
 RX phosphorylated proteins is required for the specific binding of
 RX the PID domain. However additional amino acids either N- or C-

CC terminal to the NPXY motif are often required for complete
 CC interaction. The NPXY site is also involved in clathrin-mediated
 CC endocytosis.
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal
 CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
 CC similarity).
 CC -1- PTM: N-glycosylated.
 CC -1- PTM: O-glycosylated.
 CC -1- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
 CC Zinc-binding increases heparin binding. No Cu(II) reducing
 CC activity with copper-binding.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----
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 CC -----
 CC EMBL: L04538; AAA37247.1; -;
 CC EMBL: BC021877; AAH21877.1; -;
 CC FIR: A46362; A46362.
 CC HSP: P05067; IWP.
 CC MGD: MGI:88046; Aplp1.
 CC InterPro: IPR001868; A4_APP.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC PRINTS: PR00203; AMYLOIDA4.
 CC SMART: SM00006; A4_EXTRA; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.
 CC DR Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
 KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
 KW Glycoprotein.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 653 AMYLOID-LIKE PROTEIN 1.
 FT CHAIN 624 653 C30 (BY SIMILARITY).
 FT DOMAIN 38 583 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 584 606 POTENTIAL.
 FT DOMAIN 607 653 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 157 177 COPPER-BINDING.
 FT DOMAIN 203 210 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 313 345 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 413 444 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 445 462 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 263 271 POLY-GLU.
 FT DOMAIN 535 538 POLY-SER.
 FT DOMAIN 601 606 POLY-LEU.
 FT SITE 166 166 REQUIRED FOR COPPER(II) REDUCTION (BY
 FT SIMILARITY).
 FT SITE 607 618 BASOLATERAL SORTING SIGNAL (BY
 FT SIMILARITY).
 FT SITE 623 624 CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
 FT SITE 641 644 ENDOCYTOSIS SIGNAL.
 FT SITE 643 646 NPXY MOTIF.
 FT CARBOHYD 464 464 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 554 554 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MUTAGEN 641 641 Y->G: REDUCED BINDING OF APPB1.
 FT CONFLICT 17 17 P -> PP (IN REF. 2).
 SQ SEQUENCE 653 AA; 72750 MW; 56516DC3EA40E4B0 CRC64;
 Query Match 39.7%; Score 50; DB 1; Length 653;
 Best Local Similarity 76.9%; Pred. No. 14;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 11 GGQAGGADEDELEV 23
 II:III IIII
 Db 233 GGRAGGEDDEEV 245
 RESULT 10
 NKX1_BISBI

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ID AC NKX1_BISBI STANDARD; PRT; 300 AA.
DT 046383;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 (Na(+)/K(+)/Ca(2+)-
DE exchange protein 1) (Retinal rod Na-Ca+K exchanger) (Fragment).
GN SLC24A1 OR NCKX1.
OS Bison bison (American bison).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bison.
OX NCBI_TaxID=9901;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98138491; PubMed=9478004;
RA Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.;
RT "cDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison
RL with a revised bovine sequence.";
RL Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
CC -1- FUNCTION: Critical component of the visual transduction cascade,
CC controlling the calcium concentration of outer segments during
CC light and darkness. Light causes a rapid lowering of cytosolic
CC free calcium in the outer segment of both retinal rod and cone
CC photoreceptors and the light-induced lowering of calcium is caused
CC by extrusion via this protein which plays a key role in the
CC process of light adaptation. Transports one Ca(2+) and one K(+) in
CC exchange for four Na(+) (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q28139-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q28139-2; Sequence=VSP_006159;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Retina.
CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC
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CC -----
CC EMBL; X66481; CAA47108.1; -
CC EMBL; AF025664; AAB88884.1; -
CC PIR; S20969; S20969.
CC InterPro; IPR004817; K_NaCaexchang.
CC InterPro; IPR004481; K_NaCaexchang.
CC InterPro; IPR004837; NaCa_Exmemb.
CC Pfam; PF01699; NaCa_Ex; 2.
CC TIGRFAMs; TIGR00927; 2A1904; 1.
CC TIGRFAMs; TIGR00367; TIGR00367; 1.
KW Vision; Transport; Antiport; Symport; Calcium transport;
KW Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
KW Phosphorylation; Signal; Repeat; Alternative splicing.
FT SIGNAL 1 38
FT CHAIN 39 1216 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
FT DOMAIN 39 446 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 447 467 POTENTIAL.
FT DOMAIN 468 491 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 492 512 POTENTIAL.
FT DOMAIN 513 518 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 519 539 POTENTIAL.
FT DOMAIN 540 557 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 558 578 POTENTIAL.
FT DOMAIN 579 579 POTENTIAL.
FT TRANSMEM 580 600 POTENTIAL.
FT DOMAIN 601 1024 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1025 1045 POTENTIAL.
FT DOMAIN 1046 1052 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1053 1073 POTENTIAL..
FT DOMAIN 1074 1088 CYTOPLASMIC (POTENTIAL).
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 66-88; 232-249;
RX MEDLINE=98138491; PubMed=1582405;
RA Rellaender H., Achilles A., Friedel U., Maul G., Lottspeich F.,
RA Cook N.J.;
RT "Primary structure and functional expression of the Na/Ca,K-exchanger
RL from bovine rod photoreceptors.";
RL EMBO J. 11:1689-1695(1992).
RN [2]
RP SEQUENCE OF 725-1216 FROM N.A. (ISOFORM 1).
RX TISSUE=Retina;
RX MEDLINE=98138491; PubMed=9478004;
RA Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.M.;
RT "cDNA cloning of the human retinal rod Na-Ca + K exchanger:
RL comparison with a revised bovine sequence.";
RL Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
CC -1- FUNCTION: Critical component of the visual transduction cascade,
CC controlling the calcium concentration of outer segments during
CC light and darkness. Light causes a rapid lowering of cytosolic
CC free calcium in the outer segment of both retinal rod and cone
CC photoreceptors and the light-induced lowering of calcium is caused
CC by extrusion via this protein which plays a key role in the
CC process of light adaptation. Transports one Ca(2+) and one K(+) in
CC exchange for four Na(+) (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q28139-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q28139-2; Sequence=VSP_006159;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Retina.
CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC
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CC -----
CC EMBL; X66481; CAA47108.1; -
CC EMBL; AF025664; AAB88884.1; -
CC PIR; S20969; S20969.
CC InterPro; IPR004817; K_NaCaexchang.
CC InterPro; IPR004481; K_NaCaexchang.
CC InterPro; IPR004837; NaCa_Exmemb.
CC Pfam; PF01699; NaCa_Ex; 2.
CC TIGRFAMs; TIGR00927; 2A1904; 1.
CC TIGRFAMs; TIGR00367; TIGR00367; 1.
KW Vision; Transport; Antiport; Symport; Calcium transport;
KW Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
KW Phosphorylation; Signal; Repeat; Alternative splicing.
FT SIGNAL 1 38
FT CHAIN 39 1216 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
FT DOMAIN 39 446 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 447 467 POTENTIAL.
FT DOMAIN 468 491 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 492 512 POTENTIAL.
FT DOMAIN 513 518 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 519 539 POTENTIAL.
FT DOMAIN 540 557 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 558 578 POTENTIAL.
FT DOMAIN 579 579 POTENTIAL.
FT TRANSMEM 580 600 POTENTIAL.
FT DOMAIN 601 1024 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1025 1045 POTENTIAL.
FT DOMAIN 1046 1052 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1053 1073 POTENTIAL..
FT DOMAIN 1074 1088 CYTOPLASMIC (POTENTIAL).
RN [1]

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FT TRANSMEM 1089 1109 POTENTIAL.
FT DOMAIN 1110 1127 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1128 1148 POTENTIAL.
FT DOMAIN 1149 1157 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1158 1178 POTENTIAL.
FT DOMAIN 1179 1185 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1186 1206 POTENTIAL.
FT DOMAIN 1207 1216 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 796 928 8 X 17 AA TANDEM REPEATS OF D-E-D-E-G-E-I-Q-A-G-E-[CA]-G-E-V-[EK]-G.
FT REPEAT 796 811 1 (APPROXIMATE).
FT REPEAT 812 828 2.
FT REPEAT 829 845 3.
FT REPEAT 846 862 4.
FT REPEAT 863 879 5.
FT REPEAT 880 896 6.
FT REPEAT 897 913 7.
FT REPEAT 914 928 8 (APPROXIMATE).
FT REPEAT 488 528 ALPHA-1.
FT REPEAT 1096 1127 ALPHA-2.
FT DOMAIN 984 1009 POLY-GLU.
FT MOD_RES 652 652 PHOSPHORYLATION (POTENTIAL).
FT CARBOHYD 290 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 868 884 Missing (in isoform 2).
FT CONFLICT 84 84 /FTID=VSP_006159.
FT CONFLICT 234 234 MISSING (IN REF. 1; AA SEQUENCE).
FT CONFLICT 244 245 MISSING (IN REF. 1; AA SEQUENCE).
FT CONFLICT 857 857 A -> G (IN REF. 2).
SQ SEQUENCE 1216 AA; 131614 MW; 39F149A74D1D0523 CRC64;

Query Match 38.9%; Score 49; DB 1; Length 1216;
Best Local Similarity 42.9%; Pred. No. 36;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 4 GWLRPDGQGAEGAEDELEVR 24
I :: ::::: ||| :::::
DB 816 GEIQAGEGVEGEDEGEIQ 836

RESULT 12
SYM_METKA
ID SYM_METKA STANDARD; PRT; 668 AA.
AC Q8TX28;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
DE (METS).
GN METG OR MK0850.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Shesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natalie D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozyavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC -1- FUNCTION: Is required not only for elongation of protein synthesis
CC but also for the initiation of all mRNA translation through
CC initiator tRNA(fMet) aminoacylation (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
CC diphosphate + L-methionyl-tRNA(Met).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC MetG subfamily 1.
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
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CC -----
CC EMBL: AE010375; AAM02063.1; -.
CC HAMAP: MF_00098; fused; 1.
CC InterPro: IPR004495; MetG_Cterm.
CC InterPro: IPR002300; tRNA-synt_1a.
CC InterPro: IPR001412; tRNA-synt_1.
CC InterPro: IPR002304; tRNA-synt_met.
CC InterPro: IPR002547; tRNA-bind.
CC Pfam: PF00133; tRNA-synt_1; 1.
CC Pfam: PF01588; tRNA_bind; 1.
CC PIRSF: PIRSF001528; MetRS_dimerising; 1.
CC TIGRFAMs: TIGR00398; metG; 1.
CC TIGRFAMs: TIGR00399; metG_Cterm; 1.
CC PROSITE: PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
CC PROSITE: PS00886; TRSD; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC RNA-binding; tRNA-binding; Metal-binding; Zinc; Complete proteome.
FT SITE 11 21 "HIGH" REGION.
FT SITE 332 336 "RMSKS" REGION.
FT DOMAIN 567 668 TRNA-BINDING.
FT METAL 146 146 ZINC (BY SIMILARITY).
FT METAL 149 149 ZINC (BY SIMILARITY).
FT METAL 159 159 ZINC (BY SIMILARITY).
FT METAL 162 162 ZINC (BY SIMILARITY).
SQ SEQUENCE 668 AA; 77386 MW; FBC5734FF5FEF015 CRC64;

Query Match 38.1%; Score 48; DB 1; Length 668;
Best Local Similarity 53.3%; Pred. No. 27;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 LRPEGGQGAEGAEDE 20
I :: ::::: ||| :::::
DB 547 LPEEGSEGEQDDE 561

RESULT 13
IGFB_HUMAN
ID IGFB_HUMAN STANDARD; PRT; 195 AA.
AC P05019;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Insulin-like growth factor IB precursor (IGF-IB) (Somatomedin C).
GN IGF1 OR IBP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86168194; PubMed=2937782;
RA Rotwein P., Pollock K.M., Didier D.K., Krivi G.G.;
RT "Organization and sequence of the human insulin-like growth factor I
RT gene. Alternative RNA processing produces two insulin-like growth
RT factor I precursor peptides.";
RL J. Biol. Chem. 261:4828-4832(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86094355; PubMed=3455760;
RA Rotwein P.;
RT "Two insulin-like growth factor I messenger RNAs are expressed in

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Query Match          37.7%; Score 47.5; DB 1; Length 195;
Best Local Similarity 45.5%; Pred. No. 9.3;
Matches 10; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 4 GWLRPEDGG-QAEGAEDELEVR 24
   || : || || || | : ||
Db 151 GWPKTHPGGEQEGTEASLQIR 172

RESULT 14
OPRK_CAVPO STANDARD; PRT; 380 AA.
AC P41144;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Kappa-type opioid receptor (KOR-1).
GN OPRK1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Brain;
RX MEDLINE=94224825; PubMed=8170987;
RA Xie G.X., Meng F., Mansour A., Thompson R.C., Hoversten M.T.,
RA Goldstein A., Watson S.J., Akil H.;
RT "Primary structure and functional expression of a guinea pig kappa
RT opioid (dynorphin) receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3779-3783(1994).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U04092; A067171.1; -.
DR PIR; A55259; A55259.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL).
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 380 AA; 42736 MW; 4FF053834DBBA623 CRC64;

Query Match          37.3%; Score 47; DB 1; Length 380;
Best Local Similarity 38.1%; Pred. No. 22;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAEGAEDELE 22
   | | | : | | : | |
Db 30 LPGWAEPPDGNAGSAGPQDEQL 50

RESULT 15
DDX8_ARATH STANDARD; PRT; 1168 AA.
AC Q38953; Q9LRV0;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative pre-mRNA splicing factor ATP-dependent RNA helicase.
GN AT3G26560 OR WPE16.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=97086699; PubMed=8932388;
RA Quigley F., Dao P., Cottet A., Mache R.;
RT "Sequence analysis of an 81 kb contig from Arabidopsis thaliana
RT chromosome III."
RL Nucleic Acids Res. 24:4313-4318(1996).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty pl and TAC
RT clones."
RL DNA Res. 7:131-135(2000).
CC -1- FUNCTION: COULD ACT LATE IN THE SPLICING OF PRE-MRNA AND MEDIATE
CC THE RELEASE OF THE SPLICED MRNA FROM SPICEOSOMES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. DEAH
CC SUBFAMILY. DDX8/PRP22 ORTHOLOG.
CC -1- SIMILARITY: Contains 1 SL motif domain.
CC -1- CAUTION: Ref.1 sequences differ from that shown due to a
CC frameshift in position 57.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X98130; CAA66825.1; ALT_FRAME.
DR EMBL; X97970; CAA66613.1; ALT_FRAME.
DR EMBL; AB028611; BAB01838.1; -.
DR HSP; P05055; 1SRO.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR002464; DEAH_box.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR003029; SL.
DR Pfam; PF00271; helicase_C; 1.
DR Pfam; PF00375; SL; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR SMART; SM00316; SL; 1.
```

DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
 DR PROSITE; PS0126; S1; 1.
 KW Hypothetical protein; mRNA processing; mRNA splicing; Helicase;
 KW ATP-binding; Nuclear protein.
 FT DOMAIN 214 283 S1 MOTIF.
 FT NP_BIND 538 545 ATP (POTENTIAL).
 FT SITE 635 638 DEAH BOX.
 FT DOMAIN 777 780 POLY-PRO.
 SQ SEQUENCE 1168 AA; 134156 MW; B3632DE4A7A7690C CRC64;
 Query Match 37.38; Score 47; DB 1; Length 1168;
 Best Local Similarity 57.98; Pred. No. 66;
 Matches 11; Conservative 2; Mismatches 2; Indels 4; Gaps 1;
 OY 9 EDGG----QAEGAEDELEV 23
 DB 372 EDGDMLYQEEGAELEEI 390

Search completed: September 11, 2003, 17:21:44
 Job time : 6.46524 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 : Search time 8.98396 Seconds
(without alignments)
256.908 Million cell updates/sec

Title: US-09-853-253-4
Perfect score: 126
Sequence: 1 ALAGWLRPEDGGQAGAEDELEVR 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 126 | 100.0 | 117 | 1 A59316 | ghrelin precursor |
| 2 | 95 | 75.4 | 117 | 1 B59316 | ghrelin precursor |
| 3 | 54 | 42.9 | 200 | 2 A28169 | nucleoplasmin - Af |
| 4 | 52 | 41.3 | 232 | 2 G83609 | probable transcript |
| 5 | 51.5 | 40.9 | 249 | 2 T21920 | hypothetical prote |
| 6 | 51 | 40.5 | 91 | 2 B69811 | conserved hypothet |
| 7 | 51 | 40.5 | 604 | 2 AE2760 | chloride channel p |
| 8 | 51 | 40.5 | 604 | 2 C97541 | chloride channel |
| 9 | 50 | 39.7 | 131 | 2 B75433 | hypothetical prote |
| 10 | 50 | 39.7 | 653 | 2 A46362 | amyloid precursor- |
| 11 | 49.5 | 39.3 | 484 | 2 C75609 | amino acid ABC tra |
| 12 | 49 | 38.9 | 274 | 2 A26050 | exfoliative toxin |
| 13 | 49 | 38.9 | 1199 | 2 S20969 | Na+/Ca2+,K+-exchan |
| 14 | 48 | 38.1 | 114 | 2 T49338 | hypothetical prote |
| 15 | 47.5 | 37.7 | 195 | 1 IGHU1B | insulin-like growt |
| 16 | 47 | 37.3 | 355 | 2 T09738 | protein kinase PKI |
| 17 | 47 | 37.3 | 380 | 2 A52559 | kappa opioid recep |
| 18 | 47 | 37.3 | 1273 | 2 C96767 | unknown protein F2 |
| 19 | 46.5 | 36.9 | 80 | 2 T26398 | hypothetical prote |
| 20 | 46.5 | 36.9 | 740 | 2 T03975 | hypothetical prote |
| 21 | 46 | 36.5 | 163 | 2 T21674 | hypothetical prote |
| 22 | 46 | 36.5 | 259 | 2 A87377 | hypothetical prote |
| 23 | 46 | 36.5 | 287 | 2 C82965 | hypothetical prote |
| 24 | 46 | 36.5 | 491 | 2 H97088 | protein containing |
| 25 | 46 | 36.5 | 516 | 2 A82760 | methionyl-tRNA syn |
| 26 | 46 | 36.5 | 516 | 2 A97541 | methionyl-tRNA syn |
| 27 | 46 | 36.5 | 528 | 2 C84110 | xylan beta-1,4-xy |
| 28 | 46 | 36.5 | 871 | 2 B71039 | hypothetical prote |
| 29 | 45.5 | 36.1 | 582 | 2 I38028 | matrix metalloprot |

| | | | | | |
|----|------|------|-----|----------|--------------------|
| 30 | 45.5 | 36.1 | 582 | 2 I48673 | matrix metalloprot |
| 31 | 45.5 | 36.1 | 582 | 2 I84471 | matrix metalloprot |
| 32 | 45 | 35.7 | 69 | 2 C87574 | cold-shock domain |
| 33 | 45 | 35.7 | 184 | 2 T43321 | ribosomal protein |
| 34 | 45 | 35.7 | 191 | 2 S62409 | 40s ribosomal prot |
| 35 | 45 | 35.7 | 195 | 2 T48728 | hypothetical prote |
| 36 | 45 | 35.7 | 242 | 2 S67270 | CCAAT-binding fact |
| 37 | 45 | 35.7 | 296 | 2 T15550 | hypothetical prote |
| 38 | 45 | 35.7 | 297 | 2 G71446 | hypothetical prote |
| 39 | 45 | 35.7 | 349 | 2 F91218 | probable transport |
| 40 | 45 | 35.7 | 349 | 2 H86064 | probable transport |
| 41 | 45 | 35.7 | 349 | 2 D65182 | probable transport |
| 42 | 45 | 35.7 | 479 | 2 A75353 | mOCR protein - Del |
| 43 | 45 | 35.7 | 494 | 2 JC5919 | potassium channel |
| 44 | 45 | 35.7 | 544 | 2 B75379 | CTP synthase - Del |
| 45 | 45 | 35.7 | 600 | 2 T17436 | ATP-binding protei |

ALIGNMENTS

RESULT 1

A59316
ghrelin precursor - human
N:Alternate names: preproghrelin
C:Species: Homo sapiens (man)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C:Accession: A59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: A59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-117 <KOJ>
A:Cross-references: GB:AB029434; NID:g6691571; PIDN:BAA89371.1; PID:g6691572
A:Experimental source: tissue stomach endocrine cells
A:Note: submitted to GenBank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (gr
C:Superfamily: motilin
C:Keywords: hormone; lipoprotein; stomach
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <MAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 126; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 2

B59316
ghrelin precursor - rat
N:Alternate names: preproghrelin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C:Accession: B59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: B59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA; protein
A:Residues: 1-117 <KOJ>
A:Cross-references: GB:AB029433; NID:g6691569; PIDN:BAA89370.1; PID:g6691570
A:Experimental source: strain SD; tissue stomach endocrine cells

A;Note: submitted to GenBank, June 1999
C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth hormone) from the pituitary gland.
C;Superfamily: motilin
F;1-23/Domains: signal sequence #status predicted <SIG>
F;24-51/Product: ghrelin #status predicted <NAT>
F;52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;26/Binding site: octanotate (Ser) (covalent) #status experimental

Query Match 75.4%; Score 95; DB 1; Length 117;
Best Local Similarity 75.0%; Pred.No. 2.6e-06;
Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAELEVR 24
||| ||| ||| ||| ||| ||| :
Db 52 ALEGWLHPEDRGQAEEAEELEIR 75

RESULT 3
A26169
nucleoplasmin - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 13-Aug-1999
C;Accession: C2169
R;Dingwall, C.; Dillworth, S.M.; Black, S.J.; Kearsey, S.E.; Cox, L.S.; Laskey, R.A.
EMBO J. 6, 69-74, 1987
A;Title: Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and a cluster of serine residues
A;Reference number: A26169; MUID:87218476; PMID:2884102
A;Accession: A26169
A;Molecule type: mRNA
A;Residues: 1-200 <DTN>
A;Cross-references: GB:X04766; NID:g64939; PIDN:CAA28460.1; PID:g64940
C;Superfamily: nucleophosmin
C;Keywords: molecular chaperone; nucleus

Query Match 42.9%; Score 54; DB 2; Length 200;
Best Local Similarity 55.6%; Pred.No. 2.8;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 WLRPEDGGGAEGAEDELE 22
| || | || | || | || |
Db 126 WAEEEDGEAGEGEEEE 143

RESULT 4
G83609
probable transcription regulator PA0279 [Imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83609
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brinkman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83609
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-232 <STO>
A;Cross-references: GB:AE004466; GB:AE004091; NID:g9946120; PIDN:AAG03668.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0279

Query Match 41.3%; Score 52; DB 2; Length 232;
Best Local Similarity 72.7%; Pred.No. 6.2;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GWLRLPDGGQA 14
||||| : || : ||
Db 202 GWLRPDGGRA 212

chloride channel protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AE2760
 R:Wood, D.W.; Scubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AE2760
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <KUR>
 A:Cross-references: GB:AE008588; PIDN:AA42499.1; PID:gl7179917; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: clc
 A:Map position: circular chromosome

Query Match 40.5%; Score 51; DB 2; Length 604;
 Best Local Similarity 62.5%; Pred. No. 22;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAGWLRPDPGGQAG 16
 I: ||||| ||| |
 Db 288 AIPGWLRLPTLGGVAVG 303

RESULT 8
 C97541
 chloride channel, clc (AE005067) [imported] - Agrobacterium tumefaciens (strain C58, Cer
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C:Accession: C97541
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: C97541
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK87284.1; PID:gl15156576; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C_2753
 A:Map position: circular chromosome

Query Match 40.5%; Score 51; DB 2; Length 604;
 Best Local Similarity 62.5%; Pred. No. 22;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAGWLRPDPGGQAG 16
 I: ||||| ||| |
 Db 288 AIPGWLRLPTLGGVAVG 303

RESULT 9
 B75433
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
 C:Accession: B75433
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: B75433

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-131 <WHI>
 A:Cross-references: GB:AE001963; GB:AE000513; NID:g6458869; PIDN:AAF10714.1; PID:g645
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1139
 A:Map position: 1
 C:Superfamily: Deinococcus radiodurans hypothetical protein DR1139

Query Match 39.7%; Score 50; DB 2; Length 131;
 Best Local Similarity 47.4%; Pred. No. 6.7;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 ALAGWLRPDPGGQAG 19
 || ||||| ||| |
 Db 101 ALLAWFPFPPRGAQVOGAAE 119

RESULT 10
 A46362
 amyloid precursor-like protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
 C:Accession: A46362
 R:Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
 Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
 A:Title: Identification of a mouse brain cDNA that encodes a protein related to the A
 A:Reference number: A46362; MUID:93066322; PMID:1279693
 A:Accession: A46362
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-653 <WAS>
 A:Experimental source: brain
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBIP:118684)
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
 C:Keywords: transmembrane protein

Query Match 39.7%; Score 50; DB 2; Length 653;
 Best Local Similarity 76.9%; Pred. No. 34;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGAAGAGADELEV 23
 ||:|||| ||| ||
 Db 233 GGRAEGGEDEEV 245

RESULT 11
 C75609
 amino acid ABC transporter, permease protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: C75609
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: C75609
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <WHI>
 A:Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF12224.1; PID:g646
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DRA0136
 A:Map position: 2

Query Match 39.3%; Score 49.5; DB 2; Length 484;
 Best Local Similarity 61.1%; Pred. No. 29;
 Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 2 LAGWLRPEDGGQAEAGD 19
||||| | :||| |
Db 468 LAGWLTPR-GLRAEGGEE 484

RESULT 12
A26050
exfoliative toxin B precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 18-Nov-2002
C:Accession: A26050
R:Jackson, M.P.; Iandolo, J.J.
J. Bacteriol. 167, 726-728, 1986
A:Title: Sequence of the exfoliative toxin B gene of Staphylococcus aureus.
A:Reference number: A26050; MUID:86277939; PMID:3733674
A:Accession: A26050
A:Molecule type: DNA
A:Residues: 1-274 <JAC>
C:Superfamily: staphylococcal serine proteinase
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-274/Product: exfoliative toxin B #status predicted <MAT>

Query Match 38.9%; Score 49; DB 2; Length 274;
Best Local Similarity 44.4%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 5 WLRPEDGGQAEAGDELE 22
||: |||| | ||: |
Db 86 WLKIQDGGDTTGEEQPE 103

RESULT 13
S20969
Na+/Ca2+,K+-exchanging protein - bovine
N:Alternate names: Na+/Ca2+,K+ antiporter; Na/Ca,K-exchanger
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S20969
R:Reilaender, H.; Achilles, A.; Friedel, U.; Maul, G.; Lottspeich, F.; Cook, N.J.
EMBO J. 11, 1689-1695, 1992
A:Title: Primary structure and functional expression of the Na/Ca,K-exchanger from bovine
A:Reference number: S20969; MUID:92258377; PMID:1582405
A:Accession: S20969
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1199 <REI>
A:Cross-references: GB:X66481; NID:g505578; PIDN:CAA47108.1; PID:g505579

Query Match 38.9%; Score 49; DB 2; Length 1199;
Best Local Similarity 42.9%; Pred. No. 86;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGQAEAGDELEVR 24
|::: ||: || |||| |::
Db 816 GEIQAGEGGEVGEDEGEIQ 836

RESULT 14
T49338
hypothetical protein B13N20.230 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C:Accession: T49338
R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T49338
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <SCH>
A:Cross-references: EMBL:AL355925; GSPDB:GN00116; NCSP:B13N20.230
A:Experimental source: BAC clone B13N20; strain OR74A

C:Genetics:
A:Gene: NCSP:B13N20.230
A:Map position: 6
C:Superfamily: Neurospora crassa hypothetical protein B13N20.230

Query Match 38.1%; Score 48; DB 2; Length 114;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 9 EDGGQAEAGDELEVR 23
||| | |||||
Db 44 EDGFDDEGKEDQLEV 58

RESULT 15
IGHULB
insulin-like growth factor I precursor, splice form B [validated] - human
N:Alternate names: IGF-IB; somatomedin C
N:Contains: insulin-like growth factor IB-E1 amide
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-2000
C:Accession: A01611; A26181; S30540; B48960; A42664
R:Rotwein, P.; Pollock, K.M.; Didier, D.K.; Krivl, G.G.
J. Biol. Chem. 261, 4828-4832, 1986
A:Title: Organization and sequence of the human insulin-like growth factor I gene. A1
A:Reference number: A92581; MUID:86168194; PMID:2937782
A:Accession: A01611
A:Molecule type: DNA
A:Residues: 1-195 <ROT1>
A:Cross-references: GB:M14155; NID:gi83106; PIDN:AAA52537.1; PID:gi83109
R:Rotwein, P.
Proc. Natl. Acad. Sci. U.S.A. 83, 77-81, 1986
A:Title: Two insulin-like growth factor I messenger RNAs are expressed in human liver
A:Reference number: A26181; MUID:86094355; PMID:3455760
A:Accession: A26181
A:Molecule type: mRNA
A:Residues: 1-195 <ROT2>
A:Cross-references: GB:M11568; NID:gi83111; PIDN:AAA52539.1; PID:gi83112
R:Sandberg Nordqvist, A.C.; Stahlbom, P.A.; Lake, M.; Sara, V.R.
submitted to the EMBL Data Library, November 1990
A:Description: Nucleotide sequence of the human fetal brain IGF-1b.
A:Reference number: S30540
A:Accession: S30540
A:Molecule type: mRNA
A:Residues: 1-195 <SAN>
A:Cross-references: EMBL:X56774; NID:g32991; PIDN:CAA40093.1; PID:g32992
R:Sandberg Nordqvist, A.C.; Stahlbom, P.A.; Reinecke, M.; Collins, V.P.; von Holst, H.
Cancer Res. 53, 2475-2478, 1993
A:Title: Characterization of insulin-like growth factor 1 in human primary brain tumor
A:Reference number: A48960; MUID:93265440; PMID:8495408
A:Accession: B48960
A:Molecule type: mRNA
A:Residues: 1-195 <SA2>
A:Cross-references: GB:X56774; GB:S61860; NID:g32991; PIDN:CAA40093.1; PID:g32992
A:Experimental source: anaplastic oligodendroglioma
A:Note: sequence modified after extraction from NCBI backbone
A:Note: the authors translated the codon CAG for residues 124 and 133 as Glu
A:Note: sequence extracted from NCBI backbone (NCBIN:133058)
R:Siegfried, J.M.; Kasprzyk, P.G.; Treston, A.M.; Mulshine, J.L.; Quinn, K.A.; Cuttitt
Proc. Natl. Acad. Sci. U.S.A. 89, 8107-8111, 1992
A:Title: A mitogenic peptide amide encoded within the E peptide domain of the insulin
A:Reference number: A42664; MUID:92390398; PMID:1325646
A:Contents: annotation; IBE-1; amidated carboxyl end
C:Comment: For an alternative splice form, see PIR:IGHUL.
C:Genetics:
A:Gene: GDB:IGF1
A:Cross-references: GDB:120081; OMIM:147440
A:Map position: 12q22-12q24.1
A:Introns: 21/3; 74/1; 134/3
C:Superfamily: insulin
C:Keywords: alternative splicing; amidated carboxyl end; growth factor; plasma
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-48/Domain: propeptide #status predicted <PRO>

F:49-118/Product: insulin-like growth factor I #status predicted <MAT>
 F:49-77/Domain: insulin chain B-like #status predicted <CHB>
 F:78-89/Domain: insulin connecting C peptide-like #status predicted <CHC>
 F:90-110/Domain: insulin chain A-like #status predicted <CHA>
 F:111-118/Domain: D peptide #status predicted <CHD>
 F:119-195/Domain: carboxyl-terminal propeptide (E peptide) #status predicted <CHE>
 F:151-172/Product: insulin-like growth factor IB-EI amide #status predicted <MA2>
 F:54-96,66-109,95-100/Disulfide bonds: #status predicted
 F:172/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl

Query Match 37.7%; Score 47.5; DB 1; Length 195;
 Best Local Similarity 45.5%; Pred. No. 23;
 Matches 10; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 4 GWLRPEDGG-QAEGAEDELEVR 24
 II : II | II | | : I
 Db 151 GWPKTHPGGEQKEGTEASLQIR 172

Search completed: September 11, 2003, 17:26:23
 Job time : 10.984 secs

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